KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2170 TTTTTTTTTTTTTTTTTAACT 2190
||||||||||||||||||| ||
Db 1 TTTTTTTTTTTTTTTTTAGCT 21

RESULT 694
AAQ75777
ID AAQ75777 standard; DNA; 21 BP.
XX
AC AAQ75777;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 9; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 1 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2186
|||||||||||||||||| |||
Db 1 TTTTTTTTTTTTTTTTTCTTT 21

RESULT 695
AAQ75644
ID AAQ75644 standard; DNA; 21 BP.
XX
AC AAQ75644;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 6; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2168 TTTTTTTTTTTTTTTTTTAA 2188
|||||||||||||||||| |||
Db 1 TTTTTTTTTTTTTTTTTGTAA 21

RESULT 696

```
AAQ75761/c
ID   AAQ75761 standard; DNA; 21 BP.
XX
AC   AAQ75761;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAAAA 2802
              | ||||||||||||||||||||
Db         21 AATGAAAAAAAAAAAAAAAAA 1


RESULT 697
AAQ75765
ID   AAQ75765 standard; DNA; 21 BP.
XX
AC   AAQ75765;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAACT 2190
              |||||||||||||||||| |||
Db          1 TTTTTTTTTTTTTTTTTCACT 21


RESULT 698
AAQ75765/c
ID   AAQ75765 standard; DNA; 21 BP.
XX
AC   AAQ75765;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;
```

```
  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAAAA 2802
              | ||||||||||||||||||||
Db         21 AGTGAAAAAAAAAAAAAAAAA 1


RESULT 699
AAQ75772
ID   AAQ75772 standard; DNA; 21 BP.
XX
AC   AAQ75772;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTAA 2188
              |||||||||||||||||| |||
Db          1 TTTTTTTTTTTTTTTTCTAA 21


RESULT 700
AAQ75789/c
ID   AAQ75789 standard; DNA; 21 BP.
XX
AC   AAQ75789;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAAAA 2802
              || ||||||||||||||||||
Db         21 ATGGAAAAAAAAAAAAAAAAA 1


RESULT 701
AAQ75701
ID   AAQ75701 standard; DNA; 21 BP.
XX
AC   AAQ75701;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
```

```
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAACT 2190
              |||||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTTTACCT 21


RESULT 702
AAQ75721
ID   AAQ75721 standard; DNA; 21 BP.
XX
AC   AAQ75721;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAACT 2190
              |||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTTAAGT 21


RESULT 703
AAF24290
ID   AAF24290 standard; DNA; 21 BP.
XX
AC   AAF24290;
XX
DT   03-APR-2001  (first entry)
XX
DE   Complementary nucleic acid detection method related sequence #5.
XX
KW   Complementary nucleic acid; gene analysis; polymorphism; variation;
KW   DNA chip; primer; ss.
XX
OS   Unidentified.
XX
PN   EP1065278-A2.
XX
PD   03-JAN-2001.
XX
PF   07-JUN-2000; 2000EP-00112235.
XX
PR   07-JUN-1999;   99JP-00159339.
XX
PA   (FUJF ) FUJI PHOTO FILM CO LTD.
XX
PI   Makino Y,  Abe Y,  Ogawa M,  Takagi M,  Takenaka S,  Yamashita K;
XX
DR   WPI; 2001-140003/15.
XX
PT   Determining complementarity of nucleotide fragment for gene analysis, by
PT   comparing flow of electric current from or to electroconductive substrate
PT   through DNA fragment, with reference obtained from its complement.
XX
PS   Example 1; Page 12; 28pp; English.
XX
CC   The present invention provides a method for analysing a nucleic acid
CC   strand to determine the degree of complementarity between two sequences.
CC   This involves the measurement of an electric current along the annealed
CC   strands compared to a standard. This is useful in the analysis of genetic
CC   polymorphisms and variation between genes
XX
SQ   Sequence 21 BP; 1 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              |||||||||||| |||||||||
Db          1 TTTTTTTTTTTATTTTTTTTT 21


RESULT 704
ABX79794
ID   ABX79794 standard; cDNA; 21 BP.
XX
AC   ABX79794;
XX
DT   17-APR-2003  (first entry)
XX
DE   EST polymorphic DNA repeat polynucleotide #119.
XX
KW   EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
KW   polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
KW   Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
KW   Haw River syndrome; Huntington's disease; fragile-X syndrome;
KW   Fredreich's ataxis; myotonic dystrophy; hyperandrogenaemia;
KW   spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
XX
OS   Homo sapiens.
XX
PN   US6472154-B1.
XX
PD   29-OCT-2002.
XX
```

```
PF   31-DEC-1999;   99US-00475947.
XX
PR   31-DEC-1999;   99US-00475947.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Garner HR,  Wren JD,  Minna JD,  Fondon JW;
XX
DR   WPI; 2003-208818/20.
XX
PT   Identifying a candidate polymorphic repeat within a coding sequence, for
PT   understanding or treating genetic disease, comprises detecting tandem
PT   repeats in a target coding sequence and scoring the repeats for
PT   polymorphic probability.
XX
PS   Example; Col 495; 588pp; English.
XX
CC   The invention discloses a method for identifying a candidate polymorphic
CC   repeat within a coding sequence (expressed sequence tag, EST), which
CC   comprises detecting tandem repeats in a target coding sequence, scoring
CC   the repeats for polymorphic probability and generating a dataset
CC   correlating the repeats with polymorphic probability to identify a
CC   candidate polymorphic repeat. The computational methods (polymorphic
CC   marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
CC   useful for identifying and detecting candidate polymorphic repeats in
CC   human genes, which can be used to understand, treat or eliminate genetic
CC   diseases, predispositions or adverse drug-treatment reactions. Examples
CC   of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
CC   syndrome, Huntington's disease, fragile-X syndrome, Fredreich's ataxis,
CC   myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
CC   spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
CC   the polymorphic repeats identified for a search of human ESTs
XX
SQ   Sequence 21 BP; 1 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              |||||||||| |||||||||
Db          1 TTTTTTTTTTATTTTTTTT 21


RESULT 705
AAQ30431/c
ID   AAQ30431 standard; DNA; 23 BP.
XX
AC   AAQ30431;
XX
DT   25-MAR-2003  (revised)
DT   07-DEC-1992  (first entry)
XX
DE   Oligomer IL6804 for forming triplex with HUMIL6 target duplex.
XX
KW   Human interleukin-6 gene; herpes simplex; AIDS; modified; HIV; RSV; HPV;
KW   malignancy; hepatitis; inflammation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "OTHER= N4 N4 ethanocytosine"
FT   misc_feature     11. .12
FT                    /*tag=  d
FT                    /note= "o-xyloso dimer synthon linkage"
FT   misc_feature     12. .23
FT                    /*tag=  c
FT                    /label= inverted_polarity_region
FT                    /note= "see comments"
FT   modified_base    23
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
XX
PN   WO9209705-A1.
XX
PD   11-JUN-1992.
XX
PF   25-NOV-1991;   91WO-US008811.
XX
PR   23-NOV-1990;   90US-00617907.
PR   18-JAN-1991;   91US-00643382.
PR   08-APR-1991;   91US-00683420.
PR   17-APR-1991;   91US-00686544.
PR   17-APR-1991;   91US-00686546.
PR   17-APR-1991;   91US-00686547.
PR   27-SEP-1991;   91US-00766733.
XX
PA   (GILE-) GILEAD SCI INC.
XX
PI   Froehler B,  Krawczyk S,  Matteucci MD,  Milligan J;
XX
DR   WPI; 1992-217083/26.
XX
PT   New oligomers contg. modified bases - which form a triplex with G-C
PT   doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
PT   herpes malignancy and inflammation.
XX
PS   Claim 12; Page 71; 77pp; English.
XX
CC   The synthetic oligomer is capable of forming a triplex at physiological
CC   pH with a purine rich target sequence by coupling into the major groove
CC   of the duplex. The specific target sequence of this oligomer is the human
CC   interleukin 6 gene untranslated sequence contg. a purine rich sequence
CC   concd. on one strand of the duplex. The oligomer, and others like it are
CC   useful in diagnosis and therapy of diseases characterised by specific DNA
CC   duplex targets, e.g. HPV, HER, HIV, hepatitis B, herpes, malignant
CC   tumours and inflammation. The triple helices form under mild conditions
CC   thus assays may be carried out without subjecting the test specimen to
CC   harsh conditions. The oligomer contains an inverted polarity region
CC   formed from an o-xyloso dimer synthon. The linking gp. is o-xyloso
CC   (nucleotides have the 3'positions of xylose sugars linked via the o-
CC   xylene ring). Two nucleotides are coupled through a xylene residue to
CC   form the dimer synthon. This additional modifications may render the
CC   oligomer stable to nuclease activity. The oligomer is able to inhibit
CC   gene expression, as verified by in vitro systems. See also AAQ25452-25501
CC   and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 23 BP; 1 A; 1 C; 0 G; 21 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 23;
  Best Local Similarity   95.2%;  Pred. No. 7.6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAAA 2804
              | ||||||||||||||||||||
Db         23 TAAAAAAAAAAAAAAAAAAAA 3


RESULT 706
AAQ30430/c
ID   AAQ30430 standard; DNA; 23 BP.
XX
AC   AAQ30430;
XX
DT   25-MAR-2003  (revised)
DT   07-DEC-1992  (first entry)
XX
DE   Oligomer IL6803 for forming triplex with HUMIL6 target duplex.
XX
KW   Human interleukin-6 gene; herpes simplex; AIDS; modified; HIV; RSV; HPV;
KW   malignancy; hepatitis; inflammation; ss.
XX
```

```
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
FT   misc_feature    11. .12
FT                   /*tag=  d
FT                   /note= "o-xyloso dimer synthon linkage"
FT   misc_feature    12. .23
FT                   /*tag=  c
FT                   /label= inverted_polarity_region
FT                   /note= "see comments"
FT   modified_base   23
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
XX
PN   WO9209705-A1.
XX
PD   11-JUN-1992.
XX
PF   25-NOV-1991;   91WO-US008811.
XX
PR   23-NOV-1990;   90US-00617907.
PR   18-JAN-1991;   91US-00643382.
PR   08-APR-1991;   91US-00683420.
PR   17-APR-1991;   91US-00686544.
PR   17-APR-1991;   91US-00686546.
PR   17-APR-1991;   91US-00686547.
PR   27-SEP-1991;   91US-00766733.
XX
PA   (GILE-) GILEAD SCI INC.
XX
PI   Froehler B,  Krawczyk S,  Matteucci MD,  Milligan J;
XX
DR   WPI; 1992-217083/26.
XX
PT   New oligomers contg. modified bases - which form a triplex with G-C
PT   doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
PT   herpes malignancy and inflammation.
XX
PS   Claim 12; Page 71; 77pp; English.
XX
CC   The syntnetic oligomer is capable of forming a triplex at physiological
CC   pH with a purine rich target sequence by coupling into the major groove
CC   of the duplex. The specific target sequence of this oligomer is the human
CC   interleukin 6 gene untranslated sequence contg. a purine rich sequence
CC   concd. on one strand of the duplex. The oligomer, and others like it are
CC   useful in diagnosis and therapy of diseases characterised by specific DNA
CC   duplex targets, e.g. HPV, HER, HIV, hepatitis B, herpes, malignant
CC   tumours and inflammation. The triple helices form under mild conditions
CC   thus assays may be carried out without subjecting the test specimen to
CC   harsh conditions. The oligomer contains an inverted polarity region
CC   formed from an o-xyloso dimer synthon. The linking gp. is o-xyloso
CC   (nucleotides have the 3'positions of xylose sugars linked via the o-
CC   xylene ring). Two nucleotides are coupled through a xylene residue to
CC   form the dimer synthon. This additional modifications may render the
CC   oligomer stable to nuclease activity. The oligomer is able to inhibit
CC   gene expression, as verified by in vitro systems. See also AAQ25452-25501
CC   and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 23 BP; 2 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 23;
  Best Local Similarity   95.2%;  Pred. No. 7.6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAAA 2804
              | ||||||||||||||||||||
Db         23 TAAAAAAAAAAAAAAAAAAAA 3
```

```
RESULT 707
ABL01773
ID   ABL01773 standard; DNA; 23 BP.
XX
AC   ABL01773;
XX
DT   18-MAR-2002  (first entry)
XX
DE   Human MSH2 (hMSH2) intronic sequence SEQ ID NO:126.
XX
KW   Human; MLH1; MSH2; hMLH1; hMSH2; variant gene; diagnosis; HNPCC;
KW   hereditary non-polyposis colorectal cancer; ds.
XX
OS   Homo sapiens.
XX
PN   US2001044936-A1.
XX
PD   22-NOV-2001.
XX
PF   22-OCT-1999;   99US-00426548.
XX
PR   22-OCT-1998;   98US-0105180P.
XX
PA   (ROBB/) ROBBINS D.
PA   (LING/) LIN-GOERKE J L.
PA   (LING/) LING J C.
XX
PI   Robbins D,  Lin-Goerke JL,  Ling JC;
XX
DR   WPI; 2002-105577/14.
XX
PT   New variants of the human MLH1 and MSH2 genes for diagnosing or
PT   determining a predisposition for hereditary non-polyposis colorectal
PT   cancer.
XX
PS   Disclosure; Page 4; 38pp; English.
XX
CC   The present invention describes a variant human MLH1 or MSH2 gene. Also
CC   described are: (1) a method for diagnosing or predicting susceptibility
CC   to hereditary non-polyposis colorectal cancer (HNPCC), comprising
CC   screening a DNA sample for the variant MLH1 or MSH2 gene where presence
CC   of the variant indicates presence of, or susceptibility to HNPCC; (2) a
CC   method of identifying mutants in splice donor or acceptor sites of a
CC   human MLH1 gene, comprising sequencing splice donor or acceptor sites of
CC   the gene with intronic primers for the human MLH1 gene and analysing the
CC   sequence to identify any mutants; (3) a method of identifying mutants in
CC   splice donor or acceptor sites of a human MSH2 gene, comprising
CC   sequencing splice donor or acceptor sites of the gene with intronic
CC   primers for the human MSH2 gene and analysing the sequence to identify
CC   any mutants; and (4) a transgenic model system for colorectal cancer
CC   comprising cells expressing the variant MLH1 or MSH2 gene. The hMLH1 and
CC   hMSH2 variants are used to diagnose or determine a patients
CC   susceptibility to hereditary non-polyposis colorectal cancer. ABL01648 to
CC   ABL01745 and ABL01746 to ABL01831 represent hMLH1 and hMSH2 gene
CC   fragments from the present invention. ABL01832 to ABL01839 represent
CC   mutagenic primers used in the exemplification of the present invention
XX
SQ   Sequence 23 BP; 21 A; 0 C; 1 G; 1 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 23;
  Best Local Similarity   95.2%;  Pred. No. 7.6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAAA 2804
              | ||||||||||||||||||||
Db          2 TAAAAAAAAAAAAAAAAAAAA 22


RESULT 708
AAH24266
ID   AAH24266 standard; DNA; 24 BP.
XX
```

```
AC   AAH24266;
XX
DT   11-SEP-2001  (first entry)
XX
DE   Human phosphatase 79 RT-PCR primer, SEQ ID NO:4.
XX
KW   Phosphatase 79; human; BAC clone CTB-54D4-encoded protein homologue;
KW   recombinant production; malignant tumour; cancer; blood disease;
KW   HIV infection; human immunodeficiency virus; immune disorder;
KW   inflammatory condition; cytostatic; anti-HIV; antiinflammatory;
KW   immunomodulator; reverse transcription-PCR; RT-PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138385-A1.
XX
PD   31-MAY-2001.
XX
PF   20-NOV-2000; 2000WO-CN000459.
XX
PR   22-NOV-1999;   99CN-00124059.
XX
PA   (BIOR-) BIOROAD GENE DEV LTD SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2001-355903/37.
XX
PT   Human phosphatase 79 and encoded polynucleotide, applicable in diagnosis
PT   and treatment of malignant tumor, hemopathy, HIV infection, immunological
PT   diseases and various inflammation.
XX
PS   Example 3; Page 12; 38pp; Chinese.
XX
CC   The invention relates to human phosphatase 79 (AAB73700), nucleic acids
CC   encoding it (AAH24264), and a method for the recombinant production of
CC   human phosphatase 79. The present invention additionally discloses an
CC   agonist of phosphatase 79 for therapeutic use, and an antibody which
CC   specifically binds to human phosphatase 79. Human phosphatase 79, and
CC   nucleotides which encode it may be used for treating a variety of
CC   diseases, such as malignant tumours, blood diseases, HIV (human
CC   immunodeficiency virus) infection, immune disorders and inflammatory
CC   conditions. The protein may also be used to screen for modulators of its
CC   activity or for peptide fingerprinting identification. The polynucleotide
CC   can be used as a primer for nucleic acid amplification reaction or as a
CC   probe for hybridisation reactions, or in producing gene chips or
CC   microarrays. Sequences AAH24265-AAH24266 represent reverse transcription-
CC   PCR (RT-PCR) primers used in an exemplification of the invention to
CC   isolate human phosphatase 79 cDNA
XX
SQ   Sequence 24 BP; 2 A; 0 C; 0 G; 22 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 24;
  Best Local Similarity   95.2%;  Pred. No. 8.5e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||| ||||||||||||||||||
Db          4 TTTATTTTTTTTTTTTTTTT 24


RESULT 709
ABN85073
ID   ABN85073 standard; DNA; 24 BP.
XX
AC   ABN85073;
XX
DT   05-SEP-2002  (first entry)
XX
DE   Human S4 ribosomal protein 13.97 PCR primer #2.
XX
KW   Human; S4 ribosomal protein 13.97; malignant tumour; haemopathy;
KW   HIV infection; immunological disease; inflammation; cytostatic; anti-HIV;
KW   PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1333268-A.
XX
PD   30-JAN-2002.
XX
PF   07-JUL-2000; 2000CN-00117077.
XX
PR   07-JUL-2000; 2000CN-00117077.
XX
PA   (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-292916/34.
XX
PT   Human S4 ribosomal protein 13.97 polypeptide and encoding polynucleotide,
PT   useful for treating malignant tumor, inflammation, hemopathy, human
PT   immunodeficiency virus infection, immunological disease and inflammation.
XX
PS   Example 2; Page 16 (Disclosure); 33pp; Chinese.
XX
CC   The present invention relates to human S4 ribosomal protein 13.97 (see
CC   ABB83379). The ribosomal protein and its coding sequence are useful for
CC   treating malignant tumours, haemopathy, HIV infection, immunological
CC   diseases and various inflammations. The present sequence is a PCR primer,
CC   which was used in an example from the invention
XX
SQ   Sequence 24 BP; 1 A; 2 C; 1 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 24;
  Best Local Similarity   95.2%;  Pred. No. 8.5e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTT 2183
              | ||||||||||||||||||||
Db          4 TGCTTTTTTTTTTTTTTTTT 24


RESULT 710
ABK91269/c
ID   ABK91269 standard; DNA; 24 BP.
XX
AC   ABK91269;
XX
DT   05-NOV-2002  (first entry)
XX
DE   Leukaemia related protein 24.09 specific RT-PCR primer #2.
XX
KW   Leukaemia related protein; leukaemia; lymphoma; primer; ss; haemopathy;
KW   growth development disturbance disease; reverse transcription; RT-PCR.
XX
OS   Unidentified.
XX
PN   CN1341647-A.
XX
PD   27-MAR-2002.
XX
PF   07-SEP-2000; 2000CN-00125055.
XX
PR   07-SEP-2000; 2000CN-00125055.
XX
PA   (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-520722/56.
XX
PT   Novel leukemia related protein 24.09.
XX
PS   Example 3; Page 17 (disclosure); 32pp; Chinese.
```

```
XX
CC   This invention relates to the DNA and protein sequences of leukemia
CC   related protein 24.09. The invention also comprises methods for producing
CC   the protein using recombinant DNA technology and antagonists of the
CC   protein which may be used for inhibiting the action of the protein. The
CC   sequences of the invention may be used for treating several diseases such
CC   as leukaemia, lymphoma, other haemopathy and growth development
CC   disturbance disease. The present sequence represents a reverse
CC   transcription (RT) PCR primer used to isolate the leukaemia related
CC   protein cDNA 24.09 of the invention
XX
SQ   Sequence 24 BP; 4 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 24;
  Best Local Similarity   95.2%;  Pred. No. 8.5e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAA 2801
              ||||||||||||||||||| |
Db         22 AATTGAAAAAAAAAAAAAACA 2

RESULT 711
ABZ23536
ID   ABZ23536 standard; DNA; 24 BP.
XX
AC   ABZ23536;
XX
DT   07-APR-2003  (first entry)
XX
DE   fragment of a plasmid used to detect somatic instability.
XX
KW   Replication error; drug development; somatic instability; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    4
FT                   /*tag=  a
FT                   /note= "this base represents an unspecified number of
FT                   bases"
FT   misc_feature    21
FT                   /*tag=  b
FT                   /note= "this base represents an unspecified number of
FT                   bases"
XX
PN   WO200295071-A2.
XX
PD   28-NOV-2002.
XX
PF   22-MAY-2002; 2002WO-NL000322.
XX
PR   22-MAY-2001; 2001EP-00201936.
XX
PA   (NEVW-) KONINK NEDERLANDSE AKAD VAN WETENSCHAPPE.
PA   (TIJS/) TIJSTERMAN M.
XX
PI   Plasterk RHA,  Tijsterman M;
XX
DR   WPI; 2003-129440/12.
XX
PT   Determining whether a product of a gene is involved in preventing a
PT   replication error in a cell comprises providing a specific inhibitor for
PT   the product and determining the level of expression of a marker gene.
XX
PS   Example 1; Fig 3; 47pp; English.
XX
CC   The specification describes a method for determining whether a product of
CC   a gene is involved in preventing a replication error in a cell. The
CC   method comprises providing the cell with a specific inhibitor for the
CC   product and determining the level of functional expression of a marker
CC   gene in the cell, where the level of expression of the marker gene is
CC   dependent on the occurrence of the replication error. The method is used
CC   for determining whether a product of a gene is involved in preventing a
CC   replication error in a cell. The identified genes are useful for
CC   developing diagnostic tools, or as targets for drug development to
CC   manipulate cells on the basis of the presence or absence of function of
CC   the gene. ABZ23535-36 represents fragments of plasmids used to detect
CC   somatic instability, in the course of the invention
XX
SQ   Sequence 24 BP; 20 A; 0 C; 1 G; 1 T; 0 U; 2 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 24;
  Best Local Similarity   87.0%;  Pred. No. 8.5e+02;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAAAAA 2804
              ||  |||||||||||||||| ||
Db          1 ATGNAAAAAAAAAAAAAAAANAA 23

RESULT 712
ABZ23536/c
ID   ABZ23536 standard; DNA; 24 BP.
XX
AC   ABZ23536;
XX
DT   07-APR-2003  (first entry)
XX
DE   fragment of a plasmid used to detect somatic instability.
XX
KW   Replication error; drug development; somatic instability; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    4
FT                   /*tag=  a
FT                   /note= "this base represents an unspecified number of
FT                   bases"
FT   misc_feature    21
FT                   /*tag=  b
FT                   /note= "this base represents an unspecified number of
FT                   bases"
XX
PN   WO200295071-A2.
XX
PD   28-NOV-2002.
XX
PF   22-MAY-2002; 2002WO-NL000322.
XX
PR   22-MAY-2001; 2001EP-00201936.
XX
PA   (NEVW-) KONINK NEDERLANDSE AKAD VAN WETENSCHAPPE.
PA   (TIJS/) TIJSTERMAN M.
XX
PI   Plasterk RHA,  Tijsterman M;
XX
DR   WPI; 2003-129440/12.
XX
PT   Determining whether a product of a gene is involved in preventing a
PT   replication error in a cell comprises providing a specific inhibitor for
PT   the product and determining the level of expression of a marker gene.
XX
PS   Example 1; Fig 3; 47pp; English.
XX
CC   The specification describes a method for determining whether a product of
CC   a gene is involved in preventing a replication error in a cell. The
CC   method comprises providing the cell with a specific inhibitor for the
CC   product and determining the level of functional expression of a marker
CC   gene in the cell, where the level of expression of the marker gene is
CC   dependent on the occurrence of the replication error. The method is used
CC   for determining whether a product of a gene is involved in preventing a
CC   replication error in a cell. The identified genes are useful for
CC   developing diagnostic tools, or as targets for drug development to
CC   manipulate cells on the basis of the presence or absence of function of
```

```
CC   the gene. ABZ23535-36 represents fragments of plasmids used to detect
CC   somatic instability, in the course of the invention
XX
SQ   Sequence 24 BP; 20 A; 0 C; 1 G; 1 T; 0 U; 2 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 24;
  Best Local Similarity   87.0%;  Pred. No. 8.5e+02;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTAA 2188
              ||| ||||||||||||||||  |
Db         24 TTTNTTTTTTTTTTTTTTTTNCA 2

RESULT 713
AAV42215/c
ID   AAV42215 standard; DNA; 25 BP.
XX
AC   AAV42215;
XX
DT   16-OCT-1998  (first entry)
XX
DE   Sequencing primer used to exemplify the invention.
XX
KW   Incyte clone 1; fluorescent label; probe; primer; DNA sequencing; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /note= "labelled with the donor carboxyfluoscein"
FT   modified_base   7
FT                   /*tag=  b
FT                   /note= "optionally laballed with the acceptor 6-
FT                   carboxyrhodamine"
FT   modified_base   14
FT                   /*tag=  b
FT                   /note= "optionally laballed with the acceptor 6-
FT                   carboxyrhodamine"
FT   modified_base   17
FT                   /*tag=  a
FT                   /note= "optionally labelled with the donor
FT                   carboxyfluoscein"
FT   modified_base   17
FT                   /*tag=  b
FT                   /note= "optionally laballed with the acceptor 6-
FT                   carboxyrhodamine"
XX
PN   WO9831834-A1.
XX
PD   23-JUL-1998.
XX
PF   12-DEC-1997;   97WO-US022914.
XX
PR   15-JAN-1997;   97US-00784162.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Ju J;
XX
DR   WPI; 1998-414127/35.
XX
PT   Set of energy-transfer fluorescent labels with donor and acceptor at
PT   different separations - useful for DNA sequencing allows use of fewer
PT   analysing wavelengths or an increased throughput.
XX
PS   Example 1; Page 14; 30pp; English.
XX
CC   The present sequence exxemplified the primer of the invention, and is
CC   used to sequence Incyte clone 1 (AAV42737). The primer of the invention
CC   is labelled with a set of at least 2 different fluorescent labels. The
CC   set comprises an energy-transfer fluorescent label with at least 1 each
CC   of a donor fluorophore and an acceptor fluorophore capable of energy
CC   transfer, and separated by a distance x, and a second similar fluorescent
CC   label in which the separation distance is y, x and y being sufficiently
CC   different for the two fluorescent labels to produce distinct fluorescent
CC   signals. Fluorescent labels are useful in multicomponent analyses, e.g.
CC   as probes for fluorescent in situ hybridisation or especially as primers
CC   for DNA sequencing
XX
SQ   Sequence 25 BP; 1 A; 1 C; 0 G; 23 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 25;
  Best Local Similarity   95.2%;  Pred. No. 9.3e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAAA 2804
              | ||||||||||||||||||||
Db         24 TAAAAAAAAAAAAAAAAAAAA 4

RESULT 714
AAX84259/c
ID   AAX84259 standard; DNA; 25 BP.
XX
AC   AAX84259;
XX
DT   08-SEP-1999  (first entry)
XX
DE   PCR primer for human Nck associated protein 1 coding sequence.
XX
KW   Nck associated protein 1; Nap1; human; apoptosis; Alzheimer's disease;
KW   therapy; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9931239-A1.
XX
PD   24-JUN-1999.
XX
PF   14-DEC-1998;   98WO-JP005646.
XX
PR   15-DEC-1997;   97JP-00363183.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
PA   (SAKA/) SAKAKI Y.
XX
PI   Sakaki Y;
XX
DR   WPI; 1999-395181/33.
XX
PT   Protein inhibiting apoptosis, useful in the diagnosis and treatment of
PT   Alzheimer's disease.
XX
PS   Disclosure; Page 76; 90pp; Japanese.
XX
CC   This sequence represents a PCR primer used to isolate DNA encoding the
CC   human Nck associated protein 1 (Nap1) of the invention. Nap1 inhibits
CC   apoptosis. The protein can be used in the investigation, diagnosis and
CC   treatment (e.g. by gene therapy) of Alzheimer's disease
XX
SQ   Sequence 25 BP; 1 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 25;
  Best Local Similarity   95.2%;  Pred. No. 9.3e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAAA 2804
              | ||||||||||||||||||||
Db         25 TAAAAAAAAAAAAAAAAAAAA 5

RESULT 715
ABZ23535
```

```
ID   ABZ23535 standard; DNA; 25 BP.
XX
AC   ABZ23535;
XX
DT   07-APR-2003  (first entry)
XX
DE   fragment of a plasmid used to detect somatic instability.
XX
KW   Replication error; drug development; somatic instability; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    4
FT                   /*tag=  a
FT                   /note= "this base represents an unspecified number of
FT                   bases"
FT   misc_feature    22
FT                   /*tag=  b
FT                   /note= "this base represents an unspecified number of
FT                   bases"
XX
PN   WO200295071-A2.
XX
PD   28-NOV-2002.
XX
PF   22-MAY-2002; 2002WO-NL000322.
XX
PR   22-MAY-2001; 2001EP-00201936.
XX
PA   (NEVW-) KONINK NEDERLANDSE AKAD VAN WETENSCHAPPE.
PA   (TIJS/) TIJSTERMAN M.
XX
PI   Plasterk RHA,  Tijsterman M;
XX
DR   WPI; 2003-129440/12.
XX
PT   Determining whether a product of a gene is involved in preventing a
PT   replication error in a cell comprises providing a specific inhibitor for
PT   the product and determining the level of expression of a marker gene.
XX
PS   Example 1; Fig 3; 47pp; English.
XX
CC   The specification describes a method for determining whether a product of
CC   a gene is involved in preventing a replication error in a cell. The
CC   method comprises providing the cell with a specific inhibitor for the
CC   product and determining the level of functional expression of a marker
CC   gene in the cell, where the level of expression of the marker gene is
CC   dependent on the occurrence of the replication error. The method is used
CC   for determining whether a product of a gene is involved in preventing a
CC   replication error in a cell. The identified genes are useful for
CC   developing diagnostic tools, or as targets for drug development to
CC   manipulate cells on the basis of the presence or absence of function of
CC   the gene. ABZ23535-36 represents fragments of plasmids used to detect
CC   somatic instability, in the course of the invention
XX
SQ   Sequence 25 BP; 21 A; 0 C; 1 G; 1 T; 0 U; 2 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 25;
  Best Local Similarity   87.0%;  Pred. No. 9.3e+02;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAAAAAA 2804
              ||  |||||||||||||||||  |
Db          1 ATGNAAAAAAAAAAAAAAAAAANA 23


RESULT 716
AAS20595/c
ID   AAS20595 standard; DNA; 26 BP.
XX
AC   AAS20595;
XX
DT   23-APR-2002  (first entry)
XX
DE   Human zsig63 cDNA sequencing primer ZC7231.
XX
KW   Human; zsig63; chromosome 4q12-4q13; salivary protein; antimicrobial; ss;
KW   microbial infection; tooth decay; periodontal disease; thrush; emphysema;
KW   gastrointestinal disease; urinary tract infection; vaginal infection;
KW   skin infection; epithelial wound; chronic tissue damage; cystic fibrosis;
KW   acquired immunodeficiency syndrome; AIDS; lung infection; sarcoidosis;
KW   chronic bronchitis; gene therapy; protein therapy; primer; ZC7231.
XX
OS   Homo sapiens.
XX
PN   US6331413-B1.
XX
PD   18-DEC-2001.
XX
PF   17-MAR-2000; 2000US-00527345.
XX
PR   17-MAR-1999;   99US-0124820P.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Adler DA,  Sheppard PO;
XX
DR   WPI; 2002-096707/13.
XX
PT   Polynucleotides encoding salivary proteins useful as anti-microbial
PT   agents.
XX
PS   Example 1; Col 53; 29pp; English.
XX
CC   The invention relates to a polynucleotide derived from the 4q12-4q13
CC   region of human chromosome 4 and encoding a zsig63 polypeptide, a
CC   secreted salivary protein with anti-microbial activity. Due to their
CC   microbial activity, the sequences can be used in the study of microbial
CC   infections, e.g. for recombinant production of anti-microbial proteins.
CC   The sequences can be used in the treatment of tooth decay, periodontal
CC   disease, thrush, gastrointestinal disease, urinary tract infections,
CC   vaginal infections, skin infections, epithelial wounds, chronic tissue
CC   damage, acquired immunodeficiency syndrome (AIDS), cystic fibrosis, lung
CC   infections, sarcoidosis, emphysema and chronic bronchitis. This sequence
CC   represents a sequencing primer for cDNA encoding human zsig63
XX
SQ   Sequence 26 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 1 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 26;
  Best Local Similarity   84.0%;  Pred. No. 1e+03;
  Matches   21;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAA 2804
                :||   ||||||||||||||||||
Db         26 BAAAAAAAAAAAAAAAAAAAAAAAA 2


RESULT 717
ABS52637/c
ID   ABS52637 standard; DNA; 26 BP.
XX
AC   ABS52637;
XX
DT   15-NOV-2002  (first entry)
XX
DE   Human secreted salivary protein zsig63 PCR primer ZC7321.
XX
KW   Human; secreted salivary protein; zsig63; immunogen; zsig63-cytokine;
KW   antibody-cytokine; in vivo killing; pathological microbe; bacteria;
KW   fungal; viral; infection; salivary gland; anti-microbial; dental caries;
KW   tooth decay; periodontal disease; thrush; gastrointestinal disease;
KW   urinary tract infection; vaginal infection; skin infection; microflora;
KW   epithelial wound; pathogenic colonisation; invasion; pro-inflammatory;
KW   chronic tissue damage; vascular system; diabetes; anti-inflammatory;
KW   incompetent immune system; AIDS; acquired immunodeficiency syndrome;
```

KW chemotherapy; radiation treatment; lung infection; cystic fibrosis;
KW digestion; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN US2002081701-A1.
XX
PD 27-JUN-2002.
XX
PF 03-AUG-2001; 2001US-00922480.
XX
PR 17-MAR-1999; 99US-0124820P.
PR 17-MAR-2000; 2000US-00527345.
XX
PA (ADLE/) ADLER D A.
PA (SHEP/) SHEPPARD P O.
XX
PI Adler DA, Sheppard PO;
XX
DR WPI; 2002-635468/68.
XX
PT Novel secreted salivary protein, zsig63 and polynucleotide encoding it
PT useful for treating microbial infections, inflammatory conditions, dental
PT caries and lung infections associated with cystic fibrosis.
XX
PS Example 1; Page 29; 33pp; English.
XX
CC The present invention relates to a new secreted salivary protein, zsig63.
CC The invention is useful for detecting in a test sample, the presence of
CC an antagonist or agonist of zsig63 protein activity. The invention is
CC also useful as an immunogen for producing an antibody to zsig63
CC polypeptide. zsig63-cytokine fusion proteins or antibody-cytokine fusion
CC protein are useful for enhancing in vivo killing of target tissues.
CC Pharmaceutical composition comprising purified zsig63 polypeptide are
CC useful in the treatment of conditions associated with pathological
CC microbes, including bacterial, fungal and viral infections. High
CC expression of zsig63 in salivary gland suggests that anti-microbial
CC polypeptides are useful for treatment of dental caries (tooth decay),
CC periodontal disease, thrush and gastrointestinal disease. Other
CC applications can be used in urinary tract infections, vaginal infections,
CC prevention of infection in skin and other epithelial wounds. The
CC polypeptides can be used to establish normal microflora and protect
CC against pathogenic colonisation and invasion. The invention is useful
CC when pro-inflammatory activity is desired. Applications for such pro-
CC inflammatory activity include the treatment of chronic tissue damage,
CC particularly in areas having a limited or damaged vascular system e.g.,
CC damage in extremities associated with diabetes. Antagonists to zsig63
CC polypeptides may be useful as anti-inflammatory agents. The invention is
CC useful for the treatment of patients having incompetent immune system,
CC such as AIDS (acquired immunodeficiency syndrome) patients or individuals
CC that have undergone chemotherapy, radiation treatment. The invention is
CC also useful for the treatment of lung infections associated with cystic
CC fibrosis and its agonists or antagonists are useful for aiding digestion.
CC The present nucleic acid sequence represents a PCR primer that was used
CC in the methods of the invention for identification of zsig63
XX
SQ Sequence 26 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 1 Other;

Query Match 0.7%; Score 19.4; DB 1; Length 26;
Best Local Similarity 84.0%; Pred. No. 1e+03;
Matches 21; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2780 GAATTGAAAAAAAAAAAAAAAAAAA 2804
:|| |||||||||||||||||||
Db 26 BAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 718
AAD45054/c
ID AAD45054 standard; DNA; 26 BP.
XX
AC AAD45054;
XX
DT 27-DEC-2002 (first entry)
XX
DE ZC7231 primer used in the identification of human zsig63 DNA.
XX
KW Human; secreted salivary protein; zsig63 protein; host defense protein;
KW immune modulating factor; antipathogenic; cell-cell signalling molecule;
KW growth factor; cytokine; growth factor hormone activity; dental carries;
KW infection; tooth decay; periodontal disease; gastrointestinal disease;
KW thrush; urinary tract infection; vaginal infection; diabetes; obesity;
KW anti-inflammatory; chronic tissue damage; lung dysfunction; restenosis;
KW gene therapy; salivary gland dysfunction; prostate gland dysfunction;
KW forensic DNA profiling; chondrosarcoma; atherosclerosis; primer; ss.
XX
OS Homo sapiens.
XX
PN US2002090677-A1.
XX
PD 11-JUL-2002.
XX
PF 03-AUG-2001; 2001US-00923236.
XX
PR 17-MAR-1999; 99US-0124820P.
PR 17-MAR-2000; 2000US-00527345.
XX
PA (ADLE/) ADLER D A.
PA (SHEP/) SHEPPARD P O.
XX
PI Adler DA, Sheppard PO;
XX
DR WPI; 2002-642378/69.
XX
PT Novel secreted salivary polypeptide, zsig63, useful as antimicrobial
PT agent for treating microbial infection, dental carries, periodontal
PT disease, thrush gastrointestinal disease, and for aiding digestion.
XX
PS Example 1; Page 29; 33pp; English.
XX
CC The invention relates to human secreted salivary polypeptide designated
CC as zsig63 and nucleic acid molecules encoding such polypeptides. zsig63
CC can be used in detecting agonists and antagonists of its activity, and is
CC also useful as a host defense polypeptide, immune modulating factor,
CC antipathogenic polypeptide, cell-cell signalling molecule, growth factor,
CC cytokine, or as secreted extracellular matrix associated proteins with
CC growth factor hormone activity. It is useful for treating conditions
CC associated with pathological microbes, including bacterial, fungal and
CC viral infections, for treating dental carries (tooth decay), periodontal
CC disease, thrush and gastrointestinal disease, for treating urinary tract
CC infection, vaginal infection and for preventing infection in skin and
CC other epithelial wounds. zsig63 is useful for establishing normal
CC microflora and protect against pathogenic colonisation and invasion, for
CC treating chronic tissue damage e.g. damage in extremities associated with
CC diabetes and useful as anti-inflammatory agents. It is useful as a marker
CC of lung dysfunction, salivary gland dysfunction, or dysfunction of
CC prostate gland. It is also therapeutically useful for aiding digestion.
CC Polynucleotides of the invention are used in gene therapy for increasing
CC or inhibiting zsig63 activity, for detecting abnormalities on human
CC chromosome 4 associated with disease or other human traits and as
CC diagnostics in forensic DNA profiling. Sequences of the invention are
CC useful for stimulating proliferation or differentiation of cardiac
CC myocytes, for proliferation or differentiation of adipocytes and for
CC inhibiting chondrosarcomas, atherosclerosis, restenosis and obesity. The
CC present sequence is a primer used in the identification of human zsig63
CC DNA
XX
SQ Sequence 26 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 1 Other;

Query Match 0.7%; Score 19.4; DB 1; Length 26;
Best Local Similarity 84.0%; Pred. No. 1e+03;
Matches 21; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2780 GAATTGAAAAAAAAAAAAAAAAAAA 2804
:|| |||||||||||||||||||
Db 26 BAAAAAAAAAAAAAAAAAAAAAAAA 2

```
RESULT 719
AAD55692/c
ID   AAD55692 standard; DNA; 26 BP.
XX
AC   AAD55692;
XX
DT   27-OCT-2003  (revised)
DT   07-AUG-2003  (first entry)
XX
DE   Bovine viral diarrhea virus gene 5' end amplifying PCR primer.
XX
KW   Bovine Viral Diarrhea Virus; BVDV; infection; vaccine; prophylaxis;
KW   gene therapy; PCR; primer; ss.
XX
OS   Pestivirus type 1.
XX
PN   WO2003023041-A2.
XX
PD   20-MAR-2003.
XX
PF   05-SEP-2002; 2002WO-EP009925.
XX
PR   06-SEP-2001; 2001DE-01043813.
XX
PA   (BOEH ) BOEHRINGER INGELHEIM VETMEDICA GMBH.
XX
PI   Elbers K,  Meyer C,  Von Freyburg M,  Meyers G;
XX
DR   WPI; 2003-333043/31.
XX
PT   New DNA molecule useful for manufacturing a vaccine for the prophylaxis
PT   and treatment of Bovine Viral Diarrhea Virus (BVDV) infections, comprises
PT   a sequence complementary to a BVDV RNA.
XX
PS   Example 1; Page 20; 73pp; English.
XX
CC   The invention relates to a DNA molecule containing a sequence
CC   complementary to a Bovine Viral Diarrhea Virus (BVDV) RNA. The RNA when
CC   introduced into susceptible host cells, induces the generation of
CC   infectious BVDV particles. The attenuated BVDV clone or strain is useful
CC   in the manufacture of a vaccine for the prophylaxis and treatment of BVDV
CC   infections. The invention is useful in gene therapy. The present sequence
CC   is a PCR primer used to amplify BVDV gene. (Updated on 27-OCT-2003 to
CC   standardise OS field)
XX
SQ   Sequence 26 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 1 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 26;
  Best Local Similarity   84.0%;  Pred. No. 1e+03;
  Matches   21;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAAA 2804
             :||   ||||||||||||||||||||
Db         26 BAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 720
ABX93598/c
ID   ABX93598 standard; DNA; 26 BP.
XX
AC   ABX93598;
XX
DT   28-MAY-2003  (first entry)
XX
DE   Human zsig63 PCR/sequencing primer ZC7231.
XX
KW   ss; PCR; zsig63; adhesin; salivary gland; dental carries;
KW   periodontal disease; thrush; gastrointestinal disease; epithelial wound;
KW   urinary tract infection; vaginal infection; skin infection; primer;
KW   pro-inflammatory; chronic tissue damage; vascular system; diabetes; AIDS;
KW   lung infection; cystic fibrosis; lung dysfunction; digestive;
KW   salivary gland carcinoma; Pneumocystis carinii infection; emphysema;
KW   chronic bronchitis; prostate dysfunction; prostate adenocarcinoma;
KW   cell culture media; gene therapy; human chromosome 4q12-4q13;
KW   dentinogenesis imperfecta; dentin dysplasia type II.
XX
OS   Synthetic.
XX
PN   US2002173027-A1.
XX
PD   21-NOV-2002.
XX
PF   03-AUG-2001; 2001US-00922469.
XX
PR   17-MAR-1999;   99US-0124820P.
PR   17-MAR-2000; 2000US-00527345.
XX
PA   (ADLE/) ADLER D A.
PA   (SHEP/) SHEPPARD P O.
XX
PI   Adler DA,  Sheppard PO;
XX
DR   WPI; 2003-328428/31.
XX
PT   Novel isolated zsig63 polypeptide, member of the adhesin family, useful
PT   for treating dental carries, periodontal disease, thrush,
PT   gastrointestinal disease, urinary tract infections, vaginal infections,
PT   skin infections.
XX
PS   Example 1; Page 29; 32pp; English.
XX
CC   The invention relates to an isolated zsig63 polypeptide comprising at
CC   least 90% identity to an amino acid sequence which comprises domain 1 of
CC   zsig63, domain 2, domain 3, mature zsig63 and full length zsig3. Also
CC   included are the polynucleotide encoding zsig63, a zsig63 expression
CC   vector, a cultured cell comprising the vector and expressing the protein,
CC   a DNA encoding a fusion protein (comprising amino acids 1-15, 16-37, 38-
CC   126, 127-219 or 16-219 of zsig63 and an additional protein), using a
CC   zsig63 reporter gene construct to identify zsig63 agonists, and producing
CC   an anti-zsig63 antibody using zsig63 immunogenic peptides, Zsig63 is
CC   useful for detecting in a test sample, the presence of antagonist of
CC   zsig63 protein activity. Zsig63 has antimicrobial activity and since
CC   exhibits high expression in salivary gland, can be used for treating
CC   dental carries, periodontal disease, thrush, and gastrointestinal
CC   disease, urinary tract infections, vaginal infections, skin infections
CC   and other epithelial wounds. The polypeptides can be used to establish
CC   normal microflora and protect against pathogenic colonization and
CC   invasion. Zsig63 can also be used for providing pro-inflammatory activity
CC   for treating chronic, tissue damage particularly in areas having limited
CC   or damaged vascular system, e.g. in diabetes, and for treating
CC   immunocompromised AIDS patients or in individuals that have undergone
CC   chemotherapy, radiation treatment, for treating lung infections e.g. in
CC   cystic fibrosis. Detection of zsig63 polypeptide at relatively high
CC   levels in the trachea may indicate that such polypeptides may serve as a
CC   marker of lung dysfunction. Zsig63 is also useful in diagnosing
CC   conditions associated with salivary gland or lung dysfunction including
CC   salivary gland carcinoma, Pneumocystis carinii infection, emphysema,
CC   chronic bronchitis, prostate dysfunctions such as prostate
CC   adenocarcinoma, aiding digestion, and as components of defined cell
CC   culture media and may be used to replace serum that is commonly used in
CC   culture. The DNA is useful in gene therapy applications to increase or
CC   inhibit zsig63 activity, and for detecting abnormalities on human
CC   chromosome 4 (e.g. 4q12-4q13, associated with dentinogenesis imperfecta,
CC   and dentin dysplasia type II). Zsig63 is an adhesin family member. The
CC   present sequence is a primer used to isolate and sequence nucleic acdis
CC   encoding human zsig63
XX
SQ   Sequence 26 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 1 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 26;
  Best Local Similarity   84.0%;  Pred. No. 1e+03;
  Matches   21;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAAA 2804
```

```
              :||   ||||||||||||||||||||
Db         26 BAAAAAAAAAAAAAAAAAAAAAAAA 2


RESULT 721
ACF36382/c
ID   ACF36382 standard; DNA; 26 BP.
XX
AC   ACF36382;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Nucleotide sequence of a second back primer.
XX
KW   Nucleic acid manipulation; mRNA profiling; polymerase chain reaction;
KW   electrophoresis; PCR; primer; ss.
XX
OS   Synthetic.
XX
PN   WO2003064691-A2.
XX
PD   07-AUG-2003.
XX
PF   28-JAN-2003; 2003WO-IB000843.
XX
PR   29-JAN-2002; 2002US-0352215P.
XX
PA   (GLOB-) GLOBAL GENOMICS AB.
XX
PI   Linnarsson S,  Ernfors P,  Bauren G,  Metsis A,  Pihlak A;
PI   Montelius A;
XX
DR   WPI; 2003-618365/58.
XX
PT   Producing a population of double-stranded product DNA molecules, useful
PT   for mRNA profiling, comprises amplification by nested polymerase chain
PT   reaction.
XX
PS   Claim 6; Page 85; 105pp; English.
XX
CC   The invention relates to producing a population of double-stranded
CC   product DNA molecules comprising amplification by a nested PCR method.
CC   The method is useful in profiling mRNA transcribed in a system under
CC   investigation. The oligonucleotides are used as size standards in
CC   electrophoresis, and as internal controls allowing for calculation of
CC   relative amounts of material present. The present sequence represents a
CC   specific example of a PCR primer used in the method of the invention
XX
SQ   Sequence 26 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 1 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 26;
  Best Local Similarity   84.0%;  Pred. No. 1e+03;
  Matches   21;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAA 2804
              :||   ||||||||||||||||||||
Db         26 BAAAAAAAAAAAAAAAAAAAAAAAA 2


RESULT 722
AAV35002
ID   AAV35002 standard; DNA; 26 BP.
XX
AC   AAV35002;
XX
DT   27-AUG-1998  (first entry)
XX
DE   Human endothelin-beta 1 receptor PCR primer Vet119.
XX
KW   Endothelin beta-1 receptor; ETB-1; screening; signal transduction;
KW   agonist; antagonist; vasoconstrictor; vasopressor; cardiogenic shock;
KW   pulmonary hypertension; acute myocardial infarct; uraemia; vasculitis;
KW   Crohn's disease; ulcerative colitis; sepsis; congestive heart failure;
KW   coronary spasm; cyclosporin nephrotoxicity; toxaemia; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US5773223-A.
XX
PD   30-JUN-1998.
XX
PF   02-SEP-1993;   93US-00117361.
XX
PR   02-SEP-1993;   93US-00117361.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Shyamala V,  Olson PT;
XX
DR   WPI; 1998-386992/33.
XX
PT   Screening for modulators of the endothelin B1 receptor - by measuring
PT   effect on signal transduction in cells engineered to express the
PT   receptor, potentially useful as agonists and antagonists of endothelin.
XX
PS   Example 1; Col 18; 23pp; English.
XX
CC   AAV35002-V35021 are primers used to amplify and isolate a novel human
CC   endothelin-beta1 receptor (ETB-1) which corresponds to a decapeptide
CC   insert. This sequence is used in a method involving the screening of
CC   compounds for their ability to bind to endothelin B1 (ETB1) receptor
CC   polypeptide and to modulate its signal transduction activity by applying
CC   test compound to host cells transformed with DNA encoding ETB-1 and
CC   optionally lysing the cells and then measuring signal transduction
CC   activity. The method is used to identify agonists and antagonists of
CC   endothelin (ET), a known vasoconstrictor/vasopressor agent, associated
CC   with cardiogenic shock, pulmonary hypertension, acute myocardial infarct,
CC   uraemia, Crohn's disease, ulcerative colitis, sepsis, congestive heart
CC   failure, coronary spasm, cyclosporin nephrotoxicity, vasculitis and
CC   toxaemia in pregnancy, and is also present at elevated levels after
CC   orthotopic liver transplantation and major abdominal surgery
XX
SQ   Sequence 26 BP; 3 A; 2 C; 1 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 26;
  Best Local Similarity   95.2%;  Pred. No. 1e+03;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTT 2183
              | ||||||||||||||||||||
Db          6 TACTTTTTTTTTTTTTTTTT 26


RESULT 723
AAF74913/c
ID   AAF74913 standard; DNA; 26 BP.
XX
AC   AAF74913;
XX
DT   23-MAY-2001  (first entry)
XX
DE   CD40L poly-A tract sequence SEQ ID NO:10.
XX
KW   Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW   diagnosis; antiarthritic; antirheumatic; immunosuppressive;
KW   antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200119844-A1.
XX
PD   22-MAR-2001.
XX
PF   13-SEP-2000; 2000WO-US024966.
XX
```

```
PR   13-SEP-1999;   99US-0153625P.
XX
PA   (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
PI   Crow MK,  Li Y;
XX
DR   WPI; 2001-244776/25.
XX
PT   New altered CD40L promoter for use in the study, diagnosis and treatment
PT   of a variety of inflammatory disorders and autoimmune diseases, such as
PT   rheumatoid arthritis.
XX
PS   Example 1; Fig 3; 90pp; English.
XX
CC   The present invention describes an isolated, purified nucleic acid, which
CC   is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC   residues 331-455 of the sequence comprising 455 nucleotides given in
CC   AAF74905 where A in the wild type sequence at position 331 (corresponding
CC   to position -125) is replaced with C. (I) has antiarthritic,
CC   antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC   be used in gene therapy. (I) is useful in the study, diagnosis and
CC   treatment of inflammatory and autoimmune diseases, as well as diseases in
CC   which elevated expression of CD40L is a factor, e.g., rheumatoid
CC   arthritis. The present sequence represents a CD40L poly-A tract sequence
CC   which is used in an example from the present invention
XX
SQ   Sequence 26 BP; 20 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 26;
  Best Local Similarity   95.2%;  Pred. No. 1e+03;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              |||||| ||||||||||||||
Db         21 TTTTTTGTTTTTTTTTTTTT 1


RESULT 724
ABQ76254/c
ID   ABQ76254 standard; DNA; 27 BP.
XX
AC   ABQ76254;
XX
DT   08-NOV-2002  (first entry)
XX
DE   Murine SCCE 5'-RACE oligonucleotide SEQ ID 42.
XX
KW   SCCE; murine; stratum corneum chymotryptic enzyme; kallikrein 7;
KW   serine protease; transgenic mammal; skin; skin disease; skin cancer;
KW   hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation;
KW   pruritus; atopic dermatitis; eczema; acne; itch; KLK7; ss.
XX
OS   Mus musculus.
XX
PN   WO200262135-A2.
XX
PD   15-AUG-2002.
XX
PF   08-FEB-2002; 2002WO-IB001300.
XX
PR   09-FEB-2001; 2001CA-02332655.
PR   09-FEB-2001; 2001DK-00000218.
XX
PA   (EGEL/) EGELRUD T.
PA   (HANS/) HANSSON L.
XX
PI   Egelrud T,  Hansson L;
XX
DR   WPI; 2002-643380/69.
XX
PT   Transgenic mammal or its embryo useful as model for human disease, has
PT   heterologous nucleotide sequence coding for stratum corneum chymotryptic
PT   enzyme operably linked to promoter that drives its expression in skin.
XX
PS   Example 6; Page 36; 74pp; English.
XX
CC   This invention describes a novel non-human transgenic mammal or mammalian
CC   embryo having integrated within its genome, a heterologous nucleotide
CC   sequence comprising at least a significant part of a nucleotide sequence
CC   coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant,
CC   operably linked to a promoter that drives expression of heterologous scce
CC   or its variant in skin. The product of the invention is useful as a model
CC   for the study of disease with the aim of improving treatment, to relieve
CC   or ameliorate a pathogenic condition, for development or testing of a
CC   cosmetic or a pharmaceutical formulation, and for the development of a
CC   diagnostic method. It can also be used as a model for a skin disease or
CC   skin cancer. The invention is also useful for screening or identifying a
CC   compound or composition effective for the prevention or treatment of an
CC   abnormal or unwanted phenotype, and for screening or identifying a
CC   compound or composition effective for the prevention or treatment of
CC   inflammatory skin diseases selected from diseases consisting of epidermal
CC   hyperkeratosis, acanthosis, epidermal inflammation, dermal inflammation,
CC   pruritus, atopic dermatitis, eczema, acne and inherited skin diseases
CC   with epidermal hyperkeratosis. The mammal of the invention is also useful
CC   as a model for further studies of itch mechanisms and the testing of
CC   potential compounds and compositions for relieve of various skin diseases
CC   where itch is a component. This sequence represents a 5' RACE cDNA
CC   synthesis primer used in a method of detecting homologues to human
CC   stratum corneum chymotryptic enzyme, SCCE, gene. SCCE is a serine
CC   protease synonymous with human kallikrein 7 (KLK7) and is used in the
CC   development of the transgenic mammals described in the invention
XX
SQ   Sequence 27 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 2 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 27;
  Best Local Similarity   84.0%;  Pred. No. 1.1e+03;
  Matches   21;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAA 2804
              :||   ||||||||||||||||||
Db         26 BAAAAAAAAAAAAAAAAAAAAAAAA 2


RESULT 725
AAF74926/c
ID   AAF74926 standard; DNA; 27 BP.
XX
AC   AAF74926;
XX
DT   23-MAY-2001  (first entry)
XX
DE   CD40L poly-A tract sequence SEQ ID NO:23.
XX
KW   Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW   diagnosis; antiarthritic; antirheumatic; immunosuppressive;
KW   antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200119844-A1.
XX
PD   22-MAR-2001.
XX
PF   13-SEP-2000; 2000WO-US024966.
XX
PR   13-SEP-1999;   99US-0153625P.
XX
PA   (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
PI   Crow MK,  Li Y;
XX
DR   WPI; 2001-244776/25.
XX
PT   New altered CD40L promoter for use in the study, diagnosis and treatment
PT   of a variety of inflammatory disorders and autoimmune diseases, such as
PT   rheumatoid arthritis.
```

```
XX
PS   Example 1; Fig 3; 90pp; English.
XX
CC   The present invention describes an isolated, purified nucleic acid, which
CC   is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC   residues 331-455 of the sequence comprising 455 nucleotides given in
CC   AAF74905 where A in the wild type sequence at position 331 (corresponding
CC   to position -125) is replaced with C. (I) has antiarthritic,
CC   antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC   be used in gene therapy. (I) is useful in the study, diagnosis and
CC   treatment of inflammatory and autoimmune diseases, as well as diseases in
CC   which elevated expression of CD40L is a factor, e.g., rheumatoid
CC   arthritis. The present sequence represents a CD40L poly-A tract sequence
CC   which is used in an example from the present invention
XX
SQ   Sequence 27 BP; 21 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 27;
  Best Local Similarity   95.2%;  Pred. No. 1.1e+03;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              |||||| ||||||||||||||
Db         22 TTTTTTGTTTTTTTTTTTTT 2


RESULT 726
AAF74932/c
ID   AAF74932 standard; DNA; 27 BP.
XX
AC   AAF74932;
XX
DT   23-MAY-2001  (first entry)
XX
DE   CD40L poly-A tract sequence SEQ ID NO:29.
XX
KW   Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW   diagnosis; antiarthritic; antirheumatic; immunosuppressive;
KW   antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200119844-A1.
XX
PD   22-MAR-2001.
XX
PF   13-SEP-2000; 2000WO-US024966.
XX
PR   13-SEP-1999;   99US-0153625P.
XX
PA   (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
PI   Crow MK,  Li Y;
XX
DR   WPI; 2001-244776/25.
XX
PT   New altered CD40L promoter for use in the study, diagnosis and treatment
PT   of a variety of inflammatory disorders and autoimmune diseases, such as
PT   rheumatoid arthritis.
XX
PS   Example 1; Fig 3; 90pp; English.
XX
CC   The present invention describes an isolated, purified nucleic acid, which
CC   is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC   residues 331-455 of the sequence comprising 455 nucleotides given in
CC   AAF74905 where A in the wild type sequence at position 331 (corresponding
CC   to position -125) is replaced with C. (I) has antiarthritic,
CC   antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC   be used in gene therapy. (I) is useful in the study, diagnosis and
CC   treatment of inflammatory and autoimmune diseases, as well as diseases in
CC   which elevated expression of CD40L is a factor, e.g., rheumatoid
CC   arthritis. The present sequence represents a CD40L poly-A tract sequence
CC   which is used in an example from the present invention
XX
SQ   Sequence 27 BP; 21 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 27;
  Best Local Similarity   95.2%;  Pred. No. 1.1e+03;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              |||||| ||||||||||||||
Db         22 TTTTTTGTTTTTTTTTTTTT 2


RESULT 727
AAF74931/c
ID   AAF74931 standard; DNA; 27 BP.
XX
AC   AAF74931;
XX
DT   23-MAY-2001  (first entry)
XX
DE   CD40L poly-A tract sequence SEQ ID NO:28.
XX
KW   Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW   diagnosis; antiarthritic; antirheumatic; immunosuppressive;
KW   antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200119844-A1.
XX
PD   22-MAR-2001.
XX
PF   13-SEP-2000; 2000WO-US024966.
XX
PR   13-SEP-1999;   99US-0153625P.
XX
PA   (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
PI   Crow MK,  Li Y;
XX
DR   WPI; 2001-244776/25.
XX
PT   New altered CD40L promoter for use in the study, diagnosis and treatment
PT   of a variety of inflammatory disorders and autoimmune diseases, such as
PT   rheumatoid arthritis.
XX
PS   Example 1; Fig 3; 90pp; English.
XX
CC   The present invention describes an isolated, purified nucleic acid, which
CC   is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC   residues 331-455 of the sequence comprising 455 nucleotides given in
CC   AAF74905 where A in the wild type sequence at position 331 (corresponding
CC   to position -125) is replaced with C. (I) has antiarthritic,
CC   antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC   be used in gene therapy. (I) is useful in the study, diagnosis and
CC   treatment of inflammatory and autoimmune diseases, as well as diseases in
CC   which elevated expression of CD40L is a factor, e.g., rheumatoid
CC   arthritis. The present sequence represents a CD40L poly-A tract sequence
CC   which is used in an example from the present invention
XX
SQ   Sequence 27 BP; 21 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 27;
  Best Local Similarity   95.2%;  Pred. No. 1.1e+03;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              |||||| ||||||||||||||
Db         22 TTTTTTGTTTTTTTTTTTTT 2


RESULT 728
AAF74934/c
```

```
ID   AAF74934 standard; DNA; 27 BP.
XX
AC   AAF74934;
XX
DT   23-MAY-2001  (first entry)
XX
DE   CD40L poly-A tract sequence SEQ ID NO:31.
XX
KW   Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW   diagnosis; antiarthritic; antirheumatic; immunosuppressive;
KW   antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200119844-A1.
XX
PD   22-MAR-2001.
XX
PF   13-SEP-2000; 2000WO-US024966.
XX
PR   13-SEP-1999;   99US-0153625P.
XX
PA   (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
PI   Crow MK,  Li Y;
XX
DR   WPI; 2001-244776/25.
XX
PT   New altered CD40L promoter for use in the study, diagnosis and treatment
PT   of a variety of inflammatory disorders and autoimmune diseases, such as
PT   rheumatoid arthritis.
XX
PS   Example 1; Fig 3; 90pp; English.
XX
CC   The present invention describes an isolated, purified nucleic acid, which
CC   is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC   residues 331-455 of the sequence comprising 455 nucleotides given in
CC   AAF74905 where A in the wild type sequence at position 331 (corresponding
CC   to position -125) is replaced with C. (I) has antiarthritic,
CC   antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC   be used in gene therapy. (I) is useful in the study, diagnosis and
CC   treatment of inflammatory and autoimmune diseases, as well as diseases in
CC   which elevated expression of CD40L is a factor, e.g., rheumatoid
CC   arthritis. The present sequence represents a CD40L poly-A tract sequence
CC   which is used in an example from the present invention
XX
SQ   Sequence 27 BP; 21 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 27;
  Best Local Similarity   95.2%;  Pred. No. 1.1e+03;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTT 2186
              |||||| ||||||||||||||
Db         22 TTTTTTGTTTTTTTTTTTTT 2

RESULT 729
AAT13977
ID   AAT13977 standard; DNA; 28 BP.
XX
AC   AAT13977;
XX
DT   03-OCT-1996  (first entry)
XX
DE   E. spinifera fumonisin esterase end-blocked polyT primer BamT17V.
XX
KW   Fumonisin; esterase; transgenic plant; recombinant microorganism;
KW   expression; probiotic; feed inoculant; degradation; detoxification;
KW   maize seed; grain; animal feed; end blocked; polyT primer; nested;
KW   polymerase chain reaction; Exophiala spinifera; ss.
XX
OS   Synthetic.
XX
PN   WO9606175-A2.
XX
PD   29-FEB-1996.
XX
PF   11-AUG-1995;   95WO-US010284.
XX
PR   12-AUG-1994;   94US-00289595.
PR   07-JUN-1995;   95US-00484815.
XX
PA   (PION-) PIONEER HI-BRED INT INC.
XX
PI   Duvick J,  Rood TA;
XX
DR   WPI; 1996-151378/15.
XX
PT   Detoxification of fumonisin and related mycotoxin cpds. in grains - using
PT   an enzyme esp. an esterase, from Exophiala spinifera, Rhinocladiella
PT   atrovirens or a bacterium.
XX
PS   Example 8; Page 33; 54pp; English.
XX
CC   The present sequence is a primer for the nested PCR amplification of the
CC   Exophiala spinifera (ATCC 74269), fumonisin esterase, cDNA, which was
CC   isolated from a maize seed. The esterase cDNA can be used to produce
CC   transgenic plants and genetically engineered microorganisms, capable of
CC   expressing the esterase. The microorganisms can be used as a probiotic or
CC   feed inoculant, along with the esterase to degrade fumonisins and related
CC   cpds., partic. for the detoxification of maize seed pre- or post-harvest
CC   (i.e. during the storage or processing of the harvested grain, or in the
CC   processed grain) prior to its use as an animal feed
XX
SQ   Sequence 28 BP; 1 A; 4 C; 4 G; 18 T; 0 U; 1 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 28;
  Best Local Similarity   95.2%;  Pred. No. 1.2e+03;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTT 2183
              ||| ||||||||||||||||||
Db          7 TCCGTTTTTTTTTTTTTTTTT 27


RESULT 730
AAT70108
ID   AAT70108 standard; DNA; 28 BP.
XX
AC   AAT70108;
XX
DT   24-SEP-1997  (first entry)
XX
DE   PolyTV primer 3.
XX
KW   primer; polymerase chain reaction; cDNA library; anchored end; PCSUB;
KW   lock-docking; screening; PCR-based cDNA subtractive cloning; ss.
XX
OS   Synthetic.
XX
PN   WO9640998-A1.
XX
PD   19-DEC-1996.
XX
PF   05-JUN-1996;   96WO-US008582.
XX
PR   07-JUN-1995;   95US-00481687.
XX
PA   (PION-) PIONEER HI-BRED INT INC.
XX
PI   Wang X,  Duvick JP,  Briggs SP;
XX
DR   WPI; 1997-087067/08.
XX
PT   Method for prodn. of cDNA libraries with anchored ends - useful for
```

```
PT   subtractive cloning of sequences of interest.
XX
PS   Claim 1; Page 27; 56pp; English.
XX
CC   The invention provides a PCR-based method for generating a full-length
CC   cDNA library with anchored ends. The method uses lock-docking primers
CC   (AAT70106-11), where one primer, poly TV (V = G,C or A) locks over the
CC   polyA tail of eukaryotic mRNA producing first strand synthesis and a
CC   second primer, polyGH (H = A, C or T) locks onto the polyC tail added by
CC   terminal deoxynucleotidyl transferase (TdT). In the final step, AAT70112-
CC   17 (polyAB and polyCD primers; B = G, T or C; D = G, A or T) are used to
CC   amplify the first strand and produce a cDNA library with anchored ends.
CC   cDNA libraries produced may be used to identify new (unique) nucleotide
CC   sequences from PCSUB (PCR-based cDNA subtractive) libraries. The new
CC   method produces discreet sized PCR products which would not necessarily
CC   require further subcloning/screening. The method also produces full-
CC   length cDNA's obtainable from the libraries as opposed to specific cDNA
CC   clones, as produced by previously known methods. Other methods such as
CC   PCR and RACE require a knowledge of the target sequence to be amplified,
CC   by using the PCSUB method no previous knowledge is necessary
XX
SQ   Sequence 28 BP; 1 A; 5 C; 4 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 28;
  Best Local Similarity   95.2%;  Pred. No. 1.2e+03;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTT 2183
              ||| |||||||||||||||||
Db          7 TCCGTTTTTTTTTTTTTTTTT 27


RESULT 731
AAT70106
ID   AAT70106 standard; DNA; 28 BP.
XX
AC   AAT70106;
XX
DT   24-SEP-1997  (first entry)
XX
DE   PolyTV primer 1.
XX
KW   primer; polymerase chain reaction; cDNA library; anchored end; PCSUB;
KW   lock-docking; screening; PCR-based cDNA subtractive cloning; ss.
XX
OS   Synthetic.
XX
PN   WO9640998-A1.
XX
PD   19-DEC-1996.
XX
PF   05-JUN-1996;   96WO-US008582.
XX
PR   07-JUN-1995;   95US-00481687.
XX
PA   (PION-) PIONEER HI-BRED INT INC.
XX
PI   Wang X,  Duvick JP,  Briggs SP;
XX
DR   WPI; 1997-087067/08.
XX
PT   Method for prodn. of cDNA libraries with anchored ends - useful for
PT   subtractive cloning of sequences of interest.
XX
PS   Claim 1; Page 26; 56pp; English.
XX
CC   The invention provides a PCR-based method for generating a full-length
CC   cDNA library with anchored ends. The method uses lock-docking primers
CC   (AAT70106-11), where one primer, poly TV (V = G,C or A) locks over the
CC   polyA tail of eukaryotic mRNA producing first strand synthesis and a
CC   second primer, polyGH (H = A, C or T) locks onto the polyC tail added by
CC   terminal deoxynucleotidyl transferase (TdT). In the final step, AAT70112-
CC   17 (polyAB and polyCD primers; B = G, T or C; D = G, A or T) are used to
CC   amplify the first strand and produce a cDNA library with anchored ends.
CC   cDNA libraries produced may be used to identify new (unique) nucleotide
CC   sequences from PCSUB (PCR-based cDNA subtractive) libraries. The new
CC   method produces discreet sized PCR products which would not necessarily
CC   require further subcloning/screening. The method also produces full-
CC   length cDNA's obtainable from the libraries as opposed to specific cDNA
CC   clones, as produced by previously known methods. Other methods such as
CC   PCR and RACE require a knowledge of the target sequence to be amplified,
CC   by using the PCSUB method no previous knowledge is necessary
XX
SQ   Sequence 28 BP; 2 A; 4 C; 4 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 28;
  Best Local Similarity   95.2%;  Pred. No. 1.2e+03;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTT 2183
              ||| |||||||||||||||||
Db          7 TCCGTTTTTTTTTTTTTTTTT 27


RESULT 732
AAT70107
ID   AAT70107 standard; DNA; 28 BP.
XX
AC   AAT70107;
XX
DT   24-SEP-1997  (first entry)
XX
DE   PolyTV primer 2.
XX
KW   primer; polymerase chain reaction; cDNA library; anchored end; PCSUB;
KW   lock-docking; screening; PCR-based cDNA subtractive cloning; ss.
XX
OS   Synthetic.
XX
PN   WO9640998-A1.
XX
PD   19-DEC-1996.
XX
PF   05-JUN-1996;   96WO-US008582.
XX
PR   07-JUN-1995;   95US-00481687.
XX
PA   (PION-) PIONEER HI-BRED INT INC.
XX
PI   Wang X,  Duvick JP,  Briggs SP;
XX
DR   WPI; 1997-087067/08.
XX
PT   Method for prodn. of cDNA libraries with anchored ends - useful for
PT   subtractive cloning of sequences of interest.
XX
PS   Claim 1; Page 27; 56pp; English.
XX
CC   The invention provides a PCR-based method for generating a full-length
CC   cDNA library with anchored ends. The method uses lock-docking primers
CC   (AAT70106-11), where one primer, poly TV (V = G,C or A) locks over the
CC   polyA tail of eukaryotic mRNA producing first strand synthesis and a
CC   second primer, polyGH (H = A, C or T) locks onto the polyC tail added by
CC   terminal deoxynucleotidyl transferase (TdT). In the final step, AAT70112-
CC   17 (polyAB and polyCD primers; B = G, T or C; D = G, A or T) are used to
CC   amplify the first strand and produce a cDNA library with anchored ends.
CC   cDNA libraries produced may be used to identify new (unique) nucleotide
CC   sequences from PCSUB (PCR-based cDNA subtractive) libraries. The new
CC   method produces discreet sized PCR products which would not necessarily
CC   require further subcloning/screening. The method also produces full-
CC   length cDNA's obtainable from the libraries as opposed to specific cDNA
CC   clones, as produced by previously known methods. Other methods such as
CC   PCR and RACE require a knowledge of the target sequence to be amplified,
CC   by using the PCSUB method no previous knowledge is necessary
XX
SQ   Sequence 28 BP; 1 A; 4 C; 5 G; 18 T; 0 U; 0 Other;
```

```
  Query Match             0.7%;  Score 19.4;  DB 1;  Length 28;
  Best Local Similarity   95.2%;  Pred. No. 1.2e+03;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTT 2183
              ||| ||||||||||||||||||
Db          7 TCCGTTTTTTTTTTTTTTTT 27


RESULT 733
AAV65735
ID   AAV65735 standard; DNA; 28 BP.
XX
AC   AAV65735;
XX
DT   17-DEC-1998  (first entry)
XX
DE   A. phoenices APOXD DNA amplifying 5' RACE primer Bam T17V.
XX
KW   APOXD; oxalate decarboxylase; oxalic acid; degradation; plant pathogen;
KW   oxalic acid toxicity; oxalate; plant tissue; diagnosis; treatment;
KW   enzyme; urinary tract disorder; hyperoxaluric syndrome; PCR primer; ss.
XX
OS   Synthetic.
OS   Aspergillus phoenicis.
XX
PN   WO9842827-A2.
XX
PD   01-OCT-1998.
XX
PF   19-MAR-1998;   98WO-US005432.
XX
PR   21-MAR-1997;   97US-00821827.
XX
PA   (PION-) PIONEER HI-BRED INT INC.
XX
PI   Scelonge CJ,  Bidney DL;
XX
DR   WPI; 1998-557032/47.
XX
PT   New isolated oxalate decarboxyalse gene - obtained from Aspergillus
PT   phoenices, used for e.g. degrading oxalic acid, protecting against oxalic
PT   toxicity or as a selectable marker in plants.
XX
PS   Example 1; Page 24; 58pp; English.
XX
CC   Sequences AAV65729 to AAV65740 represent primers used for the PCR
CC   amplification of the genomic DNA encoding an Aspergillus phoenices
CC   oxalate decarboxylase (APOXD) enzyme. A vector containing the APOXD
CC   nucleic acid can be used to transform host cells for the recombinant
CC   production of the enzyme. The APOXD can be used for the degradation of
CC   oxalic acid in providing protection against oxalic acid toxicity. It is
CC   useful in combating and providing protection against plant pathogens that
CC   utilise oxalate to gain access to plant tissue or otherwise in the course
CC   of the pathogenesis of the disease. The APOXD gene is also useful as a
CC   selectable marker of transformed cells, for diagnostic assay of oxalate,
CC   and for production of the enzyme in plants. The product can also be used
CC   in diagnostic assays to quantify oxalate, e.g. in the diagnosis and
CC   treatment of patients with urinary tract disorders or hyperoxaluric
CC   syndromes
XX
SQ   Sequence 28 BP; 1 A; 4 C; 4 G; 18 T; 0 U; 1 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 28;
  Best Local Similarity   95.2%;  Pred. No. 1.2e+03;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTT 2183
              ||| ||||||||||||||||||
Db          7 TCCGTTTTTTTTTTTTTTTT 27


RESULT 734
AAX05727
ID   AAX05727 standard; DNA; 28 BP.
XX
AC   AAX05727;
XX
DT   07-MAY-1999  (first entry)
XX
DE   E. spinifera fumonisin esterase (ESP26-1) cDNA amplifying polyT primer.
XX
KW   Fumonisin esterase; enzyme; fumonisin; degrade; harvesting; grain; ss;
KW   animal feed; plant tissue; silage; fruit; vegetable; detoxification;
KW   mycotoxin; phytohormone; tricarballylic acid; TCA; bacterium; PCR primer.
XX
OS   Synthetic.
OS   Exophiala spinifera.
XX
PN   WO9902703-A1.
XX
PD   21-JAN-1999.
XX
PF   07-JUL-1998;   98WO-US013987.
XX
PR   07-JUL-1997;   97US-00888949.
PR   07-JUL-1997;   97US-00888950.
XX
PA   (PION-) PIONEER HI-BRED INT INC.
XX
PI   Duvick J,  Maddox JR,  Rood TA,  Wang X,  Bowen BA,  Gilliam JT;
XX
DR   WPI; 1999-120904/10.
XX
PT   Newly isolated polynucleotides useful for degrading and detoxifying
PT   fumonisins - and methods for identifying transformed plant cells.
XX
PS   Example 8; Page 37; 88pp; English.
XX
CC   The invention relates to fumonisin esterases from E. spinifera and Gram-
CC   negative bacteria. This enzyme can degrade fumonisin. The polynucleotides
CC   encoding fumonisin degrading enzymes are useful for degrading fumonisins
CC   during the process of harvesting grain for animal feed, or in plant
CC   tissues, which are used for silage or as a spray on grain, fruit or
CC   vegetables. They are also useful for detoxifying fumonisins, structurally
CC   related mycotoxins, and fumonisin hydrolysis products of both. The
CC   fumonisin esterase genes (contained within an expression cassette,
CC   encoding a fumonisin degradative enzyme) is introduced into plant cells
CC   that are cultured on a medium containing a phytohormone linked to a
CC   tricarballylic acid (TCA), which inactivates the phytohormone unless it
CC   is cleaved by an esterase. The polynucleotides are also used in a method
CC   for measuring gene expression, comprising transforming cells with the
CC   esterase genes operably linked to a promoter, adding substrate, and
CC   measuring the level of hydrolysed product. The isolation of the
CC   polynucleotides encoding the fumonisin degrading enzymes permits the
CC   degradation and detoxification of fumonisins, which are toxic and
CC   potentially widespread in food and feed. The present sequence represents
CC   a E. spinifera fumonisin esterase gene specific primer used for the
CC   isolation of a full-length cDNA of ESP26-1
XX
SQ   Sequence 28 BP; 1 A; 4 C; 4 G; 18 T; 0 U; 1 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 28;
  Best Local Similarity   95.2%;  Pred. No. 1.2e+03;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTT 2183
              ||| ||||||||||||||||||
Db          7 TCCGTTTTTTTTTTTTTTTT 27


RESULT 735
AAF74920/c
ID   AAF74920 standard; DNA; 28 BP.
XX
```

AC AAF74920;
XX
DT 23-MAY-2001 (first entry)
XX
DE CD40L poly-A tract sequence SEQ ID NO:17.
XX
KW Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW diagnosis; antiarthritic; antirheumatic; immunosuppressive;
KW antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
OS Homo sapiens.
XX
PN WO200119844-A1.
XX
PD 22-MAR-2001.
XX
PF 13-SEP-2000; 2000WO-US024966.
XX
PR 13-SEP-1999; 99US-0153625P.
XX
PA (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
PI Crow MK, Li Y;
XX
DR WPI; 2001-244776/25.
XX
PT New altered CD40L promoter for use in the study, diagnosis and treatment
PT of a variety of inflammatory disorders and autoimmune diseases, such as
PT rheumatoid arthritis.
XX
PS Example 1; Fig 3; 90pp; English.
XX
CC The present invention describes an isolated, purified nucleic acid, which
CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC residues 331-455 of the sequence comprising 455 nucleotides given in
CC AAF74905 where A in the wild type sequence at position 331 (corresponding
CC to position -125) is replaced with C. (I) has antiarthritic,
CC antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC be used in gene therapy. (I) is useful in the study, diagnosis and
CC treatment of inflammatory and autoimmune diseases, as well as diseases in
CC which elevated expression of CD40L is a factor, e.g., rheumatoid
CC arthritis. The present sequence represents a CD40L poly-A tract sequence
CC which is used in an example from the present invention
XX
SQ Sequence 28 BP; 22 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.4; DB 1; Length 28;
Best Local Similarity 95.2%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2186
||||||||||||||||||||
Db 23 TTTTTTGTTTTTTTTTTTTT 3

RESULT 736
AAF74906/c
ID AAF74906 standard; DNA; 28 BP.
XX
AC AAF74906;
XX
DT 23-MAY-2001 (first entry)
XX
DE CD40L poly-A tract sequence SEQ ID NO:3.
XX
KW Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW diagnosis; antiarthritic; antirheumatic; immunosuppressive;
KW antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
OS Homo sapiens.
XX
PN WO200119844-A1.
XX
PD 22-MAR-2001.
XX
PF 13-SEP-2000; 2000WO-US024966.
XX
PR 13-SEP-1999; 99US-0153625P.
XX
PA (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
PI Crow MK, Li Y;
XX
DR WPI; 2001-244776/25.
XX
PT New altered CD40L promoter for use in the study, diagnosis and treatment
PT of a variety of inflammatory disorders and autoimmune diseases, such as
PT rheumatoid arthritis.
XX
PS Example 1; Fig 3; 90pp; English.
XX
CC The present invention describes an isolated, purified nucleic acid, which
CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC residues 331-455 of the sequence comprising 455 nucleotides given in
CC AAF74905 where A in the wild type sequence at position 331 (corresponding
CC to position -125) is replaced with C. (I) has antiarthritic,
CC antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC be used in gene therapy. (I) is useful in the study, diagnosis and
CC treatment of inflammatory and autoimmune diseases, as well as diseases in
CC which elevated expression of CD40L is a factor, e.g., rheumatoid
CC arthritis. The present sequence represents a CD40L poly-A tract sequence
CC which is used in an example from the present invention
XX
SQ Sequence 28 BP; 22 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.4; DB 1; Length 28;
Best Local Similarity 95.2%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2186
||||||||||||||||||||
Db 23 TTTTTTGTTTTTTTTTTTTT 3

RESULT 737
AAF74916/c
ID AAF74916 standard; DNA; 28 BP.
XX
AC AAF74916;
XX
DT 23-MAY-2001 (first entry)
XX
DE CD40L poly-A tract sequence SEQ ID NO:13.
XX
KW Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW diagnosis; antiarthritic; antirheumatic; immunosuppressive;
KW antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
OS Homo sapiens.
XX
PN WO200119844-A1.
XX
PD 22-MAR-2001.
XX
PF 13-SEP-2000; 2000WO-US024966.
XX
PR 13-SEP-1999; 99US-0153625P.
XX
PA (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
PI Crow MK, Li Y;
XX
DR WPI; 2001-244776/25.
XX
PT New altered CD40L promoter for use in the study, diagnosis and treatment
PT of a variety of inflammatory disorders and autoimmune diseases, such as

PT rheumatoid arthritis.
XX
PS Example 1; Fig 3; 90pp; English.
XX
CC The present invention describes an isolated, purified nucleic acid, which
CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC residues 331-455 of the sequence comprising 455 nucleotides given in
CC AAF74905 where A in the wild type sequence at position 331 (corresponding
CC to position -125) is replaced with C. (I) has antiarthritic,
CC antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC be used in gene therapy. (I) is useful in the study, diagnosis and
CC treatment of inflammatory and autoimmune diseases, as well as diseases in
CC which elevated expression of CD40L is a factor, e.g., rheumatoid
CC arthritis. The present sequence represents a CD40L poly-A tract sequence
CC which is used in an example from the present invention
XX
SQ Sequence 28 BP; 22 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.4; DB 1; Length 28;
Best Local Similarity 95.2%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2186
||||||||||||||||||||
Db 23 TTTTTTGTTTTTTTTTTTTT 3

RESULT 738
AAF74927/c
ID AAF74927 standard; DNA; 28 BP.
XX
AC AAF74927;
XX
DT 23-MAY-2001 (first entry)
XX
DE CD40L poly-A tract sequence SEQ ID NO:24.
XX
KW Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW diagnosis; antiarthritic; antirheumatic; immunosuppressive;
KW antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
OS Homo sapiens.
XX
PN WO200119844-A1.
XX
PD 22-MAR-2001.
XX
PF 13-SEP-2000; 2000WO-US024966.
XX
PR 13-SEP-1999; 99US-0153625P.
XX
PA (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
PI Crow MK, Li Y;
XX
DR WPI; 2001-244776/25.
XX
PT New altered CD40L promoter for use in the study, diagnosis and treatment
PT of a variety of inflammatory disorders and autoimmune diseases, such as
PT rheumatoid arthritis.
XX
PS Example 1; Fig 3; 90pp; English.
XX
CC The present invention describes an isolated, purified nucleic acid, which
CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC residues 331-455 of the sequence comprising 455 nucleotides given in
CC AAF74905 where A in the wild type sequence at position 331 (corresponding
CC to position -125) is replaced with C. (I) has antiarthritic,
CC antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC be used in gene therapy. (I) is useful in the study, diagnosis and
CC treatment of inflammatory and autoimmune diseases, as well as diseases in
CC which elevated expression of CD40L is a factor, e.g., rheumatoid
CC arthritis. The present sequence represents a CD40L poly-A tract sequence
CC which is used in an example from the present invention
XX
SQ Sequence 28 BP; 22 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.4; DB 1; Length 28;
Best Local Similarity 95.2%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2186
||||||||||||||||||||
Db 23 TTTTTTGTTTTTTTTTTTTT 3

RESULT 739
AAF60450
ID AAF60450 standard; DNA; 28 BP.
XX
AC AAF60450;
XX
DT 27-APR-2001 (first entry)
XX
DE RNA oligonucleotide #7.
XX
KW Protein-RNA fusion; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "C6-psoralen-2-OMe-U"
FT modified_base 28
FT /*tag= b
FT /mod_base= OTHER
FT /note= "A-TEG2"
XX
PN WO200107657-A1.
XX
PD 01-FEB-2001.
XX
PF 19-JUL-2000; 2000WO-US019653.
XX
PR 27-JUL-1999; 99US-0145834P.
XX
PA (PHYL-) PHYLOS INC.
XX
PI Kurz M, Lohse P, Wagner R;
XX
DR WPI; 2001-182803/18.
XX
PT Affixing a peptide acceptor to an RNA molecule useful for producing
PT fusion proteins for isolating proteins or nucleic acids with desired
PT properties through attachment of a peptide acceptor to the 3' end of an
PT RNA molecule.
XX
PS Example 6; Page 29; 56pp; English.
XX
CC The present invention relates to a method for affixing a peptide acceptor
CC to an RNA molecule through the formation of a covalent bond, noncovalent
CC bond, or by chemical ligation. The method is useful for producing RNA-
CC protein fusions which can be used for the isolation of proteins or
CC nucleic aids with desired properties from large pools of partially or
CC completely random amino acid or nucleic acid sequences. The present
CC sequence is an RNA oligonucleotide used in the present invention
XX
SQ Sequence 28 BP; 20 A; 2 C; 4 G; 0 T; 2 U; 0 Other;

Query Match 0.7%; Score 19.4; DB 1; Length 28;
Best Local Similarity 90.5%; Pred. No. 1.2e+03;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2784 TGAAAAAAAAAAAAAAAAAA 2804

```
              :| ||||||||||||||||||
Db          8 UGCAAAAAAAAAAAAAAAAA 28


RESULT 740
AAL45359
ID   AAL45359 standard; RNA; 28 BP.
XX
AC   AAL45359;
XX
DT   06-JUN-2002  (first entry)
XX
DE   Puromycin linker DNA sequence.
XX
KW   Peptide cleavage; chemical active ingredient targeted release; diagnosis;
KW   antiasthmatic; osteopathic; cytostatic; asthma; osteoporosis; cancer;
KW   stroke; neuronal disease; arthritis; pancreatitis; hypertension;
KW   thrombosis; infection; schistosomiasis; herbicide; insecticide;
KW   fungicide; cerebroprotective; neurological; antiarthritic; pancreatic;
KW   hypotensive; antithrombotic; virucide; protozoacide; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "modified by psoralen and 2'-O-methyl"
FT   modified_base    28
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "modified by (PEG)2 CC (Puromycin linker)"
XX
PN   WO200216574-A2.
XX
PD   28-FEB-2002.
XX
PF   07-AUG-2001; 2001WO-EP009102.
XX
PR   22-AUG-2000; 2000DE-01041238.
XX
PA   (XZIL-) XZILLION GMBH & CO KG.
XX
PI   Reimholz R,  Ploeger F;
XX
DR   WPI; 2002-269356/31.
XX
PT   Identifying specifically cleavable peptide, useful for targeted drug
PT   delivery and developing protease inhibitors, by incubating test compound
PT   with peptide-nucleic acid fusion.
XX
PS   Example 1; Page 19; 38pp; German.
XX
CC   The present invention relates to the identification of specific
CC   proteolytically cleavable peptides by incubating a library of fusion
CC   molecules, comprising a peptide and nucleic acid encoding said peptide,
CC   with a proteolytically active sample, then isolating the cleavage
CC   fragments and determining the coding sequences in the separated fusion
CC   molecules. The coding sequences identified by the method are used for
CC   production of specifically proteolytically cleavable substances, which
CC   are useful in the treatment of asthma, osteoporosis, cancer, stroke,
CC   neuronal diseases, arthritis, pancreatitis, hypertension, thrombosis,
CC   viral infections and schistosomiasis. Also contemplated are similar
CC   compounds designed to release herbicides, insecticides and fungicides,
CC   when cleaved. The present sequence is a puromycin linker described in the
CC   exemplification of the invention
XX
SQ   Sequence 28 BP; 20 A; 2 C; 4 G; 0 T; 2 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 28;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAA 2804
              :| ||||||||||||||||||
Db          8 UGCAAAAAAAAAAAAAAAAA 28


RESULT 741
ABZ70568
ID   ABZ70568 standard; DNA; 28 BP.
XX
AC   ABZ70568;
XX
DT   23-MAY-2003  (first entry)
XX
DE   5' RACE primer Bam T17V.
XX
KW   Oxalate decarboxylase; APOXD; enzyme; selectable marker;
KW   transgenic plant; crop protection; oxalic acid; degradation;
KW   Aspergillus phoenices; PCR; RACE; primer; ss.
XX
OS   Synthetic.
XX
PN   CA2350328-A1.
XX
PD   26-DEC-2002.
XX
PF   26-JUN-2001; 2001CA-02350328.
XX
PR   26-JUN-2001; 2001CA-02350328.
XX
PA   (PION-) PIONEER HI-BRED INT INC.
XX
PI   Scelonge C,  Bidney D;
XX
DR   WPI; 2003-248733/25.
XX
PT   New isolated nucleic acid encoding oxalate decarboxylase from Aspergillus
PT   phoenices, for degrading oxalic acid, identifying transformed plant
PT   cells, and preventing pathogenic disease in plants.
XX
PS   Example 1; Page 28; 60pp; English.
XX
CC   The present sequence is that of a dT-based primer, which was used in a 5'
CC   RACE to obtained a fragment of the Aspergillus phoenices oxalate-
CC   decarboxylase (APOXD) gene. Following 3' and 5' RACE, a full-length
CC   nucleic acid (see ABZ70560) encoding APOXD enzyme (see ABP72475) was
CC   obtained. The APOXD gene and its encoded protein are useful for degrading
CC   oxalate, protecting plants from pathogenic disease, in diagnostic assays
CC   of oxalate, and as a selectable marker
XX
SQ   Sequence 28 BP; 1 A; 4 C; 4 G; 18 T; 0 U; 1 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 28;
  Best Local Similarity   95.2%;  Pred. No. 1.2e+03;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTT 2183
              ||| ||||||||||||||||
Db          7 TCCGTTTTTTTTTTTTTTTT 27


RESULT 742
AAQ49467
ID   AAQ49467 standard; DNA; 29 BP.
XX
AC   AAQ49467;
XX
DT   14-APR-1994  (first entry)
XX
DE   Oligo-dT primer "not1dt" to amplify human NK3R C-terminal clone.
XX
KW   human; neurokinin-3 receptor; NK3R; eledoisin; neurokinin B; tachykinin;
KW   enkephalin release; ss.
XX
```

```
OS   Synthetic.
XX
PN   GB2265375-A.
XX
PD   29-SEP-1993.
XX
PF   08-MAR-1993;   93GB-00004708.
XX
PR   16-MAR-1992;   92US-00851974.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Fong TM,  Huang RRC,  Strader CD;
XX
DR   WPI; 1993-305585/39.
XX
PT   New recombinant human neurokinin-receptor - used to identify binding
PT   ligands, antagonists and agonists of the receptor.
XX
PS   Example 1; Page 17; 46pp; English.
XX
CC   Degenerate PCR primers were designed based on the known sequence of rat
CC   NK3R central transmembrane core. The corresponding human cDNA sequence
CC   was obtained by amplification of human brain cDNA. New primers corresp.
CC   to the human sequence were designed and anchored PCR was performed using
CC   the human primer in the core region. A primary PCR was carried out using
CC   primers "not1dt" and "s1068" (AAQ49467 and AAQ49468, respectively) on
CC   template cDNA whose synthesis was initiated by "not1dt". After two
CC   further rounds of PCR using "not1dt", first with "s1106" (AAQ49469) and
CC   then with "s1137" (AAQ49470), a 600bp cDNA fragment which encodes the C-
CC   terminal region of human NK3R and the 3'-UTR was obtained and sequenced.
CC   The N-terminal coding region was similarly obtained. Finally a full-
CC   length cDNA (AAQ49461) was obtained in a single step using primers from
CC   the 5' and 3' untranslated regions. The human NK3R sequence will be
CC   useful for developing novel NK3 agonists and antagonists
XX
SQ   Sequence 29 BP; 0 A; 4 C; 4 G; 21 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 29;
  Best Local Similarity   79.3%;  Pred. No. 1.3e+03;
  Matches   23;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTTTTTTTTTTTTTT 2184
              ||||    ||  ||||||||||||||||
Db          1 TTTTGCGGCCGCTTTTTTTTTTTTTTTT 29


RESULT 743
AAF74918/c
ID   AAF74918 standard; DNA; 29 BP.
XX
AC   AAF74918;
XX
DT   23-MAY-2001  (first entry)
XX
DE   CD40L poly-A tract sequence SEQ ID NO:15.
XX
KW   Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW   diagnosis; antiarthritic; antirheumatic; immunosuppressive;
KW   antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200119844-A1.
XX
PD   22-MAR-2001.
XX
PF   13-SEP-2000; 2000WO-US024966.
XX
PR   13-SEP-1999;   99US-0153625P.
XX
PA   (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
PI   Crow MK,  Li Y;
XX
DR   WPI; 2001-244776/25.
XX
PT   New altered CD40L promoter for use in the study, diagnosis and treatment
PT   of a variety of inflammatory disorders and autoimmune diseases, such as
PT   rheumatoid arthritis.
XX
PS   Example 1; Fig 3; 90pp; English.
XX
CC   The present invention describes an isolated, purified nucleic acid, which
CC   is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC   residues 331-455 of the sequence comprising 455 nucleotides given in
CC   AAF74905 where A in the wild type sequence at position 331 (corresponding
CC   to position -125) is replaced with C. (I) has antiarthritic,
CC   antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC   be used in gene therapy. (I) is useful in the study, diagnosis and
CC   treatment of inflammatory and autoimmune diseases, as well as diseases in
CC   which elevated expression of CD40L is a factor, e.g., rheumatoid
CC   arthritis. The present sequence represents a CD40L poly-A tract sequence
CC   which is used in an example from the present invention
XX
SQ   Sequence 29 BP; 23 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 29;
  Best Local Similarity   95.2%;  Pred. No. 1.3e+03;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              |||||| ||||||||||||||
Db         24 TTTTTTGTTTTTTTTTTTTT 4


RESULT 744
AAF74907/c
ID   AAF74907 standard; DNA; 29 BP.
XX
AC   AAF74907;
XX
DT   23-MAY-2001  (first entry)
XX
DE   CD40L poly-A tract sequence SEQ ID NO:4.
XX
KW   Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW   diagnosis; antiarthritic; antirheumatic; immunosuppressive;
KW   antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200119844-A1.
XX
PD   22-MAR-2001.
XX
PF   13-SEP-2000; 2000WO-US024966.
XX
PR   13-SEP-1999;   99US-0153625P.
XX
PA   (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
PI   Crow MK,  Li Y;
XX
DR   WPI; 2001-244776/25.
XX
PT   New altered CD40L promoter for use in the study, diagnosis and treatment
PT   of a variety of inflammatory disorders and autoimmune diseases, such as
PT   rheumatoid arthritis.
XX
PS   Example 1; Fig 3; 90pp; English.
XX
CC   The present invention describes an isolated, purified nucleic acid, which
CC   is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC   residues 331-455 of the sequence comprising 455 nucleotides given in
CC   AAF74905 where A in the wild type sequence at position 331 (corresponding
```

```
CC   to position -125) is replaced with C. (I) has antiarthritic,
CC   antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC   be used in gene therapy. (I) is useful in the study, diagnosis and
CC   treatment of inflammatory and autoimmune diseases, as well as diseases in
CC   which elevated expression of CD40L is a factor, e.g., rheumatoid
CC   arthritis. The present sequence represents a CD40L poly-A tract sequence
CC   which is used in an example from the present invention
XX
SQ   Sequence 29 BP; 23 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 29;
  Best Local Similarity   95.2%;  Pred. No. 1.3e+03;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              |||||| ||||||||||||||
Db         24 TTTTTTGTTTTTTTTTTTTT 4


RESULT 745
AAF74935/c
ID   AAF74935 standard; DNA; 29 BP.
XX
AC   AAF74935;
XX
DT   23-MAY-2001  (first entry)
XX
DE   CD40L poly-A tract sequence SEQ ID NO:32.
XX
KW   Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW   diagnosis; antiarthritic; antirheumatic; immunosuppressive;
KW   antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200119844-A1.
XX
PD   22-MAR-2001.
XX
PF   13-SEP-2000; 2000WO-US024966.
XX
PR   13-SEP-1999;   99US-0153625P.
XX
PA   (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
PI   Crow MK,  Li Y;
XX
DR   WPI; 2001-244776/25.
XX
PT   New altered CD40L promoter for use in the study, diagnosis and treatment
PT   of a variety of inflammatory disorders and autoimmune diseases, such as
PT   rheumatoid arthritis.
XX
PS   Example 1; Fig 3; 90pp; English.
XX
CC   The present invention describes an isolated, purified nucleic acid, which
CC   is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC   residues 331-455 of the sequence comprising 455 nucleotides given in
CC   AAF74905 where A in the wild type sequence at position 331 (corresponding
CC   to position -125) is replaced with C. (I) has antiarthritic,
CC   antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC   be used in gene therapy. (I) is useful in the study, diagnosis and
CC   treatment of inflammatory and autoimmune diseases, as well as diseases in
CC   which elevated expression of CD40L is a factor, e.g., rheumatoid
CC   arthritis. The present sequence represents a CD40L poly-A tract sequence
CC   which is used in an example from the present invention
XX
SQ   Sequence 29 BP; 23 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 29;
  Best Local Similarity   95.2%;  Pred. No. 1.3e+03;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              |||||| ||||||||||||||
Db         24 TTTTTTGTTTTTTTTTTTTT 4


RESULT 746
AAF74921/c
ID   AAF74921 standard; DNA; 29 BP.
XX
AC   AAF74921;
XX
DT   23-MAY-2001  (first entry)
XX
DE   CD40L poly-A tract sequence SEQ ID NO:18.
XX
KW   Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW   diagnosis; antiarthritic; antirheumatic; immunosuppressive;
KW   antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200119844-A1.
XX
PD   22-MAR-2001.
XX
PF   13-SEP-2000; 2000WO-US024966.
XX
PR   13-SEP-1999;   99US-0153625P.
XX
PA   (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
PI   Crow MK,  Li Y;
XX
DR   WPI; 2001-244776/25.
XX
PT   New altered CD40L promoter for use in the study, diagnosis and treatment
PT   of a variety of inflammatory disorders and autoimmune diseases, such as
PT   rheumatoid arthritis.
XX
PS   Example 1; Fig 3; 90pp; English.
XX
CC   The present invention describes an isolated, purified nucleic acid, which
CC   is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC   residues 331-455 of the sequence comprising 455 nucleotides given in
CC   AAF74905 where A in the wild type sequence at position 331 (corresponding
CC   to position -125) is replaced with C. (I) has antiarthritic,
CC   antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC   be used in gene therapy. (I) is useful in the study, diagnosis and
CC   treatment of inflammatory and autoimmune diseases, as well as diseases in
CC   which elevated expression of CD40L is a factor, e.g., rheumatoid
CC   arthritis. The present sequence represents a CD40L poly-A tract sequence
CC   which is used in an example from the present invention
XX
SQ   Sequence 29 BP; 23 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 29;
  Best Local Similarity   95.2%;  Pred. No. 1.3e+03;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              |||||| ||||||||||||||
Db         24 TTTTTTGTTTTTTTTTTTTT 4


RESULT 747
AAF74928/c
ID   AAF74928 standard; DNA; 29 BP.
XX
AC   AAF74928;
XX
DT   23-MAY-2001  (first entry)
XX
DE   CD40L poly-A tract sequence SEQ ID NO:25.
```

```
XX
KW   Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW   diagnosis; antiarthritic; antirheumatic; immunosuppressive;
KW   antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200119844-A1.
XX
PD   22-MAR-2001.
XX
PF   13-SEP-2000; 2000WO-US024966.
XX
PR   13-SEP-1999;   99US-0153625P.
XX
PA   (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
PI   Crow MK,  Li Y;
XX
DR   WPI; 2001-244776/25.
XX
PT   New altered CD40L promoter for use in the study, diagnosis and treatment
PT   of a variety of inflammatory disorders and autoimmune diseases, such as
PT   rheumatoid arthritis.
XX
PS   Example 1; Fig 3; 90pp; English.
XX
CC   The present invention describes an isolated, purified nucleic acid, which
CC   is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC   residues 331-455 of the sequence comprising 455 nucleotides given in
CC   AAF74905 where A in the wild type sequence at position 331 (corresponding
CC   to position -125) is replaced with C. (I) has antiarthritic,
CC   antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC   be used in gene therapy. (I) is useful in the study, diagnosis and
CC   treatment of inflammatory and autoimmune diseases, as well as diseases in
CC   which elevated expression of CD40L is a factor, e.g., rheumatoid
CC   arthritis. The present sequence represents a CD40L poly-A tract sequence
CC   which is used in an example from the present invention
XX
SQ   Sequence 29 BP; 23 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 29;
  Best Local Similarity   95.2%;  Pred. No. 1.3e+03;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              |||||| ||||||||||||||
Db         24 TTTTTTGTTTTTTTTTTTTT 4


RESULT 748
AAH28298
ID   AAH28298 standard; RNA; 29 BP.
XX
AC   AAH28298;
XX
DT   05-SEP-2001  (first entry)
XX
DE   3' untranslated region sequence from neuronal cadherin gene.
XX
KW   mRNA protein complex; tumour development; cell aging; death;
KW   ribonomic profile; RNA-binding protein; ss.
XX
OS   Unidentified.
XX
PN   WO200148480-A1.
XX
PD   05-JUL-2001.
XX
PF   28-DEC-2000; 2000WO-US035583.
XX
PR   28-DEC-1999;   99US-0173338P.
XX
PA   (KEEN/) KEENE J D.
XX
PI   Keene JD,  Tenenbaum SA,  Carson C;
XX
DR   WPI; 2001-425706/45.
XX
PT   Partitioning endogenous mRNA-protein complexes in vivo, by contacting
PT   sample comprising the complex with ligand that binds to a component of
PT   the complex and separating complex by binding ligand with a binding
PT   molecule.
XX
PS   Example 6; Page 31; 49pp; English.
XX
CC   The specification describes a method for partitioning endogenous cellular
CC   mRNA-protein (mRNP) complexes. The method comprises contacting a
CC   biological sample comprising mRNP complex with ligand that specifically
CC   binds a component of mRNP complex, separating mRNP complex by binding the
CC   ligand with a molecule specific for ligand, which is attached to the
CC   solid support and then collecting the mRNP complex by removing the
CC   complex from the support. The method is useful for in vivo partitioning
CC   of cellular mRNA protein complexes in a biological sample. The method is
CC   useful for determining the ribonomic profile of a cell which has numerous
CC   uses including monitoring of tumour development, state of growth or state
CC   of development, perturbations of a biological system such as disease,
CC   drug or toxin treatment and the state of cell aging or death,
CC   distinguishing ribonomic profiles among organisms, to discriminate
CC   between transcriptional and post-transcriptional contributions to gene
CC   expression and to track the movement of RNAs through RNP complexes,
CC   including the interactions of combinations of proteins with RNAs in RNP
CC   complexes. AAH28281-AAH28316 represent sequences derived from the 3'
CC   untranslated region (UTR) of mRNA of various genes. The sequences contain
CC   target sequences for RNA-binding proteins
XX
SQ   Sequence 29 BP; 4 A; 1 C; 0 G; 0 T; 24 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 29;
  Best Local Similarity   0.0%;  Pred. No. 1.3e+03;
  Matches    0;  Conservative   23;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTT 2183
              ::::::: ::::::: :::: :::::
Db          1 UUUUUUUUAAAUUUUUUUAUUUUCUUUU 29


RESULT 749
AAD33515/c
ID   AAD33515 standard; DNA; 29 BP.
XX
AC   AAD33515;
XX
DT   01-JUL-2002  (first entry)
XX
DE   T7T18Apad_PS6-29-0001 probe for calibration of molecular array data.
XX
KW   Molecular array; probe; ss.
XX
OS   Unidentified.
XX
PN   EP1186673-A2.
XX
PD   13-MAR-2002.
XX
PF   10-SEP-2001; 2001EP-00307665.
XX
PR   11-SEP-2000; 2000US-00659173.
XX
PA   (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI   Wobler PK,  Delenstarr GC;
XX
DR   WPI; 2002-282886/33.
XX
PT   Calibration of molecular array data by employing calibration probes that
```

```
PT   generate signals proportional to total concentrations of labeled target
PT   molecules, and molecular arrays incorporating sets of calibration probes.
XX
PS   Disclosure; Page 14; 32pp; English.
XX
CC   The invention relates to a method for calibrating data scanned from a
CC   molecular array. The method involves employing calibration probes that
CC   generate signals proportional to the total concentrations of labelled
CC   target molecules to which the molecular array probes are directed over an
CC   entire range of sample solutions and molecular arrays incorporating sets
CC   of calibration probes. Method is useful for calibrating different types
CC   of signals scanned from a molecular array, or calibrating signals scanned
CC   from different molecular arrays. The present sequence is poly (A)
CC   normalisation probe used in calibration of molecular array data
XX
SQ   Sequence 29 BP; 23 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 29;
  Best Local Similarity   79.3%;  Pred. No. 1.3e+03;
  Matches   23;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTT 2183
                ||||||      ||||||||||||||||||
Db         29 TTTTTGGGAGATTTTTTTTTTTTTTTT 1


RESULT 750
AAD33516/c
ID   AAD33516 standard; DNA; 29 BP.
XX
AC   AAD33516;
XX
DT   01-JUL-2002  (first entry)
XX
DE   T7T18Apad_PS18-29-0003 probe for calibration of molecular array data.
XX
KW   Molecular array; probe; ss.
XX
OS   Unidentified.
XX
PN   EP1186673-A2.
XX
PD   13-MAR-2002.
XX
PF   10-SEP-2001; 2001EP-00307665.
XX
PR   11-SEP-2000; 2000US-00659173.
XX
PA   (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI   Wobler PK,  Delenstarr GC;
XX
DR   WPI; 2002-282886/33.
XX
PT   Calibration of molecular array data by employing calibration probes that
PT   generate signals proportional to total concentrations of labeled target
PT   molecules, and molecular arrays incorporating sets of calibration probes.
XX
PS   Disclosure; Page 14; 32pp; English.
XX
CC   The invention relates to a method for calibrating data scanned from a
CC   molecular array. The method involves employing calibration probes that
CC   generate signals proportional to the total concentrations of labelled
CC   target molecules to which the molecular array probes are directed over an
CC   entire range of sample solutions and molecular arrays incorporating sets
CC   of calibration probes. Method is useful for calibrating different types
CC   of signals scanned from a molecular array, or calibrating signals scanned
CC   from different molecular arrays. The present sequence is poly (A)
CC   normalisation probe used in calibration of molecular array data
XX
SQ   Sequence 29 BP; 23 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 29;
  Best Local Similarity   79.3%;  Pred. No. 1.3e+03;
  Matches   23;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTT 2183
                ||||||      ||||||||||||||||||
Db         29 TTTTTTGGGAGATTTTTTTTTTTTTTTT 1


RESULT 751
ADC16682/c
ID   ADC16682 standard; DNA; 30 BP.
XX
AC   ADC16682;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Aminoacylation RNA molecule related DNA oligo, P3-2.
XX
KW   ribozyme; aminoacylate; tRNA; non-cognate; catalytic RNA molecule; cis;
KW   aminoacylation; trans; proteomic; ds.
XX
OS   Unidentified.
XX
PN   WO2003070740-A1.
XX
PD   28-AUG-2003.
XX
PF   18-FEB-2003; 2003WO-US005007.
XX
PR   15-FEB-2002; 2002US-0357424P.
XX
PA   (UYNY ) UNIV NEW YORK STATE RES FOUND.
XX
PI   Suga H,  Murakami H,  Saito H;
XX
DR   WPI; 2003-748198/70.
XX
PT   New polynucleotide, useful for preparing peptides containing non-cognate
PT   amino acids, encodes ribozyme that can aminoacylate tRNA with such amino
PT   acids.
XX
PS   Example 3; SEQ ID NO 42; 85pp; English.
XX
CC   The invention relates to a novel polynucleotide comprising a sequence
CC   encoding a ribozyme that can aminoacylate tRNA with a non-cognate amino
CC   acid. Ribozymes encoded by the polynucleotide of the invention are used
CC   to prepare polypeptides that contain non-cognate, including non-natural,
CC   amino acids. The invention more specifically provides catalytic RNA
CC   molecules having cis aminoacylation activity with a catalytic and
CC   aminoacylation domain, or an RNA molecule with trans aminoacylation
CC   activity with only a catalytic domain. The products of the invention are
CC   potentially useful for biomedical and therapeutic use, e.g. for probing
CC   the structure and function of proteins; preparation of peptide libraries
CC   and in proteomics. This polynucleotide sequence represents a DNA oligo
CC   relating to the RNA molecule with aminoacylation activity of the
CC   invention.
XX
SQ   Sequence 30 BP; 3 A; 5 C; 1 G; 21 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 30;
  Best Local Similarity   95.2%;  Pred. No. 1.4e+03;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAAA 2804
                | ||||||||||||||||||||
Db         21 TAAAAAAAAAAAAAAAAAAAA 1


RESULT 752
ACC42844
ID   ACC42844 standard; DNA; 33 BP.
XX
AC   ACC42844;
```

```
XX
DT   01-SEP-2003  (first entry)
XX
DE   Nuclear transition protein I-9.57 PCR primer #4.
XX
KW   Nuclear transition protein I-9.57; tumour; cytostatic; haemopathy; PCR;
KW   HIV infection; anti-HIV; immunological disease; inflammation; primer; ss.
XX
OS   Unidentified.
XX
PN   CN1380328-A.
XX
PD   20-NOV-2002.
XX
PF   10-APR-2001; 2001CN-00105924.
XX
PR   10-APR-2001; 2001CN-00105924.
XX
PA   (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2003-222560/22.
XX
PT   Polypeptide-nuclear transformation protein -9.57 and polynucleotide for
PT   coding this polypeptide.
XX
PS   Example 5; Page 27; 29pp; Chinese.
XX
CC   The present invention relates to nuclear transition protein I-9.57 and
CC   its coding sequence. The protein can be used for treating several
CC   diseases, such as malignant tumours, haemopathy, HIV infection,
CC   immunological disease and various inflammations. The present sequence is
CC   a PCR primer, which was used in an example from the invention. Note: The
CC   present sequence is SEQ ID 6 from the sequence listing. This sequence
CC   differs from the SEQ ID 6 shown in the disclosure (see ACC42932)
XX
SQ   Sequence 33 BP; 24 A; 4 C; 2 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 33;
  Best Local Similarity   95.2%;  Pred. No. 1.7e+03;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAAA 2804
              | ||||||||||||||||||||
Db         11 TAAAAAAAAAAAAAAAAAAAA 31


RESULT 753
ACC48482
ID   ACC48482 standard; DNA; 21 BP.
XX
AC   ACC48482;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Locked nucleic acid anchored oligo(I) primer ON12.
XX
KW   Locked nucleic acid; LNA; gene therapy; primer; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   3
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   5
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   7
FT                   /*tag=  d
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   9
FT                   /*tag=  e
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   11
FT                   /*tag=  f
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   13
FT                   /*tag=  g
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   15
FT                   /*tag=  h
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   17
FT                   /*tag=  i
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   19
FT                   /*tag=  j
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   21
FT                   /*tag=  k
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   22
FT                   /*tag=  l
FT                   /mod_base= OTHER
FT                   /note= "OTHER= Compound 17d"
XX
PN   WO2003020739-A2.
XX
PD   13-MAR-2003.
XX
PF   04-SEP-2002; 2002WO-IB003911.
XX
PR   04-SEP-2001; 2001US-0317034P.
PR   22-SEP-2001; 2001US-0323967P.
XX
PA   (EXIQ-) EXIQON AS.
XX
PI   Wengel J,  Kauppinen S;
XX
DR   WPI; 2003-363021/34.
XX
PT   Novel nucleic acid comprising a locked nucleic acid unit having a
PT   modified base that comprises an optionally substituted carbocyclic aryl
PT   moiety, or modified nucleobase or nucleosidic base other than
PT   oxazole/imidazole.
XX
PS   Example 24a; Page 90; 119pp; English.
XX
CC   The present sequence is that of pyrene-anchored locked nucleic acid (LNA)
CC   oligo(dT) primer ON12, which was used in first-strand cDNA synthesis from
CC   eukaryotic mRNA. It includes compound '17d' at its 3' end, which is based
CC   on an LNA-type 2'-O,4'-C-methylene- beta-D-ribofuranosyl moiety. It is
CC   one of a set of such primers (see also ACC48483-85) that were used in an
CC   example from the invention to demonstrate improved reverse transcription
CC   of mRNA using pyrene-LNA anchored oligo(T) primers. The following results
CC   were observed: efficient priming on mRNAs with short poly(A) tails;
CC   efficient anchoring of the oligo(T) primer by pyrene-LNA and LNA-C/G/T
CC   units resulting in an improved T20-VN anchor primer and thus avoiding
CC   reverse transcription of long poly(A) tracts; and improved reverse
CC   transcription of eukaryotic poly(A)+RNA directly from total RNA extracts
```

```
CC   due to increased specificity. The invention relates to modified LNA units
CC   that comprise unique base groups. Desirable nucleobase and nucleosidic
CC   base substitutions can mediate universal hybridisation when incorporated
CC   into nucleic acid strands. The novel LNA compounds can be used e.g. as
CC   PCR primers, in sequencing, the synthesis of antisense oligonucleotides,
CC   and in diagnostics
XX
SQ   Sequence 21 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 2 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 6.6e+02;
  Matches   19;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||:
Db          1 TTTTTTTTTTTTTTTTTTV 20


RESULT 754
ACC48482/c
ID   ACC48482 standard; DNA; 21 BP.
XX
AC   ACC48482;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Locked nucleic acid anchored oligo(I) primer ON12.
XX
KW   Locked nucleic acid; LNA; gene therapy; primer; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   3
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   5
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   7
FT                   /*tag=  d
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   9
FT                   /*tag=  e
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   11
FT                   /*tag=  f
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   13
FT                   /*tag=  g
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   15
FT                   /*tag=  h
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   17
FT                   /*tag=  i
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   19
FT                   /*tag=  j
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   21
FT                   /*tag=  k
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   22
FT                   /*tag=  l
FT                   /mod_base= OTHER
FT                   /note= "OTHER= Compound 17d"
XX
PN   WO2003020739-A2.
XX
PD   13-MAR-2003.
XX
PF   04-SEP-2002; 2002WO-IB003911.
XX
PR   04-SEP-2001; 2001US-0317034P.
PR   22-SEP-2001; 2001US-0323967P.
XX
PA   (EXIQ-) EXIQON AS.
XX
PI   Wengel J,  Kauppinen S;
XX
DR   WPI; 2003-363021/34.
XX
PT   Novel nucleic acid comprising a locked nucleic acid unit having a
PT   modified base that comprises an optionally substituted carbocyclic aryl
PT   moiety, or modified nucleobase or nucleosidic base other than
PT   oxazole/imidazole.
XX
PS   Example 24a; Page 90; 119pp; English.
XX
CC   The present sequence is that of pyrene-anchored locked nucleic acid (LNA)
CC   oligo(dT) primer ON12, which was used in first-strand cDNA synthesis from
CC   eukaryotic mRNA. It includes compound '17d' at its 3' end, which is based
CC   on an LNA-type 2'-O,4'-C-methylene- beta-D-ribofuranosyl moiety. It is
CC   one of a set of such primers (see also ACC48483-85) that were used in an
CC   example from the invention to demonstrate improved reverse transcription
CC   of mRNA using pyrene-LNA anchored oligo(T) primers. The following results
CC   were observed: efficient priming on mRNAs with short poly(A) tails;
CC   efficient anchoring of the oligo(T) primer by pyrene-LNA and LNA-C/G/T
CC   units resulting in an improved T20-VN anchor primer and thus avoiding
CC   reverse transcription of long poly(A) tracts; and improved reverse
CC   transcription of eukaryotic poly(A)+RNA directly from total RNA extracts
CC   due to increased specificity. The invention relates to modified LNA units
CC   that comprise unique base groups. Desirable nucleobase and nucleosidic
CC   base substitutions can mediate universal hybridisation when incorporated
CC   into nucleic acid strands. The novel LNA compounds can be used e.g. as
CC   PCR primers, in sequencing, the synthesis of antisense oligonucleotides,
CC   and in diagnostics
XX
SQ   Sequence 21 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 2 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 6.6e+02;
  Matches   19;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              :||||||||||||||||||
Db         20 BAAAAAAAAAAAAAAAAAAA 1


RESULT 755
ACC99729
ID   ACC99729 standard; DNA; 21 BP.
XX
AC   ACC99729;
XX
DT   02-SEP-2003  (first entry)
XX
DE   Oligonucleotide.
XX
KW   Multiplex real-time quantitative PCR; PCR primer; copy number;
KW   Alzheimer's disease; ss.
```

```
XX
OS   Synthetic.
XX
PN   WO2003048377-A2.
XX
PD   12-JUN-2003.
XX
PF   02-DEC-2002; 2002WO-US038806.
XX
PR   30-NOV-2001; 2001US-0336095P.
PR   19-JUL-2002; 2002US-0397475P.
XX
PA   (UYRP ) UNIV ROCHESTER.
PA   (THER/) THERIANOS S.
XX
PI   Zhu M,  Coleman P;
XX
DR   WPI; 2003-532841/50.
XX
PT   Determining the relative copy number of a group of target nucleic acid
PT   molecules present in a sample by performing a first or second PCR in a
PT   PCR mixture and quantifying the number of copies of the second target
PT   nucleic acid product.
XX
PS   Example 1; Page 68; 118pp; English.
XX
CC   The present invention describes a multiplex real-time quantitative PCR
CC   method for determining the relative copy number of a group of target
CC   nucleic acid molecules present in a sample. The method comprises: (1)
CC   performing a first PCR in a PCR mixture; (2) performing a second PCR in a
CC   PCR mixture; and (3) quantifying the number of copies of the second
CC   target nucleic acid product present in the sample containing the target
CC   nucleic acid molecule. Also described: (1) quantifying the copy number of
CC   a group of target nucleic acids in a sample; and (2) determining whether
CC   a subject is at risk of acquiring Alzheimer's disease. The method is
CC   useful for determining the relative copy number of a group of target
CC   nucleic acid molecules present in a sample for determining whether a
CC   subject is at risk of acquiring Alzheimer's disease. ACC99620 to ACC99730
CC   represent PCR primer used in the exemplification of the present invention
XX
SQ   Sequence 21 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 2 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 6.6e+02;
  Matches   19;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||:
Db          1 TTTTTTTTTTTTTTTTTTV 20


RESULT 756
ACC99729/c
ID   ACC99729 standard; DNA; 21 BP.
XX
AC   ACC99729;
XX
DT   02-SEP-2003  (first entry)
XX
DE   Oligonucleotide.
XX
KW   Multiplex real-time quantitative PCR; PCR primer; copy number;
KW   Alzheimer's disease; ss.
XX
OS   Synthetic.
XX
PN   WO2003048377-A2.
XX
PD   12-JUN-2003.
XX
PF   02-DEC-2002; 2002WO-US038806.
XX
PR   30-NOV-2001; 2001US-0336095P.
PR   19-JUL-2002; 2002US-0397475P.
XX
PA   (UYRP ) UNIV ROCHESTER.
PA   (THER/) THERIANOS S.
XX
PI   Zhu M,  Coleman P;
XX
DR   WPI; 2003-532841/50.
XX
PT   Determining the relative copy number of a group of target nucleic acid
PT   molecules present in a sample by performing a first or second PCR in a
PT   PCR mixture and quantifying the number of copies of the second target
PT   nucleic acid product.
XX
PS   Example 1; Page 68; 118pp; English.
XX
CC   The present invention describes a multiplex real-time quantitative PCR
CC   method for determining the relative copy number of a group of target
CC   nucleic acid molecules present in a sample. The method comprises: (1)
CC   performing a first PCR in a PCR mixture; (2) performing a second PCR in a
CC   PCR mixture; and (3) quantifying the number of copies of the second
CC   target nucleic acid product present in the sample containing the target
CC   nucleic acid molecule. Also described: (1) quantifying the copy number of
CC   a group of target nucleic acids in a sample; and (2) determining whether
CC   a subject is at risk of acquiring Alzheimer's disease. The method is
CC   useful for determining the relative copy number of a group of target
CC   nucleic acid molecules present in a sample for determining whether a
CC   subject is at risk of acquiring Alzheimer's disease. ACC99620 to ACC99730
CC   represent PCR primer used in the exemplification of the present invention
XX
SQ   Sequence 21 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 2 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 6.6e+02;
  Matches   19;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              :||||||||||||||||||:
Db         20 BAAAAAAAAAAAAAAAAAAA 1


RESULT 757
AAL50570/c
ID   AAL50570 standard; DNA; 22 BP.
XX
AC   AAL50570;
XX
DT   12-DEC-2002  (first entry)
XX
DE   Molecular array production method-related PCR primer.
XX
KW   Molecular array; ss; target molecule identification; genetic analysis;
KW   gene expression; SNP detection; haplotyping; sequencing; PCR; primer.
XX
OS   Unidentified.
XX
PN   WO200274988-A2.
XX
PD   26-SEP-2002.
XX
PF   18-MAR-2002; 2002WO-GB001245.
XX
PR   16-MAR-2001; 2001GB-00006635.
PR   02-AUG-2001; 2001GB-00018879.
XX
PA   (UYCH-) UNIV CHANCELLOR MASTER & SCHOLARS OXF.
XX
PI   Mir K;
XX
DR   WPI; 2002-732872/79.
XX
PT   Producing a molecular array with a plurality of molecules immobilized to
PT   a solid substrate, useful in genetic analysis, gene expression studies or
```

```
PT   the detection or typing of single nucleotide polymorphisms in a sample of
PT   nucleic acids.
XX
PS   Example 15; Page 122; 166pp; English.
XX
CC   The invention comprises a method for producing a molecular array, the
CC   method involves immobilising molecules to a solid phase at a density
CC   which allows individual immobilised molecules to be individually
CC   resolved. The molecular array produced by the method of the invention is
CC   useful for identifying one or more target molecules in a sample. The
CC   molecular array is also useful in genetic analysis, gene expression
CC   studies, identifying molecules which interact with a target molecule,
CC   detection/typing of single nucleotide polymorphisms, haplotyping and
CC   sequencing. The present DNA sequence represents a PCR primer that was
CC   used in an example of the invention
XX
SQ   Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 2 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 22;
  Best Local Similarity   95.0%;  Pred. No. 7.4e+02;
  Matches   19;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              :||||||||||||||||||||
Db         21 BAAAAAAAAAAAAAAAAAAA 2


RESULT 758
ABX74887/c
ID   ABX74887 standard; DNA; 22 BP.
XX
AC   ABX74887;
XX
DT   21-MAR-2003  (first entry)
XX
DE   Oligo-dT primer used in human CC-RCC invention.
XX
KW   Microarray; solid surface; immobilised probe; CC-RCC;
KW   differential expression profile; aggressive CC-RCC tumour type;
KW   non-aggressive CC-RCC tumour type; clear cell renal carcinoma;
KW   gene expression profiling; tumour tissue; oligo-dT; primer; ss.
XX
OS   Synthetic.
XX
PN   WO200279411-A2.
XX
PD   10-OCT-2002.
XX
PF   29-MAR-2002; 2002WO-US009576.
XX
PR   29-MAR-2001; 2001US-0279411P.
XX
PA   (VAND-) VAN ANDEL INST.
XX
PI   Haab B,  Rhodes D,  Teh BT,  Takashi M;
XX
DR   WPI; 2003-040679/03.
XX
PT   New microarray, comprising a matrix of cDNA probe from a set of probes
PT   immobilized to a solid surface in predetermined order, useful in the
PT   prognosis of patients with clear cell renal carcinoma.
XX
PS   Example 2; Page 30; 179pp; English.
XX
CC   The present invention relates to a microarray comprising a matrix of at
CC   least one cDNA probe from a set of probes immobilised to a solid surface
CC   in a predetermined order, where a row of pixels corresponds to replicates
CC   of one distinct probe from the set. The probes are complementary to
CC   nucleic acid sequences that are expressed differentially in aggressive as
CC   compared to non-aggressive types of clear cell renal carcinoma (CC-RCC)
CC   and that hybridise to the probes under high stringency conditions. The
CC   microarray is useful for the prognosis of patients with CC-RCC, wherein
CC   aggressive and non-aggressive CC-RCC tumour types are characterised by
CC   differential expression profiles of genes that hybridise with one or more
CC   probes immobilised on the microarray. The arrays are useful for gene
CC   expression profiling of tumour and normal tissues. The present sequence
CC   represents an oligo-dT primer used in the examples of the present
CC   invention
XX
SQ   Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 2 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 22;
  Best Local Similarity   95.0%;  Pred. No. 7.4e+02;
  Matches   19;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              :||||||||||||||||||||
Db         21 BAAAAAAAAAAAAAAAAAAA 2


RESULT 759
ACC48484/c
ID   ACC48484 standard; DNA; 22 BP.
XX
AC   ACC48484;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Locked nucleic acid anchored oligo(I) primer ON14.
XX
KW   Locked nucleic acid; LNA; gene therapy; primer; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .21
FT                   /*tag=  m
FT                   /mod_base= um
FT                   /note= "2'-O-methyluridine"
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   3
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   5
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   7
FT                   /*tag=  d
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   9
FT                   /*tag=  e
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   11
FT                   /*tag=  f
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   13
FT                   /*tag=  g
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   15
FT                   /*tag=  h
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   17
FT                   /*tag=  i
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   19
```

```
FT                   /*tag=  j
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   21
FT                   /*tag=  k
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   22
FT                   /*tag=  l
FT                   /mod_base= OTHER
FT                   /note= "OTHER= Compound 17d"
XX
PN   WO2003020739-A2.
XX
PD   13-MAR-2003.
XX
PF   04-SEP-2002; 2002WO-IB003911.
XX
PR   04-SEP-2001; 2001US-0317034P.
PR   22-SEP-2001; 2001US-0323967P.
XX
PA   (EXIQ-) EXIQON AS.
XX
PI   Wengel J,  Kauppinen S;
XX
DR   WPI; 2003-363021/34.
XX
PT   Novel nucleic acid comprising a locked nucleic acid unit having a
PT   modified base that comprises an optionally substituted carbocyclic aryl
PT   moiety, or modified nucleobase or nucleosidic base other than
PT   oxazole/imidazole.
XX
PS   Example 24a; Page 90; 119pp; English.
XX
CC   The present sequence is that of pyrene-anchored locked nucleic acid (LNA)
CC   oligo(dT) primer ON14, which was used in first-strand cDNA synthesis from
CC   eukaryotic mRNA. It includes compound '17d' at its 3' end, which is based
CC   on an LNA-type 2'-O,4'-C-methylene- beta-D-ribofuranosyl moiety. It is
CC   one of a set of such primers (see also ACC48482-85) that were used in an
CC   example from the invention to demonstrate improved reverse transcription
CC   of mRNA using pyrene-LNA anchored oligo(T) primers. The following results
CC   were observed: efficient priming on mRNAs with short poly(A) tails;
CC   efficient anchoring of the oligo(T) primer by pyrene-LNA and LNA-C/G/T
CC   units resulting in an improved T20-VN anchor primer and thus avoiding
CC   reverse transcription of long poly(A) tracts; and improved reverse
CC   transcription of eukaryotic poly(A)+RNA directly from total RNA extracts
CC   due to increased specificity. The invention relates to modified LNA units
CC   that comprise unique base groups. Desirable nucleobase and nucleosidic
CC   base substitutions can mediate universal hybridisation when incorporated
CC   into nucleic acid strands. The novel LNA compounds can be used e.g. as
CC   PCR primers, in sequencing, the synthesis of antisense oligonucleotides,
CC   and in diagnostics
XX
SQ   Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 2 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 22;
  Best Local Similarity   95.0%;  Pred. No. 7.4e+02;
  Matches   19;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              :||||||||||||||||||||
Db         21 BAAAAAAAAAAAAAAAAAAA 2


RESULT 760
ACC48485/c
ID   ACC48485 standard; DNA; 22 BP.
XX
AC   ACC48485;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Locked nucleic acid anchored oligo(I) primer ON15.
XX
KW   Locked nucleic acid; LNA; gene therapy; primer; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   21
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   22
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "OTHER= Compound 17d"
XX
PN   WO2003020739-A2.
XX
PD   13-MAR-2003.
XX
PF   04-SEP-2002; 2002WO-IB003911.
XX
PR   04-SEP-2001; 2001US-0317034P.
PR   22-SEP-2001; 2001US-0323967P.
XX
PA   (EXIQ-) EXIQON AS.
XX
PI   Wengel J,  Kauppinen S;
XX
DR   WPI; 2003-363021/34.
XX
PT   Novel nucleic acid comprising a locked nucleic acid unit having a
PT   modified base that comprises an optionally substituted carbocyclic aryl
PT   moiety, or modified nucleobase or nucleosidic base other than
PT   oxazole/imidazole.
XX
PS   Example 24a; Page 90; 119pp; English.
XX
CC   The present sequence is that of pyrene-anchored locked nucleic acid (LNA)
CC   oligo(dT) primer ON15, which was used in first-strand cDNA synthesis from
CC   eukaryotic mRNA. It includes compound '17d' at its 3' end, which is based
CC   on an LNA-type 2'-O,4'-C-methylene- beta-D-ribofuranosyl moiety. It is
CC   one of a set of such primers (see also ACC48482-84) that were used in an
CC   example from the invention to demonstrate improved reverse transcription
CC   of mRNA using pyrene-LNA anchored oligo(T) primers. The following results
CC   were observed: efficient priming on mRNAs with short poly(A) tails;
CC   efficient anchoring of the oligo(T) primer by pyrene-LNA and LNA-C/G/T
CC   units resulting in an improved T20-VN anchor primer and thus avoiding
CC   reverse transcription of long poly(A) tracts; and improved reverse
CC   transcription of eukaryotic poly(A)+RNA directly from total RNA extracts
CC   due to increased specificity. The invention relates to modified LNA units
CC   that comprise unique base groups. Desirable nucleobase and nucleosidic
CC   base substitutions can mediate universal hybridisation when incorporated
CC   into nucleic acid strands. The novel LNA compounds can be used e.g. as
CC   PCR primers, in sequencing, the synthesis of antisense oligonucleotides,
CC   and in diagnostics
XX
SQ   Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 2 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 22;
  Best Local Similarity   95.0%;  Pred. No. 7.4e+02;
  Matches   19;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              :||||||||||||||||||||
Db         21 BAAAAAAAAAAAAAAAAAAA 2


RESULT 761
ACC48483/c
ID   ACC48483 standard; DNA; 22 BP.
XX
AC   ACC48483;
XX
```

```
DT   11-AUG-2003  (first entry)
XX
DE   Locked nucleic acid anchored oligo(I) primer ON13.
XX
KW   Locked nucleic acid; LNA; gene therapy; primer; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   2
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   8
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   11
FT                   /*tag=  d
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   14
FT                   /*tag=  e
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   17
FT                   /*tag=  f
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   21
FT                   /*tag=  g
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   22
FT                   /*tag=  h
FT                   /mod_base= OTHER
FT                   /note= "OTHER= Compound 17d"
XX
PN   WO2003020739-A2.
XX
PD   13-MAR-2003.
XX
PF   04-SEP-2002; 2002WO-IB003911.
XX
PR   04-SEP-2001; 2001US-0317034P.
PR   22-SEP-2001; 2001US-0323967P.
XX
PA   (EXIQ-) EXIQON AS.
XX
PI   Wengel J,  Kauppinen S;
XX
DR   WPI; 2003-363021/34.
XX
PT   Novel nucleic acid comprising a locked nucleic acid unit having a
PT   modified base that comprises an optionally substituted carbocyclic aryl
PT   moiety, or modified nucleobase or nucleosidic base other than
PT   oxazole/imidazole.
XX
PS   Example 24a; Page 90; 119pp; English.
XX
CC   The present sequence is that of pyrene-anchored locked nucleic acid (LNA)
CC   oligo(dT) primer ON13, which was used in first-strand cDNA synthesis from
CC   eukaryotic mRNA. It includes compound '17d' at its 3' end, which is based
CC   on an LNA-type 2'-O,4'-C-methylene- beta-D-ribofuranosyl moiety. It is
CC   one of a set of such primers (see also ACC48482-85) that were used in an
CC   example from the invention to demonstrate improved reverse transcription
CC   of mRNA using pyrene-LNA anchored oligo(T) primers. The following results
CC   were observed: efficient priming on mRNAs with short poly(A) tails;
CC   efficient anchoring of the oligo(T) primer by pyrene-LNA and LNA-C/G/T
CC   units resulting in an improved T20-VN anchor primer and thus avoiding
CC   reverse transcription of long poly(A) tracts; and improved reverse
CC   transcription of eukaryotic poly(A)+RNA directly from total RNA extracts
CC   due to increased specificity. The invention relates to modified LNA units
CC   that comprise unique base groups. Desirable nucleobase and nucleosidic
CC   base substitutions can mediate universal hybridisation when incorporated
CC   into nucleic acid strands. The novel LNA compounds can be used e.g. as
CC   PCR primers, in sequencing, the synthesis of antisense oligonucleotides,
CC   and in diagnostics
XX
SQ   Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 2 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 22;
  Best Local Similarity   95.0%;  Pred. No. 7.4e+02;
  Matches   19;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              :||||||||||||||||||||
Db         21 BAAAAAAAAAAAAAAAAAAA 2


RESULT 762
AAD51324/c
ID   AAD51324 standard; DNA; 22 BP.
XX
AC   AAD51324;
XX
DT   16-APR-2003  (first entry)
XX
DE   Anchored oligo dT primer used to illustrate the method of the invention.
XX
KW   Laminitis; viral disease; vaccine; bacterial disease; primer; epistaxis;
KW   gastritis; gastric ulcer; respiratory ailment; fracture; joint disease;
KW   musculoskeletal damage; ss.
XX
OS   Unidentified.
XX
PN   WO200290579-A1.
XX
PD   14-NOV-2002.
XX
PF   03-MAY-2002; 2002WO-AU000553.
XX
PR   04-MAY-2001; 2001AU-00004809.
PR   29-JUN-2001; 2001US-00896941.
XX
PA   (GENO-) GENOMICS RES PARTNERS PTY LTD.
XX
PI   Brandon RB;
XX
DR   WPI; 2003-120558/11.
XX
PT   Assessing condition e.g. athletic ability, stage of disease, presence of
PT   drugs, response to exercise, response to vaccines, therapies, nutritional
PT   states, of performance animal involves analyzing nucleic acid expression.
XX
PS   Disclosure; Page 46; 87pp; English.
XX
CC   The invention relates to a method for assessing a condition of a
CC   performance animal. The method involves determining in sample abundance
CC   of expressed target nucleic acid; transmitting digital sample signal to
CC   remote diagnostic server; processing digital sample signal at remotely
CC   located database to correlate digital signal with digital information and
CC   returning report of particular condition of animal. The method is useful
CC   for assessing a condition of a performance animal preferably human, dog
CC   or camel. The condition can be an athletic ability and a condition that
CC   enhances, hinders, impedes or does not change an expected ability of the
CC   performance animal; and also normal, pre-clinical, overt progress and/or
CC   stage of disease, undiagnosed of unclassified conditions, presence of
CC   drugs, response to exercise, response to vaccines, therapies, nutritional
CC   states and response to environmental conditions. Diseases assessed by the
CC   invention include laminitis, lameless, viral or bacterial disease,
CC   gastritis, gastric ulcers, respiratory ailments, fractures, epistaxis,
```

```
CC   musculoskeletal damage or disorders and joint diseases. The present
CC   sequence is a primer used to illustrate the method of the invention
XX
SQ   Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 2 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 22;
  Best Local Similarity   95.0%;  Pred. No. 7.4e+02;
  Matches   19;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              :||||||||||||||||||||
Db         21 BAAAAAAAAAAAAAAAAAAA 2


RESULT 763
ABK13916/c
ID   ABK13916 standard; DNA; 23 BP.
XX
AC   ABK13916;
XX
DT   21-MAY-2002  (first entry)
XX
DE   3'-PCR primer used in method of identifying transcribed genes.
XX
KW   Identification of transcribed gene; mRNA profile; gene expression;
KW   cellular process; fingerprinting; susceptibility to external factor;
KW   development; disease; PCR; primer; ss.
XX
OS   Synthetic.
XX
PN   WO200208461-A2.
XX
PD   31-JAN-2002.
XX
PF   23-JUL-2001; 2001WO-IB001539.
XX
PR   21-JUL-2000; 2000GB-00018016.
PR   21-JUL-2000; 2000US-0219925P.
XX
PA   (GLOB-) GLOBAL GENOMICS AB.
XX
PI   Linnarsson S,  Ernfors P,  Bauren G;
XX
DR   WPI; 2002-217065/27.
XX
PT   Providing mRNA profile, by generating two independent patterns
PT   characteristic of sample mRNA population, analyzing patterns, comparing
PT   gene expression by cell types under varied conditions, and identifying
PT   genes.
XX
PS   Example 2; Page 45; 67pp; English.
XX
CC   The present invention relates to a method for providing a profile of mRNA
CC   molecules present in a sample. The method comprises generating two
CC   independent patterns characteristic of the population of mRNA molecules
CC   expressed in the sample and analysing the patterns using a combinatorial
CC   algorithm, comparing gene expression by different or same cell types
CC   under different conditions, and identifying genes having a role in
CC   various cellular processes. The method is useful for the analysis and
CC   identification of transcribed genes, and fingerprinting. The method can
CC   be used to identify genes which play a role in determining various
CC   cellular processes, including susceptibility to external factors,
CC   development, and disease. The present sequence for a PCR primer is used
CC   in the methods of the present invention
XX
SQ   Sequence 23 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 3 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 23;
  Best Local Similarity   95.0%;  Pred. No. 8.3e+02;
  Matches   19;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              :||||||||||||||||||||
Db         21 BAAAAAAAAAAAAAAAAAAA 2


RESULT 764
ABK48140/c
ID   ABK48140 standard; DNA; 24 BP.
XX
AC   ABK48140;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Aspergillus niger aminopeptidase RT-PCR primer poly-T.
XX
KW   Aminopeptidase; primer; ss; food composition; dough; flavour enhancer;
KW   baked product; cheese; poly-T; reverse transcriptase PCR.
XX
OS   Synthetic.
XX
PN   WO200216618-A1.
XX
PD   28-FEB-2002.
XX
PF   22-AUG-2001; 2001WO-EP009925.
XX
PR   23-AUG-2000; 2000EP-00202995.
XX
PA   (STAM ) DSM NV.
XX
PI   Basten D,  Dekker PJT,  Schuurhuizen PW,  Schaap PJ,  Visser J;
XX
DR   WPI; 2002-257917/30.
XX
PT   An isolated polypeptide with aminopeptidase activity, for preparing food
PT   compositions, such as bread and cheese, with enhanced flavoring.
XX
PS   Example 5; Page 40; 94pp; English.
XX
CC   The invention relates to an isolated polypeptide with aminopeptidase
CC   activity and the gene encoding it (including sequences complimentary to
CC   the gene and which hybridise to it at high stringency), from Aspergillus
CC   niger. Also included are a nucleic acid construct comprising the above
CC   polynucleotide operably linked to one or more control sequences that
CC   direct the production of the polypeptide in a suitable expression host, a
CC   recombinant expression vector comprising the above nucleic acid
CC   construct, a recombinant host cell comprising the above construct or
CC   vector, and producing the protein comprising cultivating an above strain/
CC   recombinant host cell to produce a supernatant and/or cells comprising
CC   the polypeptide and recovering the polypeptide. The aminopeptidase is
CC   used to prepare a food composition such as dough to enhance the flavour
CC   of a baked product from the dough and for preparing a cheese to enhance
CC   the flavour. The invention provides a bacterial enzyme for protein
CC   hydrolysis i.e. with aminopeptidase activity, to produce flavouring
CC   agents, and the enzyme has been isolated and characterised, compared to a
CC   previously observed weak aminopeptidase activity which was detected in an
CC   Aspergillus niger culture filtrate but the source was never isolated or
CC   identified. The use of enzymes to produce flavouring agents from
CC   proteinaceous material is better than use of strong acids which can
CC   severely degrade the amino acids obtained. The present sequence is a
CC   reverse transcriptase (RT)-PCR primer used to investigate the intron-exon
CC   structure of the aminopeptidase gene
XX
SQ   Sequence 24 BP; 0 A; 0 C; 0 G; 23 T; 0 U; 1 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   95.0%;  Pred. No. 9.2e+02;
  Matches   19;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              :||||||||||||||||||||
Db         24 BAAAAAAAAAAAAAAAAAAA 5


RESULT 765
```

```
AAT99286
ID   AAT99286 standard; DNA; 24 BP.
XX
AC   AAT99286;
XX
DT   15-APR-1998  (first entry)
XX
DE   POLYA, a competitor oligonucleotide for binding human PUR-alpha.
XX
KW   PUR element; human; c-myc; inhibitor; hyperproliferative disease; ss;
KW   cancer; probe; hybridisation.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US5672479-A.
XX
PD   30-SEP-1997.
XX
PF   07-JUN-1995;   95US-00486421.
XX
PR   28-AUG-1992;   92US-00938189.
PR   02-FEB-1993;   93US-00014943.
PR   06-JUN-1995;   95US-00470911.
XX
PA   (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX
PI   Bergemann AD,  Johnson EM;
XX
DR   WPI; 1997-488859/45.
XX
PT   Assays for PUR protein ligands or modulators - using immobilised PUR
PT   protein or fragments, to treat hyper-proliferative diseases, e.g. cancer.
XX
PS   Example; Col 33; 64pp; English.
XX
CC   The oligonucleotides AAT99279-T99286 were used as competitor
CC   oligonucleotides for the binding of PUR prtein to DNA. The PUR sequence
CC   can be used to identify chemical or biological compounds that bind to PUR
CC   or binding fragments of PUR. Inhibitors of PUR activity may be used to
CC   treat hyperproliferative diseases such as cancer
XX
SQ   Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 9.2e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
                ||   ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAA 24


RESULT 766
AAV31743
ID   AAV31743 standard; DNA; 24 BP.
XX
AC   AAV31743;
XX
DT   24-SEP-1998  (first entry)
XX
DE   Nucleotide sequence of the oligonucleotide POLYA.
XX
KW   PUR-alpha gene; inhibition; viral infection; cancer; PUR element;
KW   hyperproliferative disease; ss.
XX
OS   Synthetic.
XX
PN   US5756684-A.
XX
PD   26-MAY-1998.
XX
PF   06-JUN-1995;   95US-00470911.
XX
PR   28-AUG-1992;   92US-00938189.
PR   02-FEB-1993;   93US-00014943.
XX
PA   (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX
PI   Bergemann AD,  Johnson EM;
XX
DR   WPI; 1998-321632/28.
XX
PT   PUR protein and its fragments - that inhibit PUR protein binding to PUR
PT   element or other proteins.
XX
PS   Example 7.1.1; Col 33; 63pp; English.
XX
CC   This is the nucleotide sequence of an oligonucleotide used as a
CC   competitor with the PUR element in the method of the invention, involving
CC   the use of the PUR protein and its fragments, which inhibit PUR protein
CC   binding to PUR element or other proteins. Inhibitors of PUR activity may
CC   be useful for treating viral infections and hyperproliferative diseases
CC   such as cancer
XX
SQ   Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 9.2e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
                ||   ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAA 24


RESULT 767
AAX04086
ID   AAX04086 standard; DNA; 24 BP.
XX
AC   AAX04086;
XX
DT   12-APR-1999  (first entry)
XX
DE   Oligonucleotide POLYA used in PUR cloning and sequencing.
XX
KW   PUR element; PUR-alpha; hyperproliferative disease; cancer; human;
KW   monoclonal antibody; identification; characterisation; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US5869622-A.
XX
PD   09-FEB-1999.
XX
PF   07-JUN-1995;   95US-00486809.
XX
PR   28-AUG-1992;   92US-00938189.
PR   02-FEB-1993;   93US-00014943.
PR   06-JUN-1995;   95US-00470911.
XX
PA   (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX
PI   Bergemann AD,  Johnson EM;
XX
DR   WPI; 1999-152881/13.
XX
PT   Monoclonal antibody specific for PUR protein - useful for treating
PT   cancer.
XX
PS   Example; Col 33; 64pp; English.
XX
CC   The present invention describes a monoclonal antibody that specifically
CC   binds to an epitope of the PUR protein. Antibodies that bind to the PUR
CC   protein and neutralise PUR activity may be used to treat
```

```
CC   hyperproliferative diseases such as cancer. PUR antibodies may be used
CC   diagnostically to detect aberrant expression of the PUR protein and/or
CC   mutations in the PUR gene. The present sequence represents an
CC   oligonucleotide used in the cloning and sequencing of the PUR protein and
CC   its sequence element PUR repeat, in an example from the present invention
XX
SQ   Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match              0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 9.2e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAA 24


RESULT 768
AAA40359/c
ID   AAA40359 standard; RNA; 24 BP.
XX
AC   AAA40359;
XX
DT   10-NOV-2000  (first entry)
XX
DE   pBluescriptSK+ phagemid primer SEQ ID NO: 9.
XX
KW   Primer; cloning; ligation; ss.
XX
OS   Synthetic.
XX
PN   WO200036088-A1.
XX
PD   22-JUN-2000.
XX
PF   17-DEC-1999;   99WO-US030277.
XX
PR   17-DEC-1998;   98US-00213834.
XX
PA   (ROMA/) ROMANTCHIKOV Y.
XX
PI   Romantchikov Y;
XX
DR   WPI; 2000-442381/38.
XX
PT   Inserting a nucleic acid into a circular vector comprising joining their
PT   ends, melting, and reannealing ends at two different concentrations,
PT   useful for cloning small amounts of nucleic acids and forming genomic
PT   libraries.
XX
PS   Example 3; Page 67; 71pp; English.
XX
CC   This invention describes a novel method (M1) for inserting a nucleic acid
CC   (N1) into a circular vector (V1) comprising joining ends of N1 and V1
CC   under a first nucleic acid concentration, melting hybridized cohesive
CC   circularization ends, and reannealing the ends at a second concentration.
CC   The methods are useful for the cloning small amounts of nucleic acids and
CC   forming genomic libraries of complex populations of DNA or cDNA. The
CC   methods allow the cloning of minute amounts of nucleic acids efficiently
CC   and avoids the size selection problems of prior art systems. Larger
CC   nucleic acid fragments are just as easily cloned, allowing highly
CC   representative libraries to be made. Vector to vector ligation is avoided
CC   using the methods. AAA40351-A40366 represents primers used to illustrate
CC   the method of the invention
XX
SQ   Sequence 24 BP; 0 A; 0 C; 0 G; 16 T; 8 U; 0 Other;

  Query Match              0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 9.2e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db         24 AAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 769
AAA40353/c
ID   AAA40353 standard; DNA; 24 BP.
XX
AC   AAA40353;
XX
DT   10-NOV-2000  (first entry)
XX
DE   pBluescriptSK+ phagemid primer SEQ ID NO: 3.
XX
KW   Primer; cloning; ligation; ss.
XX
OS   Synthetic.
XX
PN   WO200036088-A1.
XX
PD   22-JUN-2000.
XX
PF   17-DEC-1999;   99WO-US030277.
XX
PR   17-DEC-1998;   98US-00213834.
XX
PA   (ROMA/) ROMANTCHIKOV Y.
XX
PI   Romantchikov Y;
XX
DR   WPI; 2000-442381/38.
XX
PT   Inserting a nucleic acid into a circular vector comprising joining their
PT   ends, melting, and reannealing ends at two different concentrations,
PT   useful for cloning small amounts of nucleic acids and forming genomic
PT   libraries.
XX
PS   Example 1; Page 66; 71pp; English.
XX
CC   This invention describes a novel method (M1) for inserting a nucleic acid
CC   (N1) into a circular vector (V1) comprising joining ends of N1 and V1
CC   under a first nucleic acid concentration, melting hybridized cohesive
CC   circularization ends, and reannealing the ends at a second concentration.
CC   The methods are useful for the cloning small amounts of nucleic acids and
CC   forming genomic libraries of complex populations of DNA or cDNA. The
CC   methods allow the cloning of minute amounts of nucleic acids efficiently
CC   and avoids the size selection problems of prior art systems. Larger
CC   nucleic acid fragments are just as easily cloned, allowing highly
CC   representative libraries to be made. Vector to vector ligation is avoided
CC   using the methods. AAA40351-A40366 represents primers used to illustrate
CC   the method of the invention
XX
SQ   Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

  Query Match              0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 9.2e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db         24 AAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 770
AAF99756/c
ID   AAF99756 standard; DNA; 24 BP.
XX
AC   AAF99756;
XX
DT   12-JUN-2001  (first entry)
XX
DE   Immunostimulatory nucleic acid #872.
XX
KW   Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
```

KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200122972-A2.
XX
PD 05-APR-2001.
XX
PF 25-SEP-2000; 2000WO-US026383.
XX
PR 25-SEP-1999; 99US-0156113P.
PR 27-SEP-1999; 99US-0156135P.
PR 23-AUG-2000; 2000US-0227436P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
XX
PI Krieg AM, Schetter C, Vollmer J;
XX
DR WPI; 2001-273485/28.
XX
PT Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids.
XX
PS Claim 101; Page 57; 338pp; English.
XX
CC The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells. Note: the
CC present sequence may have a phosphorothioate backbone
XX
SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 9.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
|| |||||||||||||||||||
Db 24 AAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 771
AAF99304/c
ID AAF99304 standard; DNA; 24 BP.
XX
AC AAF99304;
XX
DT 12-JUN-2001 (first entry)
XX
DE Immunostimulatory nucleic acid #420.
XX
KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200122972-A2.
XX
PD 05-APR-2001.
XX
PF 25-SEP-2000; 2000WO-US026383.
XX
PR 25-SEP-1999; 99US-0156113P.
PR 27-SEP-1999; 99US-0156135P.
PR 23-AUG-2000; 2000US-0227436P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
XX
PI Krieg AM, Schetter C, Vollmer J;
XX
DR WPI; 2001-273485/28.
XX
PT Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids.
XX
PS Claim 101; Page 46; 338pp; English.
XX
CC The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells. Note: the
CC present sequence may have a phosphorothioate backbone
XX
SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 9.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
|| |||||||||||||||||||
Db 24 AAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 772
AAF99757
ID AAF99757 standard; DNA; 24 BP.
XX
AC AAF99757;
XX
DT 12-JUN-2001 (first entry)
XX
DE Immunostimulatory nucleic acid #873.
XX
KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200122972-A2.
XX
PD 05-APR-2001.
XX
PF 25-SEP-2000; 2000WO-US026383.
XX
PR 25-SEP-1999; 99US-0156113P.
PR 27-SEP-1999; 99US-0156135P.
PR 23-AUG-2000; 2000US-0227436P.
XX

PA (IOWA) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
XX
PI Krieg AM, Schetter C, Vollmer J;
XX
DR WPI; 2001-273485/28.
XX
PT Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids.
XX
PS Claim 101; Page 57; 338pp; English.
XX
CC The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells. Note: the
CC present sequence may have a phosphorothioate backbone
XX
SQ Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 9.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
|| ||||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAA 24

RESULT 773
ABV14842/c
ID ABV14842 standard; cDNA; 24 BP.
XX
AC ABV14842;
XX
DT 13-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 14833.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US005171.
XX
PR 17-FEB-2000; 2000US-0183319P.
PR 16-MAR-2000; 2000US-0189862P.
PR 25-MAY-2000; 2000US-0207454P.
PR 09-JUN-2000; 2000US-0211314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI; 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.
XX
PS Claim 1; Page 2483; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
XX
SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 9.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
|| ||||||||||||||||||||
Db 24 AAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 774
ABS78477/c
ID ABS78477 standard; DNA; 24 BP.
XX
AC ABS78477;
XX
DT 13-DEC-2002 (first entry)
XX
DE Angiogenesis inhibitory oligonucleotide #961.
XX
KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW plaque neovascularisation; telangiectasia; haemophiliac joint;
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW scleroderma; hypertrophic scar.
XX
OS Synthetic.
XX
PN WO200253141-A2.
XX
PD 11-JUL-2002.
XX
PF 14-DEC-2001; 2001WO-US048458.
XX
PR 14-DEC-2000; 2000US-0255534P.
XX
PA (COLE-) COLEY PHARM GROUP INC.
XX
PI Bratzler RL;
XX
DR WPI; 2002-566690/60.
XX
PT Inhibiting angiogenesis in a subject, involves administering at least one
PT antiangiogenic nucleic acid molecule to the subject.
XX
PS Claim 2; Page 36; 276pp; English.
XX
CC The invention relates to inhibiting angiogenesis in a subject, comprising
CC administering at least one antiangiogenic nucleic acid molecule. Also
CC included is a kit comprising a first container housing the antiangiogenic
CC nucleic acids, and instructions for administering them to a subject

```
CC   having a condition characterised by unwanted angiogenesis. The method is
CC   useful for inhibiting angiogenesis associated with solid tumour growth,
CC   tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC   diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC   corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC   rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC   neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,
CC   wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC   hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC   acid of the invention
XX
SQ   Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 9.2e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||
Db         24 AAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 775
ABS77949/c
ID   ABS77949 standard; DNA; 24 BP.
XX
AC   ABS77949;
XX
DT   13-DEC-2002  (first entry)
XX
DE   Angiogenesis inhibitory oligonucleotide #433.
XX
KW   Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW   tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW   diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW   corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW   rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW   plaque neovascularisation; telangiectasia; haemophiliac joint;
KW   angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW   scleroderma; hypertrophic scar.
XX
OS   Synthetic.
XX
PN   WO200253141-A2.
XX
PD   11-JUL-2002.
XX
PF   14-DEC-2001; 2001WO-US048458.
XX
PR   14-DEC-2000; 2000US-0255534P.
XX
PA   (COLE-) COLEY PHARM GROUP INC.
XX
PI   Bratzler RL;
XX
DR   WPI; 2002-566690/60.
XX
PT   Inhibiting angiogenesis in a subject, involves administering at least one
PT   antiangiogenic nucleic acid molecule to the subject.
XX
PS   Claim 2; Page 27; 276pp; English.
XX
CC   The invention relates to inhibiting angiogenesis in a subject, comprising
CC   administering at least one antiangiogenic nucleic acid molecule. Also
CC   included is a kit comprising a first container housing the antiangiogenic
CC   nucleic acids, and instructions for administering them to a subject
CC   having a condition characterised by unwanted angiogenesis. The method is
CC   useful for inhibiting angiogenesis associated with solid tumour growth,
CC   tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC   diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC   corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC   rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC   neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,
CC   wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC   hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC   acid of the invention
XX
SQ   Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 9.2e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||
Db         24 AAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 776
ABS78478
ID   ABS78478 standard; DNA; 24 BP.
XX
AC   ABS78478;
XX
DT   13-DEC-2002  (first entry)
XX
DE   Angiogenesis inhibitory oligonucleotide #962.
XX
KW   Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW   tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW   diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW   corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW   rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW   plaque neovascularisation; telangiectasia; haemophiliac joint;
KW   angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW   scleroderma; hypertrophic scar.
XX
OS   Synthetic.
XX
PN   WO200253141-A2.
XX
PD   11-JUL-2002.
XX
PF   14-DEC-2001; 2001WO-US048458.
XX
PR   14-DEC-2000; 2000US-0255534P.
XX
PA   (COLE-) COLEY PHARM GROUP INC.
XX
PI   Bratzler RL;
XX
DR   WPI; 2002-566690/60.
XX
PT   Inhibiting angiogenesis in a subject, involves administering at least one
PT   antiangiogenic nucleic acid molecule to the subject.
XX
PS   Claim 2; Page 36; 276pp; English.
XX
CC   The invention relates to inhibiting angiogenesis in a subject, comprising
CC   administering at least one antiangiogenic nucleic acid molecule. Also
CC   included is a kit comprising a first container housing the antiangiogenic
CC   nucleic acids, and instructions for administering them to a subject
CC   having a condition characterised by unwanted angiogenesis. The method is
CC   useful for inhibiting angiogenesis associated with solid tumour growth,
CC   tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC   diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC   corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC   rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC   neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,
CC   wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC   hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC   acid of the invention
XX
SQ   Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
```

```
  Best Local Similarity   87.5%;  Pred. No. 9.2e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAA 24


RESULT 777
ABL39405/c
ID   ABL39405 standard; DNA; 24 BP.
XX
AC   ABL39405;
XX
DT   16-APR-2002  (first entry)
XX
DE   Immunostimulatory nucleic acid SEQ ID NO: 841.
XX
KW   Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
KW   angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .24
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "phosphorothioate backbone"
XX
PN   WO200197843-A2.
XX
PD   27-DEC-2001.
XX
PF   22-JUN-2001; 2001WO-US020154.
XX
PR   22-JUN-2000; 2000US-0213346P.
XX
PA   (IOWA ) UNIV IOWA RES FOUND.
XX
PI   Weiner G,  Hartmann G;
XX
DR   WPI; 2002-154611/20.
XX
PT   Treating or preventing cancer, such as basal cell carcinoma, comprises
PT   administering immunostimulatory nucleic acids that induce expression of
PT   cell surface antigens and antibodies to a subject having or at risk of
PT   developing cancer.
XX
PS   Disclosure; Page 309; 312pp; English.
XX
CC   The present invention relates to methods for treating or preventing
CC   cancer, involving administering to a subject having or at risk of
CC   developing cancer immunostimulatory nucleic acids that induce expression
CC   of cell surface antigens and antibodies. The methods are useful for
CC   treating or preventing cancer such as basal cell carcinoma, bladder
CC   cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC   breast cancer, cervical cancer, colon and rectum cancer, connective
CC   tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx
CC   cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
CC   Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC   cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC   cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC   present sequence is an immunostimulatory oligonucleotide described in the
CC   exemplification of the invention
XX
SQ   Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 9.2e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAA 24


RESULT 778
ABA98840
ID   ABA98840 standard; DNA; 24 BP.
XX
AC   ABA98840;
XX
DT   01-JUL-2002  (first entry)
XX
DE   A24 oligonucleotide for the creation of Pc-A24.
XX
KW   Component detection; clinical diagnosis; cell detection; drug detection;
KW   metabolite detection; pesticide detection; ligand detection; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    24
FT                    /*tag=  a
FT                    /label= OTHER
FT                    /note= "modified by PO2OCH2CH2CH2SSCH2CH2CH2OH"
XX
PN   WO200184157-A2.
XX
PD   08-NOV-2001.
XX
PF   03-MAY-2001; 2001WO-US014528.
XX
PR   04-MAY-2000; 2000US-00564230.
XX
PA   (DADE-) DADE BEHRING INC.
XX
PI   Pease JS,  Cromer R,  Patel R,  Kurn N,  De Keczer S;
XX
DR   WPI; 2002-164078/21.
XX
PT   Detection of multiple analytes, e.g. ligands, receptors, polynucleotides
PT   and pollutants, involves adding a combination of sensitizer reagents and
PT   reactive reagent Actuatable by a product of the sensitizer reagents.
XX
PS   Example; Page 58; 87pp; English.
XX
CC   The invention relates to the detection of multiple components in a
CC   medium, comprising combining the medium with at least two sensitiser
CC   reagents, and at least one reactive reagent activated by a product
CC   generated by the sensitiser reagents when activated; and differentially
CC   activating the sensitiser reagents. The combination of sensitiser
CC   reagents and reactive reagent(s) allows differential detection of the
CC   components. Methods of the invention may be used for the detection of
CC   ligands, receptors and polynucleotides, and also for the detection of
CC   e.g. cells, various drugs, metabolites, pesticides (e.g. polyhalogenated
CC   biphenyls, phosphate esters, thiophosphates, carbamates and
CC   polyhalogenated sulfenamides) and pollutants. Methods of the invention
CC   allow the detection of multiple analytes in a single test medium. An
CC   application of the methods of the present invention would be in the field
CC   of clinical diagnostics. The current sequence represents A24
CC   oligonucleotide for the creation of oligonucleotide coated phthalocyanine
CC   sensitiser particles (Pc-A24)
XX
SQ   Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 9.2e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAA 24


RESULT 779
```

```
AAS17869
ID   AAS17869 standard; DNA; 24 BP.
XX
AC   AAS17869;
XX
DT   08-MAY-2002  (first entry)
XX
DE   A24 oligonucleotide used to create dopTAR chemiluminescer particles.
XX
KW   Polymorphism detection; sequence detection; mutation detection; A24;
KW   probe; non-dissociative termolecular complex; dopTAR sensitiser particle;
KW   single nucleotide polymorphism; SNP; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   24
FT                   /*tag=  a
FT                   /note= "A is covalently linked to a
FT                   PO2OCH2CH2CH2SSCH2CH2CH2OH moiety"
XX
PN   WO200190399-A2.
XX
PD   29-NOV-2001.
XX
PF   17-MAY-2001; 2001WO-US016089.
XX
PR   19-MAY-2000; 2000US-00574596.
XX
PA   (DADE-) DADE BEHRING INC.
XX
PI   Patel RD;
XX
DR   WPI; 2002-097664/13.
XX
PT   Detecting presence of polynucleotide, differences between polynucleotide
PT   sequences, useful for detecting single nucleotide polymorphism and
PT   alleles of polynucleotide sequence involves use of three competitive
PT   probes.
XX
PS   Example; Page 47; 75pp; English.
XX
CC   This invention represents a method for detecting the presence of a
CC   polynucleotide sequence, differences in polynucleotide sequences or
CC   mutations in genomic DNA. The method involves contacting 3
CC   oligonucleotide probes with a sample containing a polynucleotide. The
CC   first probe hybridises to a region of the polynucleotide sequence and the
CC   second and third probes can bind a second region of the polynucleotide
CC   sequence. The second and third probes are identical except for the
CC   presence or difference of one or more nucleotides. The reaction medium is
CC   then subjected to conditions for forming substantially non-dissociative
CC   termolecular complexes, which can be at least one of, the polynucleotide
CC   sequence with the first and second probes or the polynucleotide sequence
CC   with the first and third probes. The oligonucleotide probes have labels
CC   non-covalently bound to allow for their detection upon binding. The
CC   method of the invention is useful for detecting the presence of a single
CC   nucleotide polymorphism (SNP) in a fragment of genomic DNA. The method
CC   can be used for the direct detection of nucleic acid in very small
CC   quantities without amplification. In addition, the method may be carried
CC   out with amplification of the target and reference sequences. This
CC   sequence represents an oligonucleotide probe A24 used to create dopTAR
CC   chimiluminescer sensitiser particles in the method of the invention.
CC   Binding the nucleic acid to a suspendable particle acts as a support and
CC   provides a means of segregating the bound polynucleotide target from the
CC   bulk solution
XX
SQ   Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 9.2e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
                 ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAA 24


RESULT 780
ABK15639/c
ID   ABK15639 standard; DNA; 24 BP.
XX
AC   ABK15639;
XX
DT   08-MAY-2002  (first entry)
XX
DE   RNA-PCR procedure primer poly(dT)24.
XX
KW   RNA-PCR; primer; ss; poly(dT)24; cytostatic; antibacterial; gene therapy;
KW   mRNA-cDNA hybrid; gene function inhibition; cancer; PTGS; antisense;
KW   high throughput screening; D-RNAi; DNA-RNA interference; RdRp;
KW   RNA dependent RNA polymerase; posttranscriptional gene silencing.
XX
OS   Synthetic.
XX
PN   WO200210374-A2.
XX
PD   07-FEB-2002.
XX
PF   02-AUG-2001; 2001WO-US024412.
XX
PR   02-AUG-2000; 2000US-0222479P.
XX
PA   (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI   Lin S,  Chuong C,  Widelitz RB;
XX
DR   WPI; 2002-188740/24.
XX
PT   Generating mRNA-cDNA hybrids for suppressing cancer-related genes, or
PT   treating or preventing microbe related genes, comprises thermocycling
PT   steps of promoter-linked double-stranded cDNA or RNA synthesis.
XX
PS   Example 5; Page 26; 53pp; English.
XX
CC   The invention relates to generating mRNA-cDNA hybrids, comprising (a)
CC   providing a solution containing a nucleic acid template, one or more
CC   primers complementary to the sense conformation of the nucleic acid
CC   template, and one or more promoter-linked primers complementary to the
CC   antisense conformation of the nucleic acid template, and with an RNA
CC   promoter, (b) treating the nucleic acid template with the one of more
CC   primers to synthesise a first cDNA strand, (c) treating the first cDNA
CC   strand with one or more promoter-linked primers to synthesise a promoter-
CC   linked double-stranded nucleic acid, (d) treating the promoter-linked
CC   double-stranded nucleic acid to synthesise amplified mRNA fragments and
CC   (e) treating the mRNA fragments with one or more primers to synthesise
CC   mRNA-cDNA hybrids by reverse transcription of the amplified mRNA
CC   fragments. The method is useful for preparing high amounts of pure and
CC   specific mRNA-cDNA hybrids for transducing biological effects of interest
CC   in vitro as well as in vivo, for inhibiting gene function in prokaryotes
CC   and eukaryotes in vivo and in vitro, for suppressing cancer-related
CC   genes, in treating or preventing microbe related genes, in studying
CC   candidate molecular pathways with systematic knock out of involved
CC   molecules, in high throughput screening of gene functions based on
CC   microarray analysis, and as a tool in studying gene function in
CC   physiological conditions. The mRNA-cDNA hybrids may be used to screen for
CC   special gene functions, for manipulating gene expression in vitro, and
CC   for designing therapy for genetic diseases in vivo. The cDNA part of a D-
CC   RNAi (DNA-RNA interference) can be modified by nucleotide analogue
CC   incorporation to increase the stability and effectiveness of transfected
CC   probe activities. The RdRp (RNA dependent RNA polymerase) enzyme may
CC   provide higher affinity of the mRNA template of a D-RNAi compared to ds-
CC   RNA due to lower binding interaction between DNA-RNA duplexes than RNA-
CC   RNA duplexes. The cDNA part of a D-RNAi provides further antisense gene
CC   knockout activity in addition to the posttranscriptional gene silencing
CC   (PTGS) mechanisms of the sense-RNA template, resulting in multiple
CC   specific gene interference effects with one probe. The present sequence
```

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CC   is a poly(dT) PCR primer used in conjunction with oligo(dC)10N primers to
CC   reverse transcribe mRNA into first strand cDNA in the method of the
CC   invention
XX
SQ   Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 9.2e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db         24 AAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 781
ACA58802/c
ID   ACA58802 standard; DNA; 24 BP.
XX
AC   ACA58802;
XX
DT   10-JUN-2003  (first entry)
XX
DE   Gastric ulcer treatment immunostimulatory nucleic acid #148.
XX
KW   Gastric ulcer; ss; immunostimulant; equine gastric ulcer syndrome; EGUS;
KW   Heliobacter pylori.
XX
OS   Synthetic.
XX
PN   US2002198165-A1.
XX
PD   26-DEC-2002.
XX
PF   01-AUG-2001; 2001US-00920313.
XX
PR   01-AUG-2000; 2000US-0222248P.
XX
PA   (BRAT/) BRATZLER R L.
PA   (PETE/) PETERSEN D M.
XX
PI   Bratzler RL,  Petersen DM;
XX
DR   WPI; 2003-370798/35.
XX
PT   Prevention or treatment of gastric ulcer involves administering nucleic
PT   acid.
XX
PS   Disclosure; Page 14; 45pp; English.
XX
CC   The invention relates to a method of prevention or treatment of gastric
CC   ulcer comprising administering a nucleic acid to a subject in need for
CC   treatment of gastric ulcer. A nucleic acid sample comprising
CC   oligonucleotide 2006 was administered to a mouse model by an oral route
CC   or a vehicle control. Colonisation of mice by Heliobacter pylori was
CC   assessed at time points from 1 day to 1 month after treatment. The
CC   ability of the nucleic acid to reduce H. pylori colonisation was
CC   assessed. The method is useful for preventing or treating a gastric ulcer
CC   on a subject e.g. human or non-human vertebrate animal including dog,
CC   cat, horse (equine gastric ulcer syndrome, EGUS), cow, goat, sheep, pig,
CC   rabbit, turkey, chicken, primate, rat and mouse. The method effectively
CC   treats or prevents gastric ulcers. The present sequence represents an
CC   immunostimulatory nucleic acid for the treatment of gastric ulcers
XX
SQ   Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 9.2e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db         24 AAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 782
ABZ80181/c
ID   ABZ80181 standard; DNA; 24 BP.
XX
AC   ABZ80181;
XX
DT   23-MAY-2003  (first entry)
XX
DE   Immunostimulatory oligonucleotide SEQ ID NO:53.
XX
KW   Immunostimulation; immune response; natural killer cell; interferon;
KW   type 1 interferon; IFN; cancer; infectious disease; allergic disorder;
KW   immune related disorder; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .24
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "optionally phosphorothioate backbone"
XX
PN   WO2003015711-A2.
XX
PD   27-FEB-2003.
XX
PF   19-AUG-2002; 2002WO-US026468.
XX
PR   17-AUG-2001; 2001US-0313273P.
PR   03-JUL-2002; 2002US-0393952P.
XX
PA   (COLE-) COLEY PHARM GROUP INC.
PA   (COLE-) COLEY PHARM GMBH.
PA   (IOWA ) UNIV IOWA RES FOUND.
XX
PI   Krieg AM,  Vollmer J,  Ulhman E;
XX
DR   WPI; 2003-268241/26.
XX
PT   New immunostimulatory nucleic acid, useful for preparing a composition
PT   for treating an allergic condition.
XX
PS   Example 1; Page 44; 115pp; English.
XX
CC   The present invention describes immunostimulatory nucleic acids of 14-100
CC   nucleotides in length comprising the formula 5' X1DCGHX2 3' (I), where X1
CC   or X2 = independently any sequence 0-10 nucleotides; D = nucleotide other
CC   than C; C = cytosine; G = guanine; H = nucleotide other than G. The
CC   immunostimulatory nucleic acid further comprises a sequence consisting of
CC   P and N positioned immediately 5' to X1 or 3' to X2 and N is a B cell
CC   neutralising sequence, where N begins with a CGG trinucleotide and is at
CC   least 10 nucleotides long and P is GC-rich palindrome containing sequence
CC   at least 10 nucleotides long. Also described: (1) a pharmaceutical
CC   composition comprising the immunostimulatory nucleic acid and a carrier;
CC   and (2) treating an allergic condition. (I) has antiallergic activity and
CC   can be used in gene therapy. (I) can be used for preparing a composition
CC   for treating a variety of immune related disorders such as cancer,
CC   infectious diseases and allergic disorders. (I) also stimulates the
CC   activation of natural killer cells and the production of type 1
CC   interferon (IFN). The present sequence represents an immunostimulatory
CC   oligonucleotide, which is used in an example from the present invention
XX
SQ   Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 9.2e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db         24 AAAAAAAAAAAAAAAAAAAAAAAA 1
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RESULT 783
ACA62284/c
ID   ACA62284 standard; DNA; 24 BP.
XX
AC   ACA62284;
XX
DT   12-AUG-2003  (first entry)
XX
DE   Oligo (dT)24 RT-PCR primer.
XX
KW   ss; PCR; RT-PCR; primer; reverse transcriptase PCR; antisense therapy;
KW   mRNA expression profile; promoter containing primer.
XX
OS   Synthetic.
XX
PN   US2003022318-A1.
XX
PD   30-JAN-2003.
XX
PF   07-SEP-2001; 2001US-00949305.
XX
PR   25-JAN-2000; 2000US-00494212.
XX
PA   (EPIC-) EPICLONE INC.
XX
PI   Lin S,  Ying S;
XX
DR   WPI; 2003-479488/45.
XX
PT   Improved polymerase thermocycling reaction for nucleic acid
PT   amplification, by thermal cycling of promoter-linked nucleic acid
PT   template synthesis and in vitro transcriptional amplification of nucleic
PT   acid sequences.
XX
PS   Example 7; Page 14; 28pp; English.
XX
CC   The invention relates to an improved polymerase thermocycling reaction
CC   (M1) for linear amplification of nucleic acid sequences, involves
CC   denaturing a number of nucleic acid templates (I), combining the
CC   denatured (I) with a promoter-containing primer (P1), a primer (P2), a
CC   number of deoxynucleotide triphosphates and ribonucleotide triphosphates,
CC   a reverse transcription enzyme, a DNA-dependent DNA polymerase and RNA
CC   polymerase, contacting P1 with (I) to generate a number of promoter-
CC   containing templates, denaturing the promoter-containing templates,
CC   contacting P2 with the denatured promoter-containing templates to
CC   generate a number of promoter-containing double-stranded DNA templates,
CC   where the double-stranded nucleic acid templates are flanked by P1 in one
CC   end and P2 in the other end of the other orientation, transcribing the
CC   promoter-containing double-stranded DNA templates to form a number of
CC   amplified RNA sequences, including the primer region of the promoter-
CC   containing double-stranded DNA templates, contacting the amplified RNA
CC   sequences with P2 to form a number of cDNAs and a number of DNA-RNA
CC   hybrid templates, and denaturing the DNA-RNA hybrid templates. The method
CC   is useful for improved polymerase thermocycling reaction for linear
CC   amplification of nucleic acid sequences, and thus for producing mRNA
CC   expression profile of a cell by M1 to generate multiple copies of the
CC   mRNA. M1 is also useful for determining aberrant protein production of
CC   cells in a diseased state, by generating an expression profile by the
CC   above method, of cells in both normal and diseased states, comparing the
CC   expression profile of the cells in the normal and diseased states,
CC   determining the differences in mRNA composition of the cell(s) in the
CC   diseased state, isolating the mRNA sequences of cell(s) in the diseased
CC   state that differ from mRNA in cell(s) in non-diseased state, amplifying
CC   the isolated mRNA by M1, and determining aberrant protein function of the
CC   protein coded for by the isolated mRNA. M1 is also useful for treating a
CC   cell in a diseased state caused by aberrant protein production, by
CC   determining protein expression of a cell in a diseased state, determining
CC   the mRNA sequence for the aberrant proteins, synthesising an antisense
CC   sequence of the mRNA, amplifying the antisense mRNA sequences by M1, and
CC   delivering a pharmaceutically effective dosage of a composition
CC   comprising the anti-sense mRNA and a compatible lipid based biological
CC   carrier. M1 is also useful for predicting the efficacy of a proposed drug
CC   targeted against an aberrant protein, by determining aberrant protein
CC   production of cell in a diseased state by the above method, amplifying
CC   the aberrant protein by M1 and using recombinant techniques to determine
CC   the effect of proposed drug on the aberrant protein. M1 is also useful
CC   for differential screening of tissue-specific gene expression at a
CC   cellular level, for preparing labeled RNA/DNA probes for a gene chip
CC   technology, and for determining the efficacy of a drug regiment against a
CC   gene or its cDNAs. The present sequence is an Oligo (dT)24 RT-(reverse
CC   transcriptase) PCR primer used to produce first strand cDNA in the method
CC   of the invention
XX
SQ   Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 9.2e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
                ||   ||||||||||||||||||
Db         24 AAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 784
ACD99729/c
ID   ACD99729 standard; DNA; 24 BP.
XX
AC   ACD99729;
XX
DT   25-SEP-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #415.
XX
KW   Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW   antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW   psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW   inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS   Synthetic.
XX
PN   US2003050268-A1.
XX
PD   13-MAR-2003.
XX
PF   29-MAR-2002; 2002US-00112653.
XX
PR   29-MAR-2001; 2001US-0279642P.
XX
PA   (KRIE/) KRIEG A M.
PA   (BERG/) BERG D J.
XX
PI   Krieg AM,  Berg DJ;
XX
DR   WPI; 2003-521815/49.
XX
PT   Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT   allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT   disease by administering an immunostimulatory nucleic acid.
XX
PS   Disclosure; Page 20; 229pp; English.
XX
CC   The invention describes a method of treating non-allergic inflammatory
CC   disease comprising administering to a subject having or at risk of
CC   developing a non-allergic inflammatory disease an immunostimulatory
CC   nucleic acid for prevention or treatment of the disease. The method is
CC   useful for treating non-allergic inflammatory diseases, such as
CC   psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC   inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC   This sequence represents an immunostimulatory nucleic acid
XX
SQ   Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
```

```
  Best Local Similarity   87.5%;  Pred. No. 9.2e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db         24 AAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 785
ACH03285
ID   ACH03285 standard; DNA; 24 BP.
XX
AC   ACH03285;
XX
DT   25-SEP-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #920.
XX
KW   Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW   antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW   psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW   inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS   Synthetic.
XX
PN   US2003050268-A1.
XX
PD   13-MAR-2003.
XX
PF   29-MAR-2002; 2002US-00112653.
XX
PR   29-MAR-2001; 2001US-0279642P.
XX
PA   (KRIE/) KRIEG A M.
PA   (BERG/) BERG D J.
XX
PI   Krieg AM,  Berg DJ;
XX
DR   WPI; 2003-521815/49.
XX
PT   Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT   allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT   disease by administering an immunostimulatory nucleic acid.
XX
PS   Disclosure; Page 34; 229pp; English.
XX
CC   The invention describes a method of treating non-allergic inflammatory
CC   disease comprising administering to a subject having or at risk of
CC   developing a non-allergic inflammatory disease an immunostimulatory
CC   nucleic acid for prevention or treatment of the disease. The method is
CC   useful for treating non-allergic inflammatory diseases, such as
CC   psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC   inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC   This sequence represents an immunostimulatory nucleic acid
XX
SQ   Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 9.2e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAA 24


RESULT 786
ACH03284/c
ID   ACH03284 standard; DNA; 24 BP.
XX
AC   ACH03284;
XX
DT   25-SEP-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #919.
XX
KW   Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW   antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW   psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW   inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS   Synthetic.
XX
PN   US2003050268-A1.
XX
PD   13-MAR-2003.
XX
PF   29-MAR-2002; 2002US-00112653.
XX
PR   29-MAR-2001; 2001US-0279642P.
XX
PA   (KRIE/) KRIEG A M.
PA   (BERG/) BERG D J.
XX
PI   Krieg AM,  Berg DJ;
XX
DR   WPI; 2003-521815/49.
XX
PT   Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT   allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT   disease by administering an immunostimulatory nucleic acid.
XX
PS   Disclosure; Page 34; 229pp; English.
XX
CC   The invention describes a method of treating non-allergic inflammatory
CC   disease comprising administering to a subject having or at risk of
CC   developing a non-allergic inflammatory disease an immunostimulatory
CC   nucleic acid for prevention or treatment of the disease. The method is
CC   useful for treating non-allergic inflammatory diseases, such as
CC   psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC   inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC   This sequence represents an immunostimulatory nucleic acid
XX
SQ   Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 9.2e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db         24 AAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 787
ADA66379
ID   ADA66379 standard; mRNA; 24 BP.
XX
AC   ADA66379;
XX
DT   20-NOV-2003  (first entry)
XX
DE   mRNA poly A.
XX
KW   ss; nucleic acid amplification; multiple step elimination;
KW   varying reaction condition elimination; poly A tract.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   primer_bind     1. .24
FT                   /*tag=  a
FT                   /note= "Binds to nucleotides 42-19 of the 1st strand cDNA
FT                   synthesis primer"
XX
PN   US6582938-B1.
```

XX
PD 24-JUN-2003.
XX
PF 11-MAY-2001; 2001US-00854317.
XX
PR 11-MAY-2001; 2001US-00854317.
XX
PA (AFFY-) AFFYMETRIX INC.
XX
PI Su X, Dong H, Ryder TB;
XX
DR WPI; 2003-656427/62.
XX
PT Amplification of nucleic acids, where the promoter is blocked from
PT extension at the 3' end, useful for eliminating multiple step reactions.
XX
PS Disclosure; Fig 2; 9pp; English.
XX
CC The invention relates to a method of amplification of nucleic acid which
CC comprises primer extension by reverse transcriptase and hybridising an
CC oligonucleotide to the single stranded DNA, where the oligonucleotide is
CC blocked from extension at the 3' end. The method is useful for
CC amplification of nucleic acids. In the new method, a promoter is
CC protected from degradation throughout the method. The promoter is
CC constructed so that it does not serve as a primer for extension of a
CC sequence that is complementary to the target sequence, i.e. it is
CC blocked. The method can be combined with other processes to eliminate the
CC need for multiple steps and varying reaction conditions and their
CC associated problems. At least three otherwise separate enzymatic
CC reactions can occur consecutively in one phase (i.e., without organic
CC extraction and precipitation), more preferably in the same reaction
CC vessel. Preferably, cDNA synthesis according to the new method may occur
CC in a modified low salt buffer. The present sequence represents the poly A
CC tract of a mRNA used to illustrate the method of the invention.
XX
SQ Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 9.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
|| |||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAA 24

RESULT 788
ADB37258/c
ID ADB37258 standard; DNA; 24 BP.
XX
AC ADB37258;
XX
DT 04-DEC-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #872.
XX
KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW hypo-responsive subject; immunostimulatory.
XX
OS Synthetic.
XX
PN US2003087848-A1.
XX
PD 08-MAY-2003.
XX
PF 02-FEB-2001; 2001US-00776479.
XX
PR 03-FEB-2000; 2000US-0179991P.
XX
PA (BRAT/) BRATZLER R L.
PA (PETE/) PETERSEN D M.
PA (FOUR/) FOURON Y.
XX
PI Bratzler RL, Petersen DM, Fouron Y;
XX
DR WPI; 2003-657977/62.
XX
PT Treating and/or preventing allergy or asthma using an immunostimulatory
PT nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS Disclosure; Page 18; 221pp; English.
XX
CC The invention relates to a method of treating or preventing allergy or
CC asthma which comprises administering to a subject a poly-G nucleic acid
CC in an aerosol formulation. The methods and compositions of the present
CC invention are useful for diagnosing and/or treating asthma and allergy
CC especially in a hypo-responsive subject. The present sequence represents
CC an immunostimulatory nucleic acid of the invention.
XX
SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 9.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
|| |||||||||||||||||||
Db 24 AAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 789
ADB36806/c
ID ADB36806 standard; DNA; 24 BP.
XX
AC ADB36806;
XX
DT 04-DEC-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #420.
XX
KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW hypo-responsive subject; immunostimulatory.
XX
OS Synthetic.
XX
PN US2003087848-A1.
XX
PD 08-MAY-2003.
XX
PF 02-FEB-2001; 2001US-00776479.
XX
PR 03-FEB-2000; 2000US-0179991P.
XX
PA (BRAT/) BRATZLER R L.
PA (PETE/) PETERSEN D M.
PA (FOUR/) FOURON Y.
XX
PI Bratzler RL, Petersen DM, Fouron Y;
XX
DR WPI; 2003-657977/62.
XX
PT Treating and/or preventing allergy or asthma using an immunostimulatory
PT nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS Disclosure; Page 11; 221pp; English.
XX
CC The invention relates to a method of treating or preventing allergy or
CC asthma which comprises administering to a subject a poly-G nucleic acid
CC in an aerosol formulation. The methods and compositions of the present
CC invention are useful for diagnosing and/or treating asthma and allergy
CC especially in a hypo-responsive subject. The present sequence represents
CC an immunostimulatory nucleic acid of the invention.
XX
SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.2; DB 1; Length 24;

```
  Best Local Similarity   87.5%;  Pred. No. 9.2e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db         24 AAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 790
ADB37259
ID   ADB37259 standard; DNA; 24 BP.
XX
AC   ADB37259;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #873.
XX
KW   ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW   hypo-responsive subject; immunostimulatory.
XX
OS   Synthetic.
XX
PN   US2003087848-A1.
XX
PD   08-MAY-2003.
XX
PF   02-FEB-2001; 2001US-00776479.
XX
PR   03-FEB-2000; 2000US-0179991P.
XX
PA   (BRAT/) BRATZLER R L.
PA   (PETE/) PETERSEN D M.
PA   (FOUR/) FOURON Y.
XX
PI   Bratzler RL,  Petersen DM,  Fouron Y;
XX
DR   WPI; 2003-657977/62.
XX
PT   Treating and/or preventing allergy or asthma using an immunostimulatory
PT   nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS   Disclosure; Page 18; 221pp; English.
XX
CC   The invention relates to a method of treating or preventing allergy or
CC   asthma which comprises administering to a subject a poly-G nucleic acid
CC   in an aerosol formulation. The methods and compositions of the present
CC   invention are useful for diagnosing and/or treating asthma and allergy
CC   especially in a hypo-responsive subject. The present sequence represents
CC   an immunostimulatory nucleic acid of the invention.
XX
SQ   Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 9.2e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAA 24


RESULT 791
ADD31867/c
ID   ADD31867 standard; DNA; 24 BP.
XX
AC   ADD31867;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Butterfly biliverdin binding protein BBP-B1X oligonucleotide SEQ ID:106.
XX
KW   recombination product; synthetic gene technology; butterfly;
KW   biliverdin binding protein; ss.
XX
OS   synthetic.
XX
PN   WO2003064611-A2.
XX
PD   07-AUG-2003.
XX
PF   29-JAN-2003; 2003WO-US002612.
XX
PR   30-JAN-2002; 2002US-00062188.
XX
PA   (EGEA-) EGEA BIOSCIENCES INC.
XX
PI   Evans GA;
XX
DR   WPI; 2003-663477/62.
XX
PT   Creating recombination products between two distinct nucleotide
PT   sequences, useful in the field of synthetic gene technology, and in
PT   assembling a library, or a population or a collection of polypeptide
PT   variants.
XX
PS   Example 3; SEQ ID NO 106; 132pp; English.
XX
CC   The present invention describes a method for creating a collection of
CC   recombination products between two nucleotide sequences. The method
CC   comprises combining an initial set of oligonucleotides corresponding to a
CC   first nucleotide sequence with a subsequent set of oligonucleotides
CC   corresponding to a distinct nucleotide sequence and further combining the
CC   initial and subsequent sets of combination oligonucleotides having a
CC   sequence region corresponding to the initial nucleotide sequence and a
CC   sequence region corresponding to the second oligonucleotide sequence.
CC   Also described is a method of creating a collection of recombination
CC   products between two genes. The methods and compositions of the present
CC   invention are useful in the field of synthetic gene technology, and more
CC   specifically, to generating a collection of recombination products
CC   between distinct nucleotide sequences. They can also be used in
CC   assembling a library, or a population or a collection of polypeptide
CC   variants that correspond to single or multiple polynucleotide
CC   recombination products. The present sequence is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 9.2e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAA 24


RESULT 792
ADE25524/c
ID   ADE25524 standard; DNA; 24 BP.
XX
AC   ADE25524;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Rolling circle amplification related probe control oigo POS1/2.
XX
KW   RCA; rolling circle amplification; genotyping;
KW   single-nucleotide polymorphism; single base extension; SBE;
KW   immuno-hybridisation; probe; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   24
FT                   /*tag=  a
```

```
FT                   /mod_base= OTHER
FT                   /note= "optional biotin label"
XX
PN   WO2003066817-A2.
XX
PD   14-AUG-2003.
XX
PF   06-FEB-2003; 2003WO-US003533.
XX
PR   06-FEB-2002; 2002US-0355374P.
XX
PA   (AMSH ) AMERSHAM BIOSCIENCES AB.
XX
PI   Xia J;
XX
DR   WPI; 2003-697450/66.
XX
PT   Detecting nucleic acid targets, useful e.g. for diagnosing single
PT   nucleotide polymorphisms, by extension of capture probe complementary to
PT   open circle probe.
XX
PS   Example 1; Fig 5; 66pp; English.
XX
CC   The invention is directed to novel methods of amplifying and detecting
CC   DNA using rolling circle amplification (RCA). The invention relates to
CC   detecting a target sequence (I), which involves using a capture probe
CC   (CP) that is complementary to an open circle probe and includes a
CC   cleavage site. The method comprises: attaching a capture probe (CP) to a
CC   substrate, at both ends, where the CP includes one domain complementary
CC   to an OCP (open circle probe) and a second domain that contains a
CC   cleavage site (CS), to form a device; treating CP with (I) and OCP for
CC   form a hybridisation complex (HC); treating HC with a ligase so that OCP
CC   is circularised, forming a second complex (HC2); treating CP with a
CC   cleavage agent, to cut at CS, and adding an extension enzyme (EE) and
CC   nucleotide triphosphates (NTPs) to form an extended CP, which is
CC   detected. The method is used for detecting (I) that comprises two target
CC   domains (TD1, TD2) and (I) that comprises two adjacent target domains.
CC   The method is used for detection, genotyping and/or quantification of
CC   target sequences, for research, clinical use, quality control or field
CC   testing, particularly detection of single-nucleotide polymorphisms. The
CC   method permits a high level of multiplexing, and since it provides
CC   localized product detection, with linear kinetics, is sensitive enough
CC   for direct detection and quantitation of unmodified targets. The present
CC   sequence is that of a single base extension (SBE) probe used in SNP
CC   genotyping with RCA signal amplification to demonstrate the method of the
CC   invention.
XX
SQ   Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 9.2e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db         24 AAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 793
ABA97997
ID   ABA97997 standard; DNA; 24 BP.
XX
AC   ABA97997;
XX
DT   26-APR-2002  (first entry)
XX
DE   Human mitochondria carrier protein 13 PCR primer SEQ ID NO 4.
XX
KW   Human; mitochondria carrier protein 13; malignant tumour; blood disease;
KW   HIV; infection; immunity disease; inflammation; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1323810-A.
XX
PD   28-NOV-2001.
XX
PF   16-MAY-2000; 2000CN-00115695.
XX
PR   16-MAY-2000; 2000CN-00115695.
XX
PA   (SHAN-) SHANGHAI BODE GENE DEV CO LTD.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-148830/20.
XX
PT   New polypeptide-human mitochondria carrier protein 13 and polynucleotide
PT   for coding same.
XX
PS   Example 2; Page 17 (Disclosure); 33pp; Chinese.
XX
CC   The invention relates to human mitochondria carrier protein 13,
CC   polynucleotide for coding this polypeptide through DNA recombination
CC   technique. This invention also discloses the method for this polypeptide
CC   to cure several diseases, such as malignant tumour, blood disease, HIV
CC   infection and immunity disease and various inflammations etc. This
CC   invention further discloses an antagonist against this polypeptide and
CC   its therapeutic action, and the application of polynucleotide for coding
CC   this new human mitochondria carrier protein 13. The present sequence is
CC   that of a PCR primer, useful to the invention
XX
SQ   Sequence 24 BP; 5 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 9.2e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTAACTTTGAA 2195
              ||||||||||||||| || ||| ||
Db          1 TTTTTTTTTTTTTTAAATTTCAA 24


RESULT 794
ABL55130
ID   ABL55130 standard; DNA; 24 BP.
XX
AC   ABL55130;
XX
DT   31-MAY-2002  (first entry)
XX
DE   Human gonadotropin-releasing hormone 10 RT-PCR primer, SEQ ID NO:4.
XX
KW   Human; gonadotropin-releasing hormone 10; recombinant production; cancer;
KW   HIV infection; human immunodeficiency virus; gene therapy; cytostatic;
KW   anti-HIV; reverse transcription-PCR; RT-PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1325900-A.
XX
PD   12-DEC-2001.
XX
PF   31-MAY-2000; 2000CN-00116266.
XX
PR   31-MAY-2000; 2000CN-00116266.
XX
PA   (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-196660/26.
XX
PT   Polypeptide-human gonadotropin-releasing hormone 10 and polynucleotide
PT   encoding it.
XX
```

```
PS   Example 2; Page 17 (Disclosure); 32pp; Chinese.
XX
CC   The invention relates to human gonadotropin-releasing hormone 10
CC   (AAM49158) and to nucleic acids encoding it (ABL55128). The protein has a
CC   molecular weight of 10 kD. The invention also relates to a method for the
CC   recombinant production of the protein, an antagonist of the protein, and
CC   the use of the protein, gene and antagonist in therapeutic applications.
CC   Gonadotropin-releasing hormone 10 can be used in the treatment of a
CC   variety of diseases such as cancer and HIV (human immunodeficiency virus)
CC   infection. Sequences ABL55129-ABL55130 represent reverse transcription-
CC   PCR (RT-PCR) primers used in an exemplification of the invention to
CC   isolate human gonadotropin-releasing hormone 10 cDNA
XX
SQ   Sequence 24 BP; 1 A; 1 C; 3 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 9.2e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTAAC 2189
              |||||||||||||||||||   ||
Db          1 TTTTTTTTTTTTTTTTTTTGGGAC 24


RESULT 795
ABA98547
ID   ABA98547 standard; DNA; 24 BP.
XX
AC   ABA98547;
XX
DT   30-APR-2002  (first entry)
XX
DE   Insulin-like growth factor binding protein 16.17 PCR primer #1.
XX
KW   Insulin-like growth factor; binding protein; cytostatic; gene therapy;
KW   cancer; PCR primer; ss.
XX
OS   Unidentified.
XX
PN   WO200212301-A1.
XX
PD   14-FEB-2002.
XX
PF   11-JUN-2001; 2001WO-CN000947.
XX
PR   14-JUN-2000; 2000CN-00116509.
XX
PA   (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-172131/22.
XX
PT   Insulin-like growth factor binding protein 16.17 and encoding
PT   polynucleotide, used in diagnosis and treatment of cancer.
XX
PS   Example 2; Page 12; 37pp; Chinese.
XX
CC   The present invention relates to insulin-like growth factor binding
CC   protein 16.17 (see AAM48365). The binding protein and its coding sequence
CC   are useful for the diagnosis and treatment of cancer. The present
CC   sequence is a PCR primer, which was used in an example from the invention
XX
SQ   Sequence 24 BP; 1 A; 3 C; 1 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 9.2e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTTTTAA 2188
              |||| ||| |||||||||||||  |
Db          1 CTTTCTTTCTTTTTTTTTTTTGA 24


RESULT 796
ADD06134
ID   ADD06134 standard; DNA; 24 BP.
XX
AC   ADD06134;
XX
DT   01-JAN-2004  (first entry)
XX
DE   N-acetylgalactosamine transferase-38.61 RT-PCR primer, SEQ ID NO:3.
XX
KW   N-acetylgalactosamine transferase-38.61; recombinant production;
KW   gene therapy; cancer; blood disease; HIV infection;
KW   human immunodeficiency virus; immune disorder; cytostatic;
KW   immunomodulator; reverse transcription-PCR; RT-PCR; primer; ss.
XX
OS   Unidentified.
XX
PN   CN1382794-A.
XX
PD   04-DEC-2002.
XX
PF   26-APR-2001; 2001CN-00112757.
XX
PR   26-APR-2001; 2001CN-00112757.
XX
PA   (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2003-269502/27.
XX
PT   Polypeptide-N-acetylgalactosamine transferase-38.61 and polynucleotide
PT   for coding it.
XX
PS   Example 3; SEQ ID NO 3; 32pp; Chinese.
XX
CC   The invention relates to N-acetylgalactosamine transferase-38.61
CC   (ADD06133) and nucleic acids encoding it (ADD06132). The protein has a
CC   molecular weight of 38.61 kD and has 55% identity and 72% homology over a
CC   319 amino acid stretch with the sequence given in ADD06141. The invention
CC   also relates to a method for the recombinant production of the protein,
CC   an antagonist of the protein, and the use of the protein, gene and
CC   antagonist in therapeutic applications. N-acetylgalactosamine transferase
CC   -38.61 can be used in the treatment of a variety of diseases such as
CC   cancer, blood diseases, HIV (human immunodeficiency virus) infection and
CC   immune disorders. Sequences ADD06134-ADD06135 represent reverse
CC   transcription-PCR (RT-PCR) primers used in an exemplification of the
CC   invention to isolate N-acetylgalactosamine transferase-38.61 cDNA.
XX
SQ   Sequence 24 BP; 1 A; 8 C; 15 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 9.2e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         49 GCGCGGCGGGGGCGGCGGCAGACG 72
              | ||||||| |||||||||| ||
Db          1 GGGCGGCGGCGGCGGCGGCAGCCG 24


RESULT 797
AAQ95960/c
ID   AAQ95960 standard; DNA; 25 BP.
XX
AC   AAQ95960;
XX
DT   06-FEB-1996  (first entry)
XX
DE   Oligonucleotide biotin-T25 for novel nucleic acid immobilisation method.
XX
KW   Immobilisation; solid support; salt; cationic detergent; capture probe;
KW   hybridisation; primer; template-dependent extension; target organism;
```

```
KW   sequencing; genetic polymorphism; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1
FT                   /*tag=  a
FT                   /note= "biotinylated"
XX
PN   WO9515970-A1.
XX
PD   15-JUN-1995.
XX
PF   06-DEC-1994;   94WO-US014096.
XX
PR   06-DEC-1993;   93US-00162397.
PR   16-NOV-1994;   94US-00341148.
XX
PA   (MOLE-) MOLECULAR TOOL INC.
XX
PI   Nikiforov T,  Knapp MR;
XX
DR   WPI; 1995-224282/29.
XX
PT   Immobilising synthetic nucleic acid on solid support - by incubation in
PT   presence of salt or cationic detergent, for use in hybridisation assays,
PT   sequencing and analysis of polymorphism.
XX
PS   Example 1; Page 18; 61pp; English.
XX
CC   Oligonucleotides AAQ95959-82 are examples of oligonucleotides used in a
CC   novel method of immobilising oligonucleotides to a solid support by
CC   incubating in the presence of a salt or cationic detergent e.g. NaCl (50-
CC   250 mM, pH 6.0-8.0) or 1-ethyl-3-(3'-dimethyl amino propyl)-1,3
CC   carbodiimide hydrochloride (ECD). The oligonucleotides can be capture
CC   probes for detection of specific nucleic acids by hybridisation or can be
CC   primers for template-dependent extension from the immobilised primers on
CC   nucleic acid from a target organism. The method can be used in
CC   hybridisation assays, sequencing and analysis of genetic polymorphism
XX
SQ   Sequence 25 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 25;
  Best Local Similarity   87.5%;  Pred. No. 1e+03;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db         25 AAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 798
AAX84258/c
ID   AAX84258 standard; DNA; 25 BP.
XX
AC   AAX84258;
XX
DT   08-SEP-1999  (first entry)
XX
DE   PCR primer for human Nck associated protein 1 coding sequence.
XX
KW   Nck associated protein 1; Nap1; human; apoptosis; Alzheimer's disease;
KW   therapy; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9931239-A1.
XX
PD   24-JUN-1999.
XX
PF   14-DEC-1998;   98WO-JP005646.
XX
PR   15-DEC-1997;   97JP-00363183.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
PA   (SAKA/) SAKAKI Y.
XX
PI   Sakaki Y;
XX
DR   WPI; 1999-395181/33.
XX
PT   Protein inhibiting apoptosis, useful in the diagnosis and treatment of
PT   Alzheimer's disease.
XX
PS   Example 1; Page 76; 90pp; Japanese.
XX
CC   This sequence represents a PCR primer used to isolate DNA encoding the
CC   human Nck associated protein 1 (Nap1) of the invention. Nap1 inhibits
CC   apoptosis. The protein can be used in the investigation, diagnosis and
CC   treatment (e.g. by gene therapy) of Alzheimer's disease
XX
SQ   Sequence 25 BP; 0 A; 0 C; 1 G; 24 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 25;
  Best Local Similarity   87.5%;  Pred. No. 1e+03;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db         24 AAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 799
AAA39306/c
ID   AAA39306 standard; RNA; 25 BP.
XX
AC   AAA39306;
XX
DT   11-SEP-2000  (first entry)
XX
DE   Rapid capture probe designated Neu-probe SEQ ID NO:1.
XX
KW   Rapid detection; probe; target nucleic acid; enzymatic amplification;
KW   isolation; detection; ss.
XX
OS   Synthetic.
XX
PN   US6060246-A.
XX
PD   09-MAY-2000.
XX
PF   13-NOV-1997;   97US-00969813.
XX
PR   15-NOV-1996;   96US-0030963P.
XX
PA   (AVIB-) AVI BIOPHARMA INC.
XX
PI   Wages JM,  Summerton JE,  Weller DD;
XX
DR   WPI; 2000-364413/31.
XX
PT   Reagent for rapidly detecting or isolating target nucleic acid sequences
PT   in polynucleotide-containing sample, comprises capture component and
PT   target-specific probe linked to solid substrate.
XX
PS   Example 3; Col 17; 24pp; English.
XX
CC   The present invention describes a rapid pairing reagent (I) for the
CC   isolation or detection of a polynucleotide (PN) analyte molecule having a
CC   selected target base sequence, in a sample containing the analyte
CC   molecule and non-target polynucleotide, comprising a capture component
CC   (A) and a target-specific probe (B) linked to a solid substrate. The
CC   isolated sequences are useful for enzymatic amplification. (I) is capable
CC   of rapidly binding nucleic acids in the sample and placing them in close
CC   proximity to target probes on the reagent, thus enabling binding under
```

```
CC   low stringency. Combination of rapid capture and concentration of
CC   polynucleotides with selective targeting of analyte molecules, greatly
CC   enhances the isolation process. Non-ionic morpholino oligomers used as
CC   probes are not extended by polymerases and therefore do not interfere
CC   with amplification of target molecule. AAA39306 to AAA39316 represent
CC   oligonucleotides used in the exemplification of the present invention
XX
SQ   Sequence 25 BP; 0 A; 0 C; 0 G; 0 T; 25 U; 0 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 25;
  Best Local Similarity   87.5%;  Pred. No. 1e+03;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db         25 AAAAAAAAAAAAAAAAAAAAAAAAA 2


RESULT 800
AAZ30267/c
ID   AAZ30267 standard; DNA; 25 BP.
XX
AC   AAZ30267;
XX
DT   11-FEB-2000  (first entry)
XX
DE   Capture probe CP125 specific for c-myc fusion targets.
XX
KW   c-myc fusion; non-nucleoside spacer; capture probe;
KW   nucleic acid-protein fusion; ribosome display particle; ss.
XX
OS   Synthetic.
XX
PN   WO9951773-A1.
XX
PD   14-OCT-1999.
XX
PF   31-MAR-1999;   99WO-US007203.
XX
PR   03-APR-1998;   98US-0080686P.
XX
PA   (PHYL-) PHYLOS INC.
XX
PI   Kuimelis RG,  Wagner R;
XX
DR   WPI; 2000-013048/01.
XX
PT   Attaching capture probes to solid phases through non-nucleic spacers,
PT   producing arrays for detecting interactions of proteins with other
PT   compounds, e.g. for drug screening.
XX
PS   Example 8; Page 29; 57pp; English.
XX
CC   The present sequence represents a capture probe specific for a c-myc
CC   fusion target. It is used in the method of the invention. The
CC   specification describes the use of non-nucleoside spacers to immobilise
CC   an array of capture probes on a solid support. The solid support carries
CC   an array of capture probes, each consisting of non-nucleoside spacers
CC   plus an oligonucleotide to which a nucleic acid-protein fusion or a
CC   ribosome display particle is bound. Non-nucleoside spacers prevent
CC   interaction of proteins with the support surface, ensuring efficient
CC   hybridisation between capture probes and bound nucleic acid/protein
CC   fusions, while minimising denaturation of the protein which may then
CC   adopt its native folded structure. The arrays of capture probes are used
CC   to screen for interactions between proteins and compounds (e.g. other
CC   proteins, ligands or nucleic acids), particularly to identify potential
CC   therapeutic agents, enzyme substrates or unknown proteins that interact
CC   with drugs, but also for diagnosis (detecting disease-associated
CC   proteins) and for quantifying target molecules in a sample
XX
SQ   Sequence 25 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 25;
  Best Local Similarity   87.5%;  Pred. No. 1e+03;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db         25 AAAAAAAAAAAAAAAAAAAAAAAAA 2


RESULT 801
ABK49986/c
ID   ABK49986 standard; DNA; 25 BP.
XX
AC   ABK49986;
XX
DT   15-JUL-2002  (first entry)
XX
DE   Example oligonucleotide #2 prepared on glass-synthetic resin membrane.
XX
KW   Glass-synthetic resin membrane; pore glass-polytetrafluoroethylene resin;
KW   chromatography membrane; PTFE; ss.
XX
OS   Synthetic.
XX
PN   US6261497-B1.
XX
PD   17-JUL-2001.
XX
PF   04-MAY-1999;   99US-00305219.
XX
PR   21-FEB-1996;   96US-00604440.
XX
PA   (CPGC-) CPG INC.
XX
PI   Wong YN,  Chen R;
XX
DR   WPI; 2001-534961/59.
XX
PT   Preparation of controlled pore glass-polytetrafluoroethylene resin
PT   chromatography membrane by heating, calendering and sintering mixture of
PT   controlled pore glass and aqueous dispersion of polytetrafluoroethylene.
XX
PS   Example 12; Col 8; 6pp; English.
XX
CC   The invention relates to a method of preparing a controlled pore glass-
CC   polytetrafluoroethylene (PTFE) resin chromatography membrane, comprising
CC   combining controlled pore glass and an aqueous dispersion of PTFE to form
CC   a paste-like mass, heating the paste-like mass at 50-70 plus oC,
CC   calendering to form a foldable sheet, and sintering the sheet to produce
CC   a rigid, porous sheet. The method prepares a controlled pore glass-PTFE
CC   resin chromatography membrane for use in various biotechnical procedures.
CC   The membrane is useful in place of controlled pore glass as a support for
CC   the synthesis, isolation, and purification of nucleic acids and for the
CC   isolation and purification of proteins. The method produces a membrane
CC   that may be used in lieu of controlled pore glass. The present sequence
CC   represents an oligonucleotide prepared on the membrane in an example
CC   which demonstrates the method of the invention
XX
SQ   Sequence 25 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 25;
  Best Local Similarity   87.5%;  Pred. No. 1e+03;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db         25 AAAAAAAAAAAAAAAAAAAAAAAAA 2


RESULT 802
ADC54009/c
ID   ADC54009 standard; DNA; 25 BP.
XX
AC   ADC54009;
```

XX
DT 18-DEC-2003 (first entry)
XX
DE Oligonucleotide of the invention SEQ ID NO:4.
XX
KW ss; probe carrier; discharge.
XX
OS Synthetic.
XX
PN JP2003035711-A.
XX
PD 07-FEB-2003.
XX
PF 28-MAR-2002; 2002JP-00093023.
XX
PR 28-MAR-2001; 2001JP-00094400.
XX
PA (CANO) CANON KK.
XX
DR WPI; 2003-535999/51.
XX
PT Probe carrier manufacturing method for inkjet system, involves scanning
PT liquid discharge head in direction orthogonal to scanning direction, at
PT angle satisfying predetermined relation.
XX
PS Example 2; SEQ ID NO 4; 17pp; Japanese.
XX
CC The invention relates to a novel probe carrier and the method for
CC manufacturing the carrier. The invention enables stable discharge of
CC solution, and removes liquid droplets adhering to discharge nozzle. The
CC present sequence is used in the exemplification of the invention.
XX
SQ Sequence 25 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 1e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2781 AATTGAAAAAAAAAAAAAAAAAAAA 2804
|| |||||||||||||||||||
Db 25 AAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 803
ADC54008
ID ADC54008 standard; DNA; 25 BP.
XX
AC ADC54008;
XX
DT 18-DEC-2003 (first entry)
XX
DE Oligonucleotide of the invention SEQ ID NO:3.
XX
KW ss; probe carrier; discharge.
XX
OS Synthetic.
XX
PN JP2003035711-A.
XX
PD 07-FEB-2003.
XX
PF 28-MAR-2002; 2002JP-00093023.
XX
PR 28-MAR-2001; 2001JP-00094400.
XX
PA (CANO) CANON KK.
XX
DR WPI; 2003-535999/51.
XX
PT Probe carrier manufacturing method for inkjet system, involves scanning
PT liquid discharge head in direction orthogonal to scanning direction, at
PT angle satisfying predetermined relation.
XX
PS Example 2; SEQ ID NO 3; 17pp; Japanese.
XX
CC The invention relates to a novel probe carrier and the method for
CC manufacturing the carrier. The invention enables stable discharge of
CC solution, and removes liquid droplets adhering to discharge nozzle. The
CC present sequence is used in the exemplification of the invention.
XX
SQ Sequence 25 BP; 25 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 1e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2781 AATTGAAAAAAAAAAAAAAAAAAAA 2804
|| |||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAA 24

RESULT 804
ABK86170/c
ID ABK86170 standard; DNA; 25 BP.
XX
AC ABK86170;
XX
DT 24-SEP-2002 (first entry)
XX
DE Oligo dT primer #3 used in method to study gene expression.
XX
KW Oligo dT primer; gene expression analysis; primer; ss.
XX
OS Synthetic.
XX
PN WO200236828-A2.
XX
PD 10-MAY-2002.
XX
PF 01-NOV-2001; 2001WO-US045401.
XX
PR 01-NOV-2000; 2000US-0244933P.
XX
PA (GENO-) GENOMIC SOLUTIONS INC.
XX
PI Kane MD, Dombkowski AA, Nagel AC;
XX
DR WPI; 2002-508123/54.
XX
PT Identifying and characterizing gene expression in samples, for
PT identifying mRNAs expressed at different levels, comprises employing an
PT identimer having a oligo-dT primer of a specific sequence and a
PT detectable marker at its 5' end.
XX
PS Example 2; Page 21; 45pp; English.
XX
CC The invention relates to systems for identification and characterisation
CC of gene expression in one or more samples, comprising an identimer having
CC a specific oligo-dT primer sequence, where the identimer comprises a
CC detectable marker at its 5' end. The system is useful for identifying any
CC or all genes expressed in a given in vivo or in vitro RNA sample, as well
CC as the relative differences in mRNA between 2 or more samples, where
CC desired, for supporting discovery of new genes, and for identifying mRNAs
CC that are expressed at different levels between 2 or more samples. The new
CC system or method addresses limitations of prior methods by comprising
CC compositions and systems that incorporate new strategies where molecular
CC or biochemical assay compositions and systems are linked to DNA or RNA
CC sequence databases for optimal resource efficiency in assaying gene
CC expression. The system has the following advantages over existing
CC methods: (a) prior sequence information or clone library construction is
CC not needed to enable the assay; (b) provides immediate sequence
CC information in addition to information concerning changes or differences
CC in mRNA level, to determine mRNA expression level and mRNA identification
CC in one assay; (c) generates cDNA fragments from all mRNAs present in the
CC sample for subsequent investigation by common molecular biology
CC techniques; and (d) does not require prior knowledge of the sequence of

```
CC   the genome of the organism under investigation and can be employed in
CC   organisms lacking significant genomic sequence in formation. The present
CC   sequence represents an oligo dT primer used in the method of the
CC   invention
XX
SQ   Sequence 25 BP; 0 A; 0 C; 2 G; 23 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 25;
  Best Local Similarity   87.5%;  Pred. No. 1e+03;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db         25 AAACCAAAAAAAAAAAAAAAAAAA 2


RESULT 805
AAC96700
ID   AAC96700 standard; DNA; 25 BP.
XX
AC   AAC96700;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA HLA-A gene PCR primer #77.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 55; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 4 A; 1 C; 4 G; 16 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 25;
  Best Local Similarity   87.5%;  Pred. No. 1e+03;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2175 TTTTTTTTTTTTAACTTTGAAAGT 2198
              |||||||||||||  |||  |||||
Db          1 TTTTTTTTTTTTAGCTTGTAAAGT 24


RESULT 806
ABL45245/c
ID   ABL45245 standard; DNA; 25 BP.
XX
AC   ABL45245;
XX
DT   11-APR-2002  (first entry)
XX
DE   Human chromosome 1p36-35 PCR primer SEQ ID NO:2289.
XX
KW   Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2001321190-A.
XX
PD   20-NOV-2001.
XX
PF   12-MAR-2001; 2001JP-00068285.
XX
PR   10-MAR-2000; 2000JP-00066716.
XX
PA   (RIKA ) RIKAGAKU KENKYUSHO.
PA   (GENO-) GENOTEX YG.
XX
DR   WPI; 2002-144136/19.
XX
PT   Arraying genome clones.
XX
PS   Claim 4; Page 49; 528pp; Japanese.
XX
CC   The present invention describes a method of arraying genome clones. The
CC   method comprises: (a) clones of the genomic libraries contained in
CC   multiwell plates numbered for discrimination are mixed in each of the
CC   multiwell plates; (b) a primer designed based on the chromosome marker
CC   sequence is added to the mixture to carry out an amplification reaction;
CC   (c) a signal corresponding to the marker is detected from the resultant
CC   amplified product to specify the discrimination Nos. of the multiwell
CC   plates containing the clones having said marker sequence; (d) the order
CC   of the markers is changed so that the same discrimination Nos. succeed to
CC   the maximum in the specified discrimination Nos. to array the multiwell
CC   plates; (e) the clones in the multiwell plates of the specified
CC   discrimination Nos. are mixed respectively in each wells of longitudinal
CC   and lateral directions; (f) the mixed clones are cultured and the
CC   resultant cultures are amplified by using the above primer; (g) signals
CC   are detected from the amplified products; (h) the clones in the multiwell
CC   plates are specified from the detected result; and (i) the clones are
CC   reconstituted as the positions on the chromosome and arrayed. The
CC   microarray is useful for gene analysis. ABL42957 to ABL45322 represent
CC   PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
CC   represent PCR primers for human chromosome 21q22.1, which are
CC   specifically claimed for use in the present invention
XX
SQ   Sequence 25 BP; 18 A; 1 C; 5 G; 1 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 25;
  Best Local Similarity   87.5%;  Pred. No. 1e+03;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTTTTTTTT 2185
              | ||||||||||||||  ||  ||||
Db         25 CACCTTTTTTTTTTTTCTTCTTTT 2


RESULT 807
AAX07466/c
ID   AAX07466 standard; cDNA; 26 BP.
XX
AC   AAX07466;
XX
DT   08-JUN-1999  (first entry)
XX
DE   Human BS124 specific EST clone oligonucleotide.
```

XX
KW BS124; breast; cancer; detection; diagnosis; prevention; treatment; EST;
KW ss.
XX
OS Synthetic.
XX
PN WO9859049-A1.
XX
PD 30-DEC-1998.
XX
PF 19-JUN-1998; 98WO-US012862.
XX
PR 20-JUN-1997; 97US-00879354.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
PI Granados EN, Hodges SC, Klass MR, Kratochvil JD, Russell JC;
PI Scheffel CP, Stroupe SD, Yu H;
XX
DR WPI; 1999-105623/09.
XX
PT New isolated BS124 polynucleotides and polypeptides - used for detecting,
PT diagnosing, preventing or treating diseases or conditions of the breast,
PT such as breast cancer.
XX
PS Disclosure; Page 97; 125pp; English.
XX
CC The sequence is that of an oligonucleotide used in the isolation of a
CC BS124-specific EST clone. It is useful for detecting, diagnosing,
CC staging, preventing or treating, or determining predisposition to
CC diseases or conditions of the breast, such as breast cancer
XX
SQ Sequence 26 BP; 0 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.2; DB 1; Length 26;
Best Local Similarity 87.5%; Pred. No. 1.1e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
|| ||||||||||||||||||||
Db 25 AAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 808
AAX78723/c
ID AAX78723 standard; DNA; 26 BP.
XX
AC AAX78723;
XX
DT 03-SEP-1999 (first entry)
XX
DE Human pancreatic PA153 EST-specific clone primer 12.
XX
KW Pancreatic disease; PA153; human; cytostatic; detection; antigen;
KW anti-PA153; antagonist; therapy; treatment; tumour; metastasis;
KW gene therapy; EST; expressed sequence tag; primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9931274-A2.
XX
PD 24-JUN-1999.
XX
PF 11-DEC-1998; 98WO-US026441.
XX
PR 15-DEC-1997; 97US-00990568.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
PI Granados EN, Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L;
PI Russell JC, Stroupe SD;
XX
DR WPI; 1999-405041/34.
XX
PT PA153 cDNA transcribed from pancreatic tissue.
XX
PS Example 2; Page 121; 123pp; English.
XX
CC This invention describes novel contiguous and partially overlapping cDNA
CC sequences and their encoded polypeptides, designated PA153, transcribed
CC from human pancreatic tissue and which have cytostatic activity. The
CC PA153 polynucleotides, proteins and antibodies are all useful in methods
CC of detection. Detection of PA153 polynucleotide, antigens or anti-PA153
CC antibodies in a sample is indicative of pancreatic disease. PA153
CC antibodies (antagonists) can also be used in vivo for therapeutic use,
CC e.g. treatment of pancreatic disease, tumours or metastases. Antisense
CC PA153 polynucleotides can be used in gene therapy of pancreatic diseases.
CC AAX78712-X78725 represent primers used in the method of the invention
XX
SQ Sequence 26 BP; 0 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.2; DB 1; Length 26;
Best Local Similarity 87.5%; Pred. No. 1.1e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
|| ||||||||||||||||||||
Db 25 AAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 809
AAV71936/c
ID AAV71936 standard; DNA; 27 BP.
XX
AC AAV71936;
XX
DT 18-FEB-1999 (first entry)
XX
DE Anchored poly T RT-PCR primer.
XX
KW Normalised; cDNA library; mRNA cloning; reverse transcription;
KW immobilise; screening; hybridisation; nucleic acid amplification;
KW expression pattern; drug development; PCR primer; RT-PCR; ss.
XX
OS Synthetic.
XX
PN WO9851789-A2.
XX
PD 19-NOV-1998.
XX
PF 13-MAY-1998; 98WO-DK000186.
XX
PR 13-MAY-1997; 97DK-00000547.
PR 19-MAY-1997; 97US-00871030.
PR 27-MAR-1998; 98DK-00000432.
XX
PA (DISP-) DISPLAY SYSTEMS BIOTECH APS.
XX
PI Warthoe PR;
XX
DR WPI; 1999-009772/01.
XX
PT Preparation of normalised, subdivided cDNA libraries from mRNA - by
PT reverse transcription and amplification, used to screen for new genes and
PT interacting proteins, potential drugs, and for diagnosis.
XX
PS Example 1; Page 29; 71pp; English.
XX
CC The invention relates to preparation of a normalised, subdivided library
CC of amplified cDNA from the coding regions of mRNA in a sample. The method
CC involves reverse transcription, with at least one cDNA primer of formula
CC 5'-Con1-dTn2-Vn3-Nn4 to form first stand cDNA where Con1 = any sequence
CC of 1-100 nucleotides; dT = deoxythymidinyl; n2 is at least 1; n3 and n4

CC are both 0, or n3 is 1 and n4 is at least 1; followed by second strand
CC cDNA synthesis using the first strand as template and a second cDNA
CC primer of a similar formula, in the presence of DNA polymerase I (or its
CC Klenow fragment) and amplification of double-stranded cDNA with a set of
CC amplification primers. Comparison of cDNA in the prepared library with a
CC database (a computer-generated list of molecular weights of restricted
CC DNA fragments of known sequence) is used to determine presence of an
CC expressed protein in a cell, also to detect changes in such expression
CC (particularly for diagnosis of disease). Surfaces (chip) having amplified
CC cDNA stably immobilised on it, obtained by a similar method, are used to
CC screen for genes of a particular family, by hybridisation with nucleic
CC acid from the family (to identify new genes) and to detect differences in
CC expression patterns between cells. The polypeptides expressed by the
CC libraries can be used for drug development. Sequences AAV71935 to
CC AAV71946 represent primers used to exemplify the method of the invention
XX
SQ Sequence 27 BP; 0 A; 1 C; 1 G; 25 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.2; DB 1; Length 27;
Best Local Similarity 87.5%; Pred. No. 1.2e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2781 AATTGAAAAAAAAAAAAAAAAAA 2804
|| ||||||||||||||||||||
Db 25 AAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 810
ABS53863/c
ID ABS53863 standard; DNA; 27 BP.
XX
AC ABS53863;
XX
DT 25-NOV-2002 (first entry)
XX
DE Human androgen receptor complex-associated protein 5'RACE PCR primer #1.
XX
KW Human; androgen receptor complex-associated protein; ARCAP; primer; ss;
KW androgen receptor; AR; cancer; liver tumour; cytostatic; PCR; 5'RACE.
XX
OS Homo sapiens.
XX
PN EP1227150-A2.
XX
PD 31-JUL-2002.
XX
PF 16-JAN-2002; 2002EP-00250305.
XX
PR 17-JAN-2001; 2001US-0262312P.
PR 12-FEB-2001; 2001US-00781693.
XX
PA (VETE-) VETERANS GEN HOSPITAL.
XX
PI Tai-Jay C;
XX
DR WPI; 2002-676576/73.
XX
PT Novel substantially pure androgen receptor (AR) complex-associated
PT protein which binds to AR and increases ability of AR to transactivate
PT androgen-responsive gene, useful as drug target for treating liver
PT cancer.
XX
PS Example; Page 11; 26pp; English.
XX
CC The invention relates to an androgen receptor complex-associated protein
CC (ARCAP) sequence and the cDNA encoding it. The protein is useful for
CC screening a compound that decreases AR-mediated (androgen receptor
CC mediated) transactivation which involves contacting the ARCAP protein
CC with a protein complex comprising an AR in the presence of a candidate
CC compound, measuring the extent of binding between the polypeptide, and
CC determining if the extent of binding is less than the extent of binding
CC between the polypeptide and the protein complex in the absence of the
CC candidate compound. The ARCAP DNA is useful for determining if a sample
CC contains cancerous cells which involves providing a sample from a human
CC patient and detecting ARCAP expression in the sample. The sequences are
CC useful for determining whether a sample contains liver tumour cells. This
CC sequence represents a 5'RACE PCR primer used to amplify human ARCAP DNA
XX
SQ Sequence 27 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 2 Other;

Query Match 0.7%; Score 19.2; DB 1; Length 27;
Best Local Similarity 87.5%; Pred. No. 1.2e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2781 AATTGAAAAAAAAAAAAAAAAAA 2804
|| ||||||||||||||||||||
Db 25 AAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 811
ABS54324/c
ID ABS54324 standard; DNA; 27 BP.
XX
AC ABS54324;
XX
DT 10-DEC-2002 (first entry)
XX
DE Human ARCAP associated 5'RACE PCR primer.
XX
KW Human; androgen receptor complex-coupled protein; ARCAP; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN JP2002262871-A.
XX
PD 17-SEP-2002.
XX
PF 28-FEB-2001; 2001JP-00055192.
XX
PR 12-FEB-2001; 2001US-00781693.
XX
PA (VETE-) VETERANS GEN HOSPITAL.
XX
PI Tai-Jay C;
XX
DR WPI; 2002-676576/73.
XX
PT Novel substantially pure androgen receptor (AR) complex-associated
PT protein which binds to AR and increases ability of AR to transactivate
PT androgen-responsive gene, useful as drug target for treating liver
PT cancer.
XX
PS Example; Page 15; 18pp; Japanese.
XX
CC The present invention relates to the isolation of human androgen receptor
CC complex-coupled protein (ARCAP), and the polynucleotide sequence encoding
CC it. The ARCAP polypeptide complexes with an androgen receptor to increase
CC the activity of the androgen receptor, transactivating the androgen
CC responsing gene. The invention also describes a a vector containing the
CC ARCAP polynucleotide sequence, and a host cell containing the ARCAP
CC polynucleotide sequence. The ARCAP polypeptide can be used as a treating
CC agent. The present sequence represents a PCR primer used in the example
CC of the present invention
XX
SQ Sequence 27 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 2 Other;

Query Match 0.7%; Score 19.2; DB 1; Length 27;
Best Local Similarity 87.5%; Pred. No. 1.2e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2781 AATTGAAAAAAAAAAAAAAAAAA 2804
|| ||||||||||||||||||||
Db 25 AAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 812

```
AAL47309
ID   AAL47309 standard; DNA; 27 BP.
XX
AC   AAL47309;
XX
DT   30-AUG-2002  (first entry)
XX
DE   Intracellular target molecule property modulation method oligo #1.
XX
KW   Intracellular target; cellular component; property modulation;
KW   antimicrobial; immunomodulatory; nootropic; neuroprotective; metabolic;
KW   neuroleptic; cytostatic; cardiant; infection; ds; immunological disorder;
KW   neurological disorder; metabolic disorder; psychiatric disorder;
KW   myopathy; cancer; cardiovascular disorder.
XX
OS   Synthetic.
XX
PN   EP1205191-A1.
XX
PD   15-MAY-2002.
XX
PF   13-NOV-2000; 2000EP-00403156.
XX
PR   13-NOV-2000; 2000EP-00403156.
XX
PA   (CNRS ) CENT NAT RECH SCI.
PA   (MASS-) MASSACHUSETTS GEN HOSPITAL.
PA   (MOLE-) MOLECULAR SCI INST.
XX
PI   Colas P,  Brent R,  Cohen BA;
XX
DR   WPI; 2002-418829/45.
XX
PT   Process for specifically modulating the properties of an intracellular
PT   target molecule used for the treatment of various disorders.
XX
PS   Example 4; Page 16; 33pp; English.
XX
CC   The present invention relates to a process for specifically modulating
CC   the properties of an intracellular target molecule T, and/or of a
CC   cellular component C which interacts directly or indirectly in a cell
CC   with the target. The process involves the introduction into the cell of a
CC   chimeric molecule known as a targeted effector, comprising a recognition
CC   moiety capable of recognising T and an effector moiety. The chimeric
CC   protein or nucleic acid can be used in the preparation of a medicament
CC   for the treatment of microbial infections, immunological disorders,
CC   neurological disorders, metabolic disorders, psychiatric disorders,
CC   myopathies, genetic disorders, cancer, cardiovascular disorders and
CC   dental disorders. The present sequence is an oligonucleotide used in the
CC   construction of a fusion protein in the exemplification of the invention
XX
SQ   Sequence 27 BP; 19 A; 1 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 27;
  Best Local Similarity   87.5%;  Pred. No. 1.2e+03;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAA 2804
             ||||||| || |||||||| ||||
Db          1 AATTGAAGAAGAAAAAAAAGAAAA 24


RESULT 813
AAA40362/c
ID   AAA40362 standard; DNA; 28 BP.
XX
AC   AAA40362;
XX
DT   10-NOV-2000  (first entry)
XX
DE   pBluescriptSK+ phagemid primer SEQ ID NO: 12.
XX
KW   Primer; cloning; ligation; ss.
XX
OS   Synthetic.
XX
PN   WO200036088-A1.
XX
PD   22-JUN-2000.
XX
PF   17-DEC-1999;   99WO-US030277.
XX
PR   17-DEC-1998;   98US-00213834.
XX
PA   (ROMA/) ROMANTCHIKOV Y.
XX
PI   Romantchikov Y;
XX
DR   WPI; 2000-442381/38.
XX
PT   Inserting a nucleic acid into a circular vector comprising joining their
PT   ends, melting, and reannealing ends at two different concentrations,
PT   useful for cloning small amounts of nucleic acids and forming genomic
PT   libraries.
XX
PS   Example 4; Page 68; 71pp; English.
XX
CC   This invention describes a novel method (M1) for inserting a nucleic acid
CC   (N1) into a circular vector (V1) comprising joining ends of N1 and V1
CC   under a first nucleic acid concentration, melting hybridized cohesive
CC   circularization ends, and reannealing the ends at a second concentration.
CC   The methods are useful for the cloning small amounts of nucleic acids and
CC   forming genomic libraries of complex populations of DNA or cDNA. The
CC   methods allow the cloning of minute amounts of nucleic acids efficiently
CC   and avoids the size selection problems of prior art systems. Larger
CC   nucleic acid fragments are just as easily cloned, allowing highly
CC   representative libraries to be made. Vector to vector ligation is avoided
CC   using the methods. AAA40351-A40366 represents primers used to illustrate
CC   the method of the invention
XX
SQ   Sequence 28 BP; 0 A; 2 C; 2 G; 24 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 28;
  Best Local Similarity   87.5%;  Pred. No. 1.3e+03;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
             ||   ||||||||||||||||||
Db         28 AAAAAAAAAAAAAAAAAAAAAAAA 5


RESULT 814
AAA40358/c
ID   AAA40358 standard; DNA; 28 BP.
XX
AC   AAA40358;
XX
DT   10-NOV-2000  (first entry)
XX
DE   pBluescriptSK+ phagemid primer SEQ ID NO: 8.
XX
KW   Primer; cloning; ligation; ss.
XX
OS   Synthetic.
XX
PN   WO200036088-A1.
XX
PD   22-JUN-2000.
XX
PF   17-DEC-1999;   99WO-US030277.
XX
PR   17-DEC-1998;   98US-00213834.
XX
PA   (ROMA/) ROMANTCHIKOV Y.
XX
PI   Romantchikov Y;
```

```
XX
DR   WPI; 2000-442381/38.
XX
PT   Inserting a nucleic acid into a circular vector comprising joining their
PT   ends, melting, and reannealing ends at two different concentrations,
PT   useful for cloning small amounts of nucleic acids and forming genomic
PT   libraries.
XX
PS   Example 3; Page 67; 71pp; English.
XX
CC   This invention describes a novel method (M1) for inserting a nucleic acid
CC   (N1) into a circular vector (V1) comprising joining ends of N1 and V1
CC   under a first nucleic acid concentration, melting hybridized cohesive
CC   circularization ends, and reannealing the ends at a second concentration.
CC   The methods are useful for the cloning small amounts of nucleic acids and
CC   forming genomic libraries of complex populations of DNA or cDNA. The
CC   methods allow the cloning of minute amounts of nucleic acids efficiently
CC   and avoids the size selection problems of prior art systems. Larger
CC   nucleic acid fragments are just as easily cloned, allowing highly
CC   representative libraries to be made. Vector to vector ligation is avoided
CC   using the methods. AAA40351-A40366 represents primers used to illustrate
CC   the method of the invention
XX
SQ   Sequence 28 BP; 1 A; 1 C; 1 G; 25 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 28;
  Best Local Similarity   87.5%;  Pred. No. 1.3e+03;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db         28 AAAAAAAAAAAAAAAAAAAAAAAA 5


RESULT 815
AAQ52308
ID   AAQ52308 standard; cDNA; 28 BP.
XX
AC   AAQ52308;
XX
DT   25-MAR-2003  (revised)
DT   03-JUN-1994  (first entry)
XX
DE   FKBP12C PCR primer VX10801.
XX
KW   Transplant rejection; monitoring; FK506 immunosuppressant therapy;
KW   tissue specific; polymerase chain reaction; ss.
XX
OS   Synthetic.
XX
PN   WO9323548-A2.
XX
PD   25-NOV-1993.
XX
PF   20-MAY-1993;   93WO-US004916.
XX
PR   20-MAY-1992;   92US-00886611.
XX
PA   (VERT-) VERTEX PHARM INC.
XX
PI   Peattie DA;
XX
DR   WPI; 1993-386579/48.
XX
PT   New cDNA for tissue specific FK506 binding proteins - and detection of
PT   its mRNA to monitor transplant rejection and effect or FK506
PT   immunosuppressant therapy.
XX
PS   Example 4; Page 36; 54pp; English.
XX
CC   The sequence is that of a PCR primer VX10801 which was used to amplify
CC   DNA specific to FKBP12C. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 28 BP; 5 A; 1 C; 4 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 28;
  Best Local Similarity   87.5%;  Pred. No. 1.3e+03;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTAACTT 2191
              ||||||||||||||||   ||||||
Db          1 TTTTTTTTTTTTTTTGAATAACTT 24


RESULT 816
ABN83378
ID   ABN83378 standard; DNA; 29 BP.
XX
AC   ABN83378;
XX
DT   15-AUG-2002  (first entry)
XX
DE   Mononucleotide repeat locus BAT25 probe #1.
XX
KW   Mononucleotide repeat locus; human; BAT25; probe; microsatellite; tumour;
KW   ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   29
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Labelled with Fluorescein"
XX
PN   EP1207210-A1.
XX
PD   22-MAY-2002.
XX
PF   13-NOV-2001; 2001EP-00126930.
XX
PR   15-NOV-2000; 2000EP-00124897.
XX
PA   (HOFF ) ROCHE DIAGNOSTICS GMBH.
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Dietmaier W;
XX
DR   WPI; 2002-437469/47.
XX
PT   Analyzing repeat sequences in DNA using a probe which hybridizes to
PT   adjacent repetitive and non-repetitive regions and determining hybrid
PT   melting point is useful to detect microsatellite instability such as in
PT   hereditary cancer.
XX
PS   Claim 16; Page 7; 19pp; English.
XX
CC   The present invention relates to a method for analysing a target nucleic
CC   acid consisting of repetitive and non-repetitive sequences. The method
CC   comprises hybridising a polynucleotide probe comprising a segment
CC   complementary to a non-repetitive region and a segment complementary to
CC   an adjacent repetitive region, where the second segment consists of a
CC   defined number of repeats, and determining the melting point temperature
CC   of the hybrid. The method is used to analyse microsatellites, especially
CC   microsatellite instability, particularly as a means for detecting
CC   hereditary tumours. Alternatively, the method is used to identify an
CC   individual in a population. The present sequence is a probe for
CC   Mononucleotide repeat locus BAT25, and was used to illustrate the
CC   invention
XX
SQ   Sequence 29 BP; 26 A; 2 C; 0 G; 1 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 29;
  Best Local Similarity   87.5%;  Pred. No. 1.4e+03;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;
```

```
Qy       2781 AATTGAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||
Db          2 AAAAAAAAAAAAAAAAAAAAAAAAA 25
```

RESULT 817
AAL44903/c
ID AAL44903 standard; DNA; 29 BP.
XX
AC AAL44903;
XX
DT 05-AUG-2002 (first entry)
XX
DE Triplex forming oligonucleotide #4.
XX
KW Cancer; cytostatic; gene therapy; triplex forming oligonucleotide; ds.
XX
OS Unidentified.
XX
PN KR2001086830-A.
XX
PD 15-SEP-2001.
XX
PF 03-MAR-2000; 2000KR-00010744.
XX
PR 03-MAR-2000; 2000KR-00010744.
XX
PA (KOCH-) KOREA CHUNGANG EDUCATIONAL FOUND.
XX
PI Choi JG, Lee DH, Lee GY, Park GH, Park MG, Son JW;
XX
DR WPI; 2002-233771/29.
XX
PT Novel triplex forming synthetic oligonucleotide, useful for gene therapy
PT of tumor.
XX
PS Claim 4; Page 11; 13pp; Korean.
XX
CC The present invention relates to a triplex forming oligonucleotide which
CC specifically binds to a specific gene. This is useful for the gene
CC therapy of cancer by binding itself to Auger electron emitters. The
CC present sequence is a triplex forming oligonucleotide of the invention
XX
SQ Sequence 29 BP; 0 A; 1 C; 3 G; 25 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.2; DB 1; Length 29;
Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       2781 AATTGAAAAAAAAAAAAAAAAAA 2804
              ||  |||||| ||||||||||||||
Db         27 AAAAGAAAAACAAAAAAAAAAAAA 4
```

RESULT 818
AAA71176
ID AAA71176 standard; DNA; 29 BP.
XX
AC AAA71176;
XX
DT 27-APR-2001 (first entry)
XX
DE Molecular interaction site DNA #157.
XX
KW Modulator; identification; molecular interaction; virtual library; ss.
XX
OS Canis familiaris.
XX
PN WO9958947-A2.
XX
PD 18-NOV-1999.
XX
PF 12-MAY-1999; 99WO-US010361.
XX
PR 12-MAY-1998; 98US-00076404.
PR 12-MAY-1998; 98US-0085092P.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
PI Hofstadler S, Mcneil J;
XX
DR WPI; 2000-086439/07.
XX
PT Identifying compounds which modulate activity of target biomolecules,
PT used to provide compounds which can be used as pharmacological,
PT agricultural and industrial compounds.
XX
PS Example 8; Fig 134; 405pp; English.
XX
CC This invention describes a novel method for identifying compounds which
CC modulate the activity of a target biomolecule. The method uses 3-
CC dimensional representations of the biomolecule and a library of compounds
CC and comprises (a) identifying at least one molecular interaction site of
CC the target RNA; (b) generating in silico a virtual library of compounds
CC predicted or calculated to interact with the molecular interaction site;
CC and (c) comparing 3-dimensional (3-D) representations of the target RNA
CC with members of the virtual library of compounds to generate a hierarchy
CC of the compounds ranked in accordance with their respective ability to
CC form physical interactions with the molecular interaction site. The
CC method also describes (1) RNA comprising a joined sequence of at least 24
CC nucleotides but not more than 70 nucleotides and having secondary
CC structure defined by: (a) 3 nucleotides forming a first side of a first
CC double stranded (ds) region; (b) 2 nucleotides forming a first side of an
CC internal loop region; (c) 4 nucleotides forming a first side of a second
CC ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
CC nucleotides forming a second side of the second ds region; (f) 4
CC nucleotides forming a second side of the internal loop region; and (g) 3
CC nucleotides forming a second side of the first ds region; (2) a purified
CC and isolated RNA fragment comprising the human sequence
CC UUUACAACAUAAUCUAGUUUACAGAAAAAUC (II). The methods and products can be
CC used for identifying agents which modulate the activity of biomolecules,
CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
CC or industrial compounds
XX
SQ Sequence 29 BP; 21 A; 2 C; 1 G; 3 T; 0 U; 2 Other;

Query Match 0.7%; Score 19.2; DB 1; Length 29;
Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       2778 TAGAATTGAAAAAAAAAAAAAAAA 2801
              ||||  | ||||||||||||||||
Db          4 TAGACCTAAAAAAAAAAAAAAAAA 27
```

RESULT 819
AAA71193
ID AAA71193 standard; RNA; 29 BP.
XX
AC AAA71193;
XX
DT 27-APR-2001 (first entry)
XX
DE Molecular interaction site RNA #230.
XX
KW Modulator; identification; molecular interaction; virtual library; ss.
XX
OS Canis familiaris.
XX
PN WO9958947-A2.
XX
PD 18-NOV-1999.
XX
PF 12-MAY-1999; 99WO-US010361.
XX

```
PR   12-MAY-1998;   98US-00076404.
PR   12-MAY-1998;   98US-0085092P.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Ecker DJ,  Griffey R,  Crooke ST,  Sampath R,  Swayze E,  Mohan V;
PI   Hofstadler S,  Mcneil J;
XX
DR   WPI; 2000-086439/07.
XX
PT   Identifying compounds which modulate activity of target biomolecules,
PT   used to provide compounds which can be used as pharmacological,
PT   agricultural and industrial compounds.
XX
PS   Example 8; Fig 135; 405pp; English.
XX
CC   This invention describes a novel method for identifying compounds which
CC   modulate the activity of a target biomolecule. The method uses 3-
CC   dimensional representations of the biomolecule and a library of compounds
CC   and comprises (a) identifying at least one molecular interaction site of
CC   the target RNA; (b) generating in silico a virtual library of compounds
CC   predicted or calculated to interact with the molecular interaction site;
CC   and (c) comparing 3-dimensional (3-D) representations of the target RNA
CC   with members of the virtual library of compounds to generate a hierarchy
CC   of the compounds ranked in accordance with their respective ability to
CC   form physical interactions with the molecular interaction site. The
CC   method also describes (1) RNA comprising a joined sequence of at least 24
CC   nucleotides but not more than 70 nucleotides and having secondary
CC   structure defined by: (a) 3 nucleotides forming a first side of a first
CC   double stranded (ds) region; (b) 2 nucleotides forming a first side of an
CC   internal loop region; (c) 4 nucleotides forming a first side of a second
CC   ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
CC   nucleotides forming a second side of the second ds region; (f) 4
CC   nucleotides forming a second side of the internal loop region; and (g) 3
CC   nucleotides forming a second side of the first ds region; (2) a purified
CC   and isolated RNA fragment comprising the human sequence
CC   UUUACAACAUAAUCUAGUUUACAGAAAAAUC (II). The methods and products can be
CC   used for identifying agents which modulate the activity of biomolecules,
CC   particularly RNA. Such agents can be used as pharmaceutical, agricultural
CC   or industrial compounds
XX
SQ   Sequence 29 BP; 21 A; 2 C; 1 G; 0 T; 3 U; 2 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 29;
  Best Local Similarity   79.2%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAAAAAAAA 2801
              :|||  : ||||||||||||||||
Db          4 UAGACCUAAAAAAAAAAAAAAAAA 27


RESULT 820
AAF74917/c
ID   AAF74917 standard; DNA; 29 BP.
XX
AC   AAF74917;
XX
DT   23-MAY-2001  (first entry)
XX
DE   CD40L poly-A tract sequence SEQ ID NO:14.
XX
KW   Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW   diagnosis; antiarthritic; antirheumatic; immunosuppressive;
KW   antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200119844-A1.
XX
PD   22-MAR-2001.
XX
PF   13-SEP-2000; 2000WO-US024966.
XX
PR   13-SEP-1999;   99US-0153625P.
XX
PA   (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
PI   Crow MK,  Li Y;
XX
DR   WPI; 2001-244776/25.
XX
PT   New altered CD40L promoter for use in the study, diagnosis and treatment
PT   of a variety of inflammatory disorders and autoimmune diseases, such as
PT   rheumatoid arthritis.
XX
PS   Example 1; Fig 3; 90pp; English.
XX
CC   The present invention describes an isolated, purified nucleic acid, which
CC   is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC   residues 331-455 of the sequence comprising 455 nucleotides given in
CC   AAF74905 where A in the wild type sequence at position 331 (corresponding
CC   to position -125) is replaced with C. (I) has antiarthritic,
CC   antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC   be used in gene therapy. (I) is useful in the study, diagnosis and
CC   treatment of inflammatory and autoimmune diseases, as well as diseases in
CC   which elevated expression of CD40L is a factor, e.g., rheumatoid
CC   arthritis. The present sequence represents a CD40L poly-A tract sequence
CC   which is used in an example from the present invention
XX
SQ   Sequence 29 BP; 22 A; 4 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 29;
  Best Local Similarity   87.5%;  Pred. No. 1.4e+03;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTT 2182
              ||| |  |||||||||||||||||
Db         24 TTTTTGGTTTTTTTTTTTTTTT 1


RESULT 821
AAF74929/c
ID   AAF74929 standard; DNA; 29 BP.
XX
AC   AAF74929;
XX
DT   23-MAY-2001  (first entry)
XX
DE   CD40L poly-A tract sequence SEQ ID NO:26.
XX
KW   Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW   diagnosis; antiarthritic; antirheumatic; immunosuppressive;
KW   antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200119844-A1.
XX
PD   22-MAR-2001.
XX
PF   13-SEP-2000; 2000WO-US024966.
XX
PR   13-SEP-1999;   99US-0153625P.
XX
PA   (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
PI   Crow MK,  Li Y;
XX
DR   WPI; 2001-244776/25.
XX
PT   New altered CD40L promoter for use in the study, diagnosis and treatment
PT   of a variety of inflammatory disorders and autoimmune diseases, such as
PT   rheumatoid arthritis.
XX
PS   Example 1; Fig 3; 90pp; English.
```

```
XX
CC   The present invention describes an isolated, purified nucleic acid, which
CC   is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC   residues 331-455 of the sequence comprising 455 nucleotides given in
CC   AAF74905 where A in the wild type sequence at position 331 (corresponding
CC   to position -125) is replaced with C. (I) has antiarthritic,
CC   antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC   be used in gene therapy. (I) is useful in the study, diagnosis and
CC   treatment of inflammatory and autoimmune diseases, as well as diseases in
CC   which elevated expression of CD40L is a factor, e.g., rheumatoid
CC   arthritis. The present sequence represents a CD40L poly-A tract sequence
CC   which is used in an example from the present invention
XX
SQ   Sequence 29 BP; 22 A; 4 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 29;
  Best Local Similarity   87.5%;  Pred. No. 1.4e+03;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTT 2182
              ||| |  ||||||||||||||||||
Db         24 TTTTTGGTTTTTTTTTTTTTTTT 1


RESULT 822
ABS53433/c
ID   ABS53433 standard; DNA; 32 BP.
XX
AC   ABS53433;
XX
DT   29-NOV-2002  (first entry)
XX
DE   First strand synthesis - first primer.
XX
KW   Terminal continuation; TC; ss; second strand cDNA synthesis; primer.
XX
OS   Synthetic.
XX
PN   WO200265093-A2.
XX
PD   22-AUG-2002.
XX
PF   14-FEB-2002; 2002WO-US005713.
XX
PR   14-FEB-2001; 2001US-0268645P.
PR   14-FEB-2001; 2001US-0268664P.
PR   18-JUL-2001; 2001US-0306216P.
PR   07-NOV-2001; 2001US-0344557P.
PR   07-NOV-2001; 2001US-0348242P.
PR   09-NOV-2001; 2001US-0350176P.
XX
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (REME-) RES FOUND MENTAL HYGIENE INC.
XX
PI   Ginsberg SD,  Che S;
XX
DR   WPI; 2002-567050/60.
XX
PT   Increasing efficiency of second strand cDNA synthesis using terminal
PT   continuation model before performing further RNA amplification by RNA
PT   transcription.
XX
PS   Example 4; Page 78; 128pp; English.
XX
CC   This invention relates to a novel method for increasing the efficiency of
CC   second strand cDNA synthesis through a mechanism of terminal
CC   continuation. In the method an RNA molecule is obtained and a first
CC   primer is added that comprises a region that hybridises to a
CC   complementary region of the molecule before a second primer is added
CC   comprising at least one riboguanine at the 3' end of the primer. A first
CC   complementary nucleic acid molecule is synthesised, the RNA molecule and
CC   second primer are removed and a second complementary nucleic acid
CC   molecule is synthesised to form a second hybrid with an extension product
CC   of the third primer bound to the first complementary molecule. The method
CC   of the invention is useful for increasing the efficiency of second strand
CC   cDNA synthesis and may be used for linear amplification of genetic
CC   signals from histologically stained tissue. The present sequence
CC   represents a first strand synthesis - first primer used in the method of
CC   the invention
XX
SQ   Sequence 32 BP; 3 A; 4 C; 1 G; 22 T; 0 U; 2 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 32;
  Best Local Similarity   95.0%;  Pred. No. 1.7e+03;
  Matches   19;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              :||||||||||||||||||
Db         31 BAAAAAAAAAAAAAAAAAAA 12


RESULT 823
AAQ43973/c
ID   AAQ43973 standard; DNA; 32 BP.
XX
AC   AAQ43973;
XX
DT   25-MAR-2003  (revised)
DT   28-OCT-1993  (first entry)
XX
DE   Triple helix forming oligonucleotide I.
XX
KW   Purine; pyrimidine; tracts; intramolecular triplex; therapeutic;
KW   diagnostic; control; gene expresssion; mRNA synthesis suppression; ss.
XX
OS   Synthetic.
XX
PN   WO9312230-A1.
XX
PD   24-JUN-1993.
XX
PF   11-DEC-1992;   92WO-US010792.
XX
PR   13-DEC-1991;   91US-00808452.
PR   21-JAN-1992;   92US-00826934.
XX
PA   (STRI ) SRI INT.
XX
PI   Jayasena SD,  Johnston BH;
XX
DR   WPI; 1993-214172/26.
XX
PT   New oligo:nucleotide(s) forming triple helix with target nucleic acid -
PT   contain purine and pyrimidine tracts in specific orientations, useful
PT   therapeutically or diagnostically e.g. for inactivating HIV RNA, etc.
XX
PS   Disclosure; Page 47; 101pp; English.
XX
CC   The sequence is that of an oligonucleotide, I, which is able to form a
CC   triple helix with a duplex nucleic acid (dsNA) contg. a target sequence
CC   which comprises at least one pyrimidine tract, and at least one adjacent
CC   purine tract. It is useful for therapeutic or diagnostic control of gene
CC   expression, e.g. suppression of mRNA synthesis from a target gene. A
CC   specified application is targetting of RNA in the HIV-1 genome. When
CC   appropriately labelled it may also be used as a probe. Attachment of
CC   cleavage agents caused permanent inactivation of the target by site-
CC   specific cleavage. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 32 BP; 8 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 32;
  Best Local Similarity   87.5%;  Pred. No. 1.7e+03;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAA 2804
              ||  ||||||||||||||||||
```

```
Db         32 AAAAAAAAAAAAAAAAAAAAAAAA 9


RESULT 824
AAL44170/c
ID   AAL44170 standard; DNA; 33 BP.
XX
AC   AAL44170;
XX
DT   03-OCT-2002  (first entry)
XX
DE   Porphyra yezoensis cytochrome C - related PCR primer, SEQ ID NO 4.
XX
KW   Cytochrome C; ss; maturation protein; nitrogen oxide trapping;
KW   polluted atmosphere purification; PCR; primer.
XX
OS   Porphyra yezoensis.
XX
PN   WO200259339-A1.
XX
PD   01-AUG-2002.
XX
PF   23-JAN-2002; 2002WO-JP000467.
XX
PR   23-JAN-2001; 2001JP-00014510.
XX
PA   (UYNI-) UNIV NIPPON.
XX
PI   Oku T,  Nishio T,  Satoh T;
XX
DR   WPI; 2002-557951/59.
XX
PT   Production of cytochrome c by culturing prokaryote transformed with
PT   vector containing e.g. DNA of signal peptide and of eukaryotic cytochrome
PT   c maturation protein for use in reagents and drugs for trapping nitrogen
PT   oxide.
XX
PS   Example 1; Page 7-8; 27pp; Japanese.
XX
CC   The invention comprises a method for the production of cytochrome C. The
CC   method involves culturing a prokaryote that has been transformed with a
CC   vector encoding a signal peptide and a cytochrome C maturation protein.
CC   The method of the invention is useful for producing cytochrome C.
CC   Cytochrome C produced by the method of the invention is used in reagents
CC   and drugs for trapping nitrogen oxide (e.g. in purifying polluted
CC   atmosphere by trapping nitrogen oxide). The present DNA sequence
CC   represents a Porphyra yezoensis cytochrome C - related PCR primer
XX
SQ   Sequence 33 BP; 1 A; 3 C; 3 G; 26 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 33;
  Best Local Similarity   87.5%;  Pred. No. 1.8e+03;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||
Db         33 AAAAAAAAAAAAAAAAAAAAAAAA 10


RESULT 825
ABQ80396
ID   ABQ80396 standard; DNA; 35 BP.
XX
AC   ABQ80396;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Probe APC 2.
XX
KW   Probe; target; nanoparticle; detection; DNA sequencing; pathogen;
KW   infection; screening; colour change; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /note= "Gold-S'-A"
XX
PN   WO2003048769-A1.
XX
PD   12-JUN-2003.
XX
PF   27-NOV-2002; 2002WO-US038069.
XX
PR   30-NOV-2001; 2001US-0334644P.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Storhoff JJ,  Fritz BM,  Herrmann M;
XX
DR   WPI; 2003-617993/58.
XX
PT   Detecting target polynucleotide in a sample, by amplifying target,
PT   hybridizing it to oligonucleotides bound to nanoparticles in nanoparticle
PT   detection system, and determining amount of signal generated due to
PT   binding.
XX
PS   Example 1; Page 35; 74pp; English.
XX
CC   The sequences given in ABQ80394-99 represent probes and targets which
CC   were used in the method of the invention for detecting a target
CC   polynucleotide in a sample. The method comprises amplifying the target,
CC   hybridizing the target to oligonucleotides bound to nanoparticles in a
CC   nanoparticle detection system, determining the amount of signal generated
CC   as a result of binding, optionally repeating the above steps, and
CC   detecting the presence of the target oligonucleotide by analysing for the
CC   amount of signal produced after at least one amplification cycle. The
CC   method is useful for detecting target polynucleotide in a sample, and for
CC   determining the quantity of target polynucleotide in a sample. The method
CC   is useful in research and analytical laboratories in DNA sequencing, in
CC   the field to detect the presence of specific pathogens, in the doctor's
CC   office for quick identification of an infection to assist in prescribing
CC   a drug for treatment, and in homes and health centres for inexpensive
CC   first-line screening. The method is based on observing colour change with
CC   the naked eye, hence the method is cheap, fast, simple, robust, do not
CC   require specialized or expensive equipment, and little or no
CC   instrumentation is required
XX
SQ   Sequence 35 BP; 28 A; 1 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 35;
  Best Local Similarity   87.5%;  Pred. No. 2e+03;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAA 24


RESULT 826
AAF85682/c
ID   AAF85682 standard; DNA; 37 BP.
XX
AC   AAF85682;
XX
DT   25-JUN-2001  (first entry)
XX
DE   Pea blight resistance protein related oligonucleotide #1.
XX
KW   Pea; blight resistance; nucleotide triphosphate decomposition; ds.
XX
OS   Unidentified.
XX
PN   JP2001017176-A.
XX
```

```
PD   23-JAN-2001.
XX
PF   02-JUL-1999;   99JP-00189129.
XX
PR   02-JUL-1999;   99JP-00189129.
XX
PA   (KYOU ) UNIV KYOTO.
XX
DR   WPI; 2001-320697/34.
XX
PT   New blight-resistant polypeptide useful for giving blight resistance to a
PT   plant.
XX
PS   Example; Page 6; 20pp; Japanese.
XX
CC   The present invention provides the protein and coding sequences of a pea
CC   protein with nucleotide triphosphate decomposing activity. The gene can
CC   be used for conferring blight resistance on a plant
XX
SQ   Sequence 37 BP; 2 A; 3 C; 3 G; 29 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 37;
  Best Local Similarity   87.5%;  Pred. No. 2.2e+03;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db         37 AAAAAAAAAAAAAAAAAAAAAAAA 14


RESULT 827
AAQ75552
ID   AAQ75552 standard; DNA; 19 BP.
XX
AC   AAQ75552;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 19 BP; 2 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAA 2188
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTAA 19


RESULT 828
AAQ75556/c
ID   AAQ75556 standard; DNA; 19 BP.
XX
AC   AAQ75556;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 19 BP; 1 A; 1 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||||
Db         19 TGAAAAAAAAAAAAAAAAA 1


RESULT 829
AAT10757
ID   AAT10757 standard; RNA; 19 BP.
XX
AC   AAT10757;
XX
DT   09-SEP-1996  (first entry)
XX
DE   Oligonucleotide probe, T-2.
XX
KW   Electronically self-addressable device; ED; electrode; current source;
KW   attachment layer; permeable; counterion; genetic typing; probe;
```

```
KW   detection; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /note= "5'-amino terminus"
XX
PN   WO9601836-A1.
XX
PD   25-JAN-1996.
XX
PF   05-JUL-1995;   95WO-US008570.
XX
PR   07-JUL-1994;   94US-00271882.
XX
PA   (NANO-) NANOGEN INC.
XX
PI   Heller MJ,  Tu E,  Evans GA,  Sosnowski RG;
XX
DR   WPI; 1996-097582/10.
XX
PT   Electronically self-addressable device - used for electronic control of,
PT   e.g. nucleic acid hybridisation.
XX
PS   Example 1; Page 61; 155pp; English.
XX
CC   The sequences given in AAT10742-67 are synthetic oligonucleotides which
CC   are used in the construction of the electronically self- addressable
CC   device (ED) of the invention. The ED comprises a substrate, an electrode
CC   or opt. a number of electrodes supported by the substrate, a current
CC   source operatively connected to the electrode and an attachment layer
CC   adjacent to the electrode which is permeable to a counterion but not
CC   permeable to a molecule capable of insulating or binding to the
CC   electrode. The attachment layer is capable of attaching a macromolecule.
CC   The ED is used for genetic typing and comprises a number of
CC   electronically addressable locations each comprising an electrode, and a
CC   binding entity, such as one of these probes, attached to each of the
CC   locations capable of detecting the presence of a genetic sequence
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 830
AAT10757/c
ID   AAT10757 standard; RNA; 19 BP.
XX
AC   AAT10757;
XX
DT   09-SEP-1996  (first entry)
XX
DE   Oligonucleotide probe, T-2.
XX
KW   Electronically self-addressable device; ED; electrode; current source;
KW   attachment layer; permeable; counterion; genetic typing; probe;
KW   detection; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /note= "5'-amino terminus"
XX
PN   WO9601836-A1.
XX
PD   25-JAN-1996.
XX
PF   05-JUL-1995;   95WO-US008570.
XX
PR   07-JUL-1994;   94US-00271882.
XX
PA   (NANO-) NANOGEN INC.
XX
PI   Heller MJ,  Tu E,  Evans GA,  Sosnowski RG;
XX
DR   WPI; 1996-097582/10.
XX
PT   Electronically self-addressable device - used for electronic control of,
PT   e.g. nucleic acid hybridisation.
XX
PS   Example 1; Page 61; 155pp; English.
XX
CC   The sequences given in AAT10742-67 are synthetic oligonucleotides which
CC   are used in the construction of the electronically self- addressable
CC   device (ED) of the invention. The ED comprises a substrate, an electrode
CC   or opt. a number of electrodes supported by the substrate, a current
CC   source operatively connected to the electrode and an attachment layer
CC   adjacent to the electrode which is permeable to a counterion but not
CC   permeable to a molecule capable of insulating or binding to the
CC   electrode. The attachment layer is capable of attaching a macromolecule.
CC   The ED is used for genetic typing and comprises a number of
CC   electronically addressable locations each comprising an electrode, and a
CC   binding entity, such as one of these probes, attached to each of the
CC   locations capable of detecting the presence of a genetic sequence
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 831
AAV07878
ID   AAV07878 standard; DNA; 19 BP.
XX
AC   AAV07878;
XX
DT   14-DEC-1998  (first entry)
XX
DE   Aminooxy-modified oligonucleotide.
XX
KW   phosphorothioate; ras gene; malignant cell growth; aminooxy-modified;
KW   nuclease resistance; reporter group; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   15. .18
FT                   /*tag=  a
FT                   /note= "5-methyl, 2'-aminooxyethoxy-thymidine"
XX
PN   WO9835978-A1.
XX
PD   20-AUG-1998.
XX
PF   13-FEB-1998;   98WO-US002405.
XX
PR   14-FEB-1997;   97US-0037143P.
PR   30-JAN-1998;   98US-00016520.
XX
PA   (ISIS-) ISIS PHARM INC.
```

```
XX
PI   Cook PD,  Manoharan M,  Kawasaki AM;
XX
DR   WPI; 1998-568232/48.
XX
PT   New aminooxy-modified oligonucleotides - which can show improved binding
PT   to complementary strands and improved resistance to nuclease.
XX
PS   Disclosure; Page 84; 131pp; English.
XX
CC   The invention relates to aminooxy-modified(oligo)nucleotides or
CC   nucleosides which are useful as therapeutics, diagnostics, and research
CC   reagents. They may be used, e.g., for modulation of the ras gene and may
CC   be able to modulate the process of transformation from normal to
CC   malignant cell growth. They may be prepared using known methods.
CC   Inclusion of the aminooxy moieties can improve binding of
CC   oligonucleotides to complementary strands. The moieties can also provide
CC   conjugation sites useful for conjugation of useful ligands (e.g. reporter
CC   groups and groups for modifying uptake, distribution or other
CC   pharmacodynamic properties) to oligonucleotides. The present sequence
CC   represents an example of an aminooxy-modified oligonucleotide disclosed
CC   in the specification
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 832
AAV07878/c
ID   AAV07878 standard; DNA; 19 BP.
XX
AC   AAV07878;
XX
DT   14-DEC-1998  (first entry)
XX
DE   Aminooxy-modified oligonucleotide.
XX
KW   phosphorothioate; ras gene; malignant cell growth; aminooxy-modified;
KW   nuclease resistance; reporter group; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   15. .18
FT                   /*tag=  a
FT                   /note= "5-methyl, 2'-aminooxyethoxy-thymidine"
XX
PN   WO9835978-A1.
XX
PD   20-AUG-1998.
XX
PF   13-FEB-1998;   98WO-US002405.
XX
PR   14-FEB-1997;   97US-0037143P.
PR   30-JAN-1998;   98US-00016520.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cook PD,  Manoharan M,  Kawasaki AM;
XX
DR   WPI; 1998-568232/48.
XX
PT   New aminooxy-modified oligonucleotides - which can show improved binding
PT   to complementary strands and improved resistance to nuclease.
XX
PS   Disclosure; Page 84; 131pp; English.
XX
CC   The invention relates to aminooxy-modified(oligo)nucleotides or
CC   nucleosides which are useful as therapeutics, diagnostics, and research
CC   reagents. They may be used, e.g., for modulation of the ras gene and may
CC   be able to modulate the process of transformation from normal to
CC   malignant cell growth. They may be prepared using known methods.
CC   Inclusion of the aminooxy moieties can improve binding of
CC   oligonucleotides to complementary strands. The moieties can also provide
CC   conjugation sites useful for conjugation of useful ligands (e.g. reporter
CC   groups and groups for modifying uptake, distribution or other
CC   pharmacodynamic properties) to oligonucleotides. The present sequence
CC   represents an example of an aminooxy-modified oligonucleotide disclosed
CC   in the specification
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 833
AAV06820
ID   AAV06820 standard; DNA; 19 BP.
XX
AC   AAV06820;
XX
DT   13-OCT-1998  (first entry)
XX
DE   Oligonucleotide containing modified internucleotide linkage.
XX
KW   oligonucleotide; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   16. .18
FT                   /*tag=  a
FT                   /note= "these T residues are formed as part of a
FT                   conventional phosphoramidite oligonucleotide synthesis
FT                   process but using as the reactant a thymosine nucleoside
FT                   having at the 3'-position a group of formula -CH2-
FT                   P(OCH2CH2CN)-N(iPr)2"
XX
PN   WO9747636-A2.
XX
PD   18-DEC-1997.
XX
PF   03-JUN-1997;   97WO-GB001490.
XX
PR   13-JUN-1996;   96GB-00012600.
XX
PA   (NOVS ) NOVARTIS AG.
XX
PI   Collingwood SP,  Moser HE,  Altmann K,  Douglas ME;
XX
DR   WPI; 1998-052233/05.
XX
PT   New tetra:hydro:furan derivatives - useful in the synthesis of
PT   oligo:nucleotide(s).
XX
PS   Example 12; Page 29; 37pp; English.
XX
CC   The invention relates, inter alia, to a method of preparing an
CC   oligonucleotide by coupling (1) a new nucleoside having a protected 5'-
CC   hydroxy group and at the 3'-position a group of formula -CH2-P(OR3)-
CC   NR4R5, with (2) a nucleoside or oligonucleotide having a free 5'-hydroxy
CC   group, to give (3) a precursor having an internucleoside linkage of
CC   formula -CH2-P(OR3)-O-; and converting this to a linkage of formula -CH2-
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CC   P(OR3)(=X)-O- (where X = S or O). The present sequence is a specific
CC   example of an oligonucleotide so prepared
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 834
AAV06820/c
ID   AAV06820 standard; DNA; 19 BP.
XX
AC   AAV06820;
XX
DT   13-OCT-1998  (first entry)
XX
DE   Oligonucleotide containing modified internucleotide linkage.
XX
KW   oligonucleotide; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   16. .18
FT                   /*tag=  a
FT                   /note= "these T residues are formed as part of a
FT                   conventional phosphoramidite oligonucleotide synthesis
FT                   process but using as the reactant a thymosine nucleoside
FT                   having at the 3'-position a group of formula -CH2-
FT                   P(OCH2CH2CN)-N(iPr)2"
XX
PN   WO9747636-A2.
XX
PD   18-DEC-1997.
XX
PF   03-JUN-1997;   97WO-GB001490.
XX
PR   13-JUN-1996;   96GB-00012600.
XX
PA   (NOVS ) NOVARTIS AG.
XX
PI   Collingwood SP,  Moser HE,  Altmann K,  Douglas ME;
XX
DR   WPI; 1998-052233/05.
XX
PT   New tetra:hydro:furan derivatives - useful in the synthesis of
PT   oligo:nucleotide(s).
XX
PS   Example 12; Page 29; 37pp; English.
XX
CC   The invention relates, inter alia, to a method of preparing an
CC   oligonucleotide by coupling (1) a new nucleoside having a protected 5'-
CC   hydroxy group and at the 3'-position a group of formula -CH2-P(OR3)-
CC   NR4R5, with (2) a nucleoside or oligonucleotide having a free 5'-hydroxy
CC   group, to give (3) a precursor having an internucleoside linkage of
CC   formula -CH2-P(OR3)-O-; and converting this to a linkage of formula -CH2-
CC   P(OR3)(=X)-O- (where X = S or O). The present sequence is a specific
CC   example of an oligonucleotide so prepared
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 835
AAX81316
ID   AAX81316 standard; DNA; 19 BP.
XX
AC   AAX81316;
XX
DT   20-AUG-1999  (first entry)
XX
DE   5' amino oligonucleotide probe T-2.
XX
KW   Microelectronic device; multi-step reaction; microscopic format;
KW   ion-permeable permeation layer; electrode; electrical control; transport;
KW   attachment; binding; DNA/RNA hybrid; probe; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1
FT                   /*tag=  a
FT                   /note= "amino group attached at 5' terminal"
XX
PN   WO9929711-A1.
XX
PD   17-JUN-1999.
XX
PF   01-DEC-1998;   98WO-US025475.
XX
PR   05-DEC-1997;   97US-00986065.
XX
PA   (NANO-) NANOGEN INC.
XX
PI   Sosnowski RG,  Butler WF,  Tu E,  Nerenberg MI,  Heller MJ,  Edman CF;
XX
DR   WPI; 1999-385567/32.
XX
PT   New microelectronic device designed to carry out and control multi-step
PT   and multiplex molecular biological reactions in microscopic format.
XX
PS   Example 1; Page 90; 179pp; English.
XX
CC   The specification describes a self-addressable, self-assembling
CC   microelectronic device which is designed to actively carry out and
CC   control multi-step and multiplex molecular biological reactions in
CC   microscopic formats. A key aspect of this inventions is played by the ion
CC   -permeable permeation layer which overlies the electrode. This permeation
CC   layer allows attachment of nucleic acids to permit immobilization but
CC   also separates the attached oligonucleotides and hybridized target DNA
CC   sequences from the highly reactive electrochemical environment generated
CC   immediately at the electrode surface. The microelectronic device is
CC   designed and fabricated to actively carry out and control reactions such
CC   as nucleic acid hybridizations, antibody/antigen reactions, sample
CC   preparation, diagnostics and biopolymer synthesis. The device can
CC   electronically control the transport and attachment of specific binding
CC   entities, such as nucleic acids and polypeptides, to specific micro-
CC   locations. The device can subsequently control the transport and reaction
CC   of analytes or reactants at the addressed specific micro-locations. The
CC   device is able to concentrate analytes and reactants, remove non-
CC   specifically bound molecules, provide stringency control for DNA
CC   hybridization reactions and improve the detection of analytes. The
CC   present sequence represents a probe used to exemplify the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19
```

```
RESULT 836
AAX81316/c
ID   AAX81316 standard; DNA; 19 BP.
XX
AC   AAX81316;
XX
DT   20-AUG-1999  (first entry)
XX
DE   5' amino oligonucleotide probe T-2.
XX
KW   Microelectronic device; multi-step reaction; microscopic format;
KW   ion-permeable permeation layer; electrode; electrical control; transport;
KW   attachment; binding; DNA/RNA hybrid; probe; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1
FT                   /*tag=  a
FT                   /note= "amino group attached at 5' terminal"
XX
PN   WO9929711-A1.
XX
PD   17-JUN-1999.
XX
PF   01-DEC-1998;   98WO-US025475.
XX
PR   05-DEC-1997;   97US-00986065.
XX
PA   (NANO-) NANOGEN INC.
XX
PI   Sosnowski RG,  Butler WF,  Tu E,  Nerenberg MI,  Heller MJ,  Edman CF;
XX
DR   WPI; 1999-385567/32.
XX
PT   New microelectronic device designed to carry out and control multi-step
PT   and multiplex molecular biological reactions in microscopic format.
XX
PS   Example 1; Page 90; 179pp; English.
XX
CC   The specification describes a self-addressable, self-assembling
CC   microelectronic device which is designed to actively carry out and
CC   control multi-step and multiplex molecular biological reactions in
CC   microscopic formats. A key aspect of this inventions is played by the ion
CC   -permeable permeation layer which overlies the electrode. This permeation
CC   layer allows attachment of nucleic acids to permit immobilization but
CC   also separates the attached oligonucleotides and hybridized target DNA
CC   sequences from the highly reactive electrochemical environment generated
CC   immediately at the electrode surface. The microelectronic device is
CC   designed and fabricated to actively carry out and control reactions such
CC   as nucleic acid hybridizations, antibody/antigen reactions, sample
CC   preparation, diagnostics and biopolymer synthesis. The device can
CC   electronically control the transport and attachment of specific binding
CC   entities, such as nucleic acids and polypeptides, to specific micro-
CC   locations. The device can subsequently control the transport and reaction
CC   of analytes or reactants at the addressed specific micro-locations. The
CC   device is able to concentrate analytes and reactants, remove non-
CC   specifically bound molecules, provide stringency control for DNA
CC   hybridization reactions and improve the detection of analytes. The
CC   present sequence represents a probe used to exemplify the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1
```

```
RESULT 837
AAX81927
ID   AAX81927 standard; DNA; 19 BP.
XX
AC   AAX81927;
XX
DT   07-SEP-1999  (first entry)
XX
DE   Polynucleotide strand with amino groups.
XX
KW   Enzyme-specific cleavable polynucleotide substrate;
KW   quenched fluorescent moiety; biological assay; detection; identification;
KW   microorganism; sterilization assurance; nuclease; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   7
FT                   /*tag=  a
FT                   /note= "amine-modified C6 derivative of deoxythymidine
FT                   (dT)"
FT   modified_base   9
FT                   /*tag=  b
FT                   /note= "amine-modified C6 derivative of deoxythymidine
FT                   (dT)"
FT   modified_base   11
FT                   /*tag=  c
FT                   /note= "amine-modified C6 derivative of deoxythymidine
FT                   (dT)"
FT   modified_base   13
FT                   /*tag=  d
FT                   /note= "amine-modified C6 derivative of deoxythymidine
FT                   (dT)"
XX
PN   WO9935288-A1.
XX
PD   15-JUL-1999.
XX
PF   20-AUG-1998;   98WO-US017311.
XX
PR   09-JAN-1998;   98US-00005260.
XX
PA   (MINN ) MINNESOTA MINING & MFG CO.
XX
PI   Wei A,  Mach PA;
XX
DR   WPI; 1999-419356/35.
XX
PT   An enzyme-specific cleavable polynucleotide substrate bearing quenched
PT   fluorescent moieties.
XX
PS   Example 2; Page 20; 34pp; English.
XX
CC   The specification describes an enzyme-specific cleavable polynucleotide
CC   substrate bearing quenched fluorescent moieties. The enzyme-specific
CC   cleavable polynucleotide substrate is useful in biological assays for
CC   detection and identification of microorganisms, sterilization assurance,
CC   pharmaceutical discovery, enzyme assays, immunoassays and other
CC   biological assays. The method provides a rapid and convenient approach
CC   for detection and identification of microorganisms. It can be adapted to
CC   sequence-dependent or sequence-independent tests. The invention provides
CC   improved accuracy, faster detection, and overall lower cost in detection
CC   and identification of microorganisms. The presence of nuclease is
CC   measured more accurately and sensitively by red-shifting the emission
CC   wavelength from far UV region (350-400 nm) to the 500-600 nm region of
CC   the electromagnetic spectrum and reducing the effect of background signal
CC   levels of intact reagents. The present sequence is used in the course of
CC   the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
```

```
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 838
AAX81927/c
ID   AAX81927 standard; DNA; 19 BP.
XX
AC   AAX81927;
XX
DT   07-SEP-1999  (first entry)
XX
DE   Polynucleotide strand with amino groups.
XX
KW   Enzyme-specific cleavable polynucleotide substrate;
KW   quenched fluorescent moiety; biological assay; detection; identification;
KW   microorganism; sterilization assurance; nuclease; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   7
FT                   /*tag=  a
FT                   /note= "amine-modified C6 derivative of deoxythymidine
FT                   (dT)"
FT   modified_base   9
FT                   /*tag=  b
FT                   /note= "amine-modified C6 derivative of deoxythymidine
FT                   (dT)"
FT   modified_base   11
FT                   /*tag=  c
FT                   /note= "amine-modified C6 derivative of deoxythymidine
FT                   (dT)"
FT   modified_base   13
FT                   /*tag=  d
FT                   /note= "amine-modified C6 derivative of deoxythymidine
FT                   (dT)"
XX
PN   WO9935288-A1.
XX
PD   15-JUL-1999.
XX
PF   20-AUG-1998;   98WO-US017311.
XX
PR   09-JAN-1998;   98US-00005260.
XX
PA   (MINN ) MINNESOTA MINING & MFG CO.
XX
PI   Wei A,  Mach PA;
XX
DR   WPI; 1999-419356/35.
XX
PT   An enzyme-specific cleavable polynucleotide substrate bearing quenched
PT   fluorescent moieties.
XX
PS   Example 2; Page 20; 34pp; English.
XX
CC   The specification describes an enzyme-specific cleavable polynucleotide
CC   substrate bearing quenched fluorescent moieties. The enzyme-specific
CC   cleavable polynucleotide substrate is useful in biological assays for
CC   detection and identification of microorganisms, sterilization assurance,
CC   pharmaceutical discovery, enzyme assays, immunoassays and other
CC   biological assays. The method provides a rapid and convenient approach
CC   for detection and identification of microorganisms. It can be adapted to
CC   sequence-dependent or sequence-independent tests. The invention provides
CC   improved accuracy, faster detection, and overall lower cost in detection
CC   and identification of microorganisms. The presence of nuclease is
CC   measured more accurately and sensitively by red-shifting the emission
CC   wavelength from far UV region (350-400 nm) to the 500-600 nm region of
CC   the electromagnetic spectrum and reducing the effect of background signal
CC   levels of intact reagents. The present sequence is used in the course of
CC   the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 839
AAZ01358
ID   AAZ01358 standard; DNA; 19 BP.
XX
AC   AAZ01358;
XX
DT   27-SEP-1999  (first entry)
XX
DE   PCR primer for PG1 biallelic marker 4-4-187.
XX
KW   PG1 gene; biallelic marker; PCR primer; PG1-related biallelic marker;
KW   cancer; prostate cancer; diagnosis; therapy; prostate specific antigen;
KW   PSA; human; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9932644-A2.
XX
PD   01-JUL-1999.
XX
PF   22-DEC-1998;   98WO-IB002133.
XX
PR   22-DEC-1997;   97US-00996306.
PR   09-SEP-1998;   98US-0099658P.
XX
PA   (GEST ) GENSET.
XX
PI   Cohen D,  Blumenfeld M,  Chumakov I,  Bougueleret L;
XX
DR   WPI; 1999-405178/34.
XX
PT   Use of a prostate cancer associated gene and biallelic markers derived
PT   from it.
XX
PS   Claim 4; Page 374; 385pp; English.
XX
CC   The invention relates to a mammalian PG1 gene and protein, and a set of
CC   PG1 biallelic markers. The PG1 polynucleotide and biallelic markers are
CC   used in a hybridisation assay, a sequencing assay, or in an allele-
CC   specific amplification assay for determining the identity of a nucleotide
CC   at a PG1-related biallelic marker. The methods can be used to detect and
CC   to assess the risk of developing cancer or prostate cancer. Early-stage
CC   diagnosis of prostate cancer relies on prostate specific antigen (PSA)
CC   dosage. However, the effectiveness of this is limited due to its
CC   inability to discriminate between malignant and non-malignant affections
CC   of the organ. A need exists for both a reliable diagnostic procedure
CC   which would enable early-stage diagnosis, and for preventative and
CC   curative treatments of the disease. The PG1 gene can be used for
CC   detection of prostate cancer, and the risk of developing it in the
CC   future, and can also be used to determine therapies for the disease
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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```
Qy       2166 TTTTTTTTTTTTTTTTTT 2184
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 19


RESULT 840
AAZ01358/c
ID   AAZ01358 standard; DNA; 19 BP.
XX
AC   AAZ01358;
XX
DT   27-SEP-1999  (first entry)
XX
DE   PCR primer for PG1 biallelic marker 4-4-187.
XX
KW   PG1 gene; biallelic marker; PCR primer; PG1-related biallelic marker;
KW   cancer; prostate cancer; diagnosis; therapy; prostate specific antigen;
KW   PSA; human; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9932644-A2.
XX
PD   01-JUL-1999.
XX
PF   22-DEC-1998;   98WO-IB002133.
XX
PR   22-DEC-1997;   97US-00996306.
PR   09-SEP-1998;   98US-0099658P.
XX
PA   (GEST ) GENSET.
XX
PI   Cohen D,  Blumenfeld M,  Chumakov I,  Bougueleret L;
XX
DR   WPI; 1999-405178/34.
XX
PT   Use of a prostate cancer associated gene and biallelic markers derived
PT   from it.
XX
PS   Claim 4; Page 374; 385pp; English.
XX
CC   The invention relates to a mammalian PG1 gene and protein, and a set of
CC   PG1 biallelic markers. The PG1 polynucleotide and biallelic markers are
CC   used in a hybridisation assay, a sequencing assay, or in an allele-
CC   specific amplification assay for determining the identity of a nucleotide
CC   at a PG1-related biallelic marker. The methods can be used to detect and
CC   to assess the risk of developing cancer or prostate cancer. Early-stage
CC   diagnosis of prostate cancer relies on prostate specific antigen (PSA)
CC   dosage. However, the effectiveness of this is limited due to its
CC   inability to discriminate between malignant and non-malignant affections
CC   of the organ. A need exists for both a reliable diagnostic procedure
CC   which would enable early-stage diagnosis, and for preventative and
CC   curative treatments of the disease. The PG1 gene can be used for
CC   detection of prostate cancer, and the risk of developing it in the
CC   future, and can also be used to determine therapies for the disease
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              ||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAA 1


RESULT 841
AAZ61390
ID   AAZ61390 standard; DNA; 19 BP.
XX
AC   AAZ61390;
XX
DT   19-JUN-2000  (first entry)
XX
DE   Uniform phosphodiester oligonucleotide.
XX
KW   Oligomeric compound; 2'-O-modified ribosyl nucleoside; 3' endo geometry;
KW   nuclease resistance; phosphodiester; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   16
FT                   /*tag=  a
FT                   /note= "2'-modified T"
FT   modified_base   17
FT                   /*tag=  b
FT                   /note= "2'-modified T"
FT   modified_base   18
FT                   /*tag=  c
FT                   /note= "2'-modified T"
FT   modified_base   19
FT                   /*tag=  d
FT                   /note= "2'-modified T"
XX
PN   WO200008044-A1.
XX
PD   17-FEB-2000.
XX
PF   06-AUG-1999;   99WO-US017895.
XX
PR   07-AUG-1998;   98US-00130566.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Manoharan M,  Cook PD;
XX
DR   WPI; 2000-205668/18.
XX
PT   Novel 2'-O-aminoethyloxyethyl modified nucleosides and oligonucleotides
PT   used in diagnostic, therapeutic and research reagents.
XX
PS   Disclosure; Page 44; 60pp; English.
XX
CC   The present sequence represents an uniform phosphodiester
CC   oligonucleotide. The specification describes oligomeric compounds
CC   containing 2'-O-modified ribosyl nucleosides. The 2'-O-modified
CC   nucleosides include ring structures that position the sugar moiety of the
CC   nucleosides preferentially in 3' endo geometries. The modified oligomeric
CC   compounds have increased binding affinity and increased nuclease
CC   resistance. The oligomeric compounds can be used in diagnostic,
CC   therapeutic and research reagents
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2184
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 19


RESULT 842
AAZ61390/c
ID   AAZ61390 standard; DNA; 19 BP.
XX
AC   AAZ61390;
XX
DT   19-JUN-2000  (first entry)
XX
DE   Uniform phosphodiester oligonucleotide.
XX
```

```
KW   Oligomeric compound; 2'-O-modified ribosyl nucleoside; 3' endo geometry;
KW   nuclease resistance; phosphodiester; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   16
FT                   /*tag=  a
FT                   /note= "2'-modified T"
FT   modified_base   17
FT                   /*tag=  b
FT                   /note= "2'-modified T"
FT   modified_base   18
FT                   /*tag=  c
FT                   /note= "2'-modified T"
FT   modified_base   19
FT                   /*tag=  d
FT                   /note= "2'-modified T"
XX
PN   WO200008044-A1.
XX
PD   17-FEB-2000.
XX
PF   06-AUG-1999;   99WO-US017895.
XX
PR   07-AUG-1998;   98US-00130566.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Manoharan M,  Cook PD;
XX
DR   WPI; 2000-205668/18.
XX
PT   Novel 2'-O-aminoethyloxyethyl modified nucleosides and oligonucleotides
PT   used in diagnostic, therapeutic and research reagents.
XX
PS   Disclosure; Page 44; 60pp; English.
XX
CC   The present sequence represents an uniform phosphodiester
CC   oligonucleotide. The specification describes oligomeric compounds
CC   containing 2'-O-modified ribosyl nucleosides. The 2'-O-modified
CC   nucleosides include ring structures that position the sugar moiety of the
CC   nucleosides preferentially in 3' endo geometries. The modified oligomeric
CC   compounds have increased binding affinity and increased nuclease
CC   resistance. The oligomeric compounds can be used in diagnostic,
CC   therapeutic and research reagents
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 843
AAZ61404
ID   AAZ61404 standard; DNA; 19 BP.
XX
AC   AAZ61404;
XX
DT   19-JUN-2000  (first entry)
XX
DE   2'-O-modified ribosyl oligonucleotide with phosphodiester linkages.
XX
KW   Oligomeric compound; 2'-O-modified ribosyl nucleoside; 3' endo geometry;
KW   nuclease resistance; phosphorothioate; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .19
FT                   /*tag=  a
FT                   /note= "nucleosides linked by phosphodiester linkages"
FT   modified_base   16. .19
FT                   /*tag=  b
FT                   /note= "2'-O-[2-N,N-dimethylaminoethyl)oxyethyl-5- methyl
FT                   uridine"
XX
PN   WO200008044-A1.
XX
PD   17-FEB-2000.
XX
PF   06-AUG-1999;   99WO-US017895.
XX
PR   07-AUG-1998;   98US-00130566.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Manoharan M,  Cook PD;
XX
DR   WPI; 2000-205668/18.
XX
PT   Novel 2'-O-aminoethyloxyethyl modified nucleosides and oligonucleotides
PT   used in diagnostic, therapeutic and research reagents.
XX
PS   Disclosure; Page 51; 60pp; English.
XX
CC   The present sequence represents an oligomeric compound containing 2'-O-
CC   modified ribosyl nucleosides. The oligomeric compound contains
CC   phosphodiester linkages. The 2'-O-modified nucleosides include ring
CC   structures that position the sugar moiety of the nucleosides
CC   preferentially in 3' endo geometries. The modified oligomeric compounds
CC   have increased binding affinity and increased nuclease resistance. The
CC   oligomeric compounds can be used in diagnostic, therapeutic and research
CC   reagents
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 844
AAZ61404/c
ID   AAZ61404 standard; DNA; 19 BP.
XX
AC   AAZ61404;
XX
DT   19-JUN-2000  (first entry)
XX
DE   2'-O-modified ribosyl oligonucleotide with phosphodiester linkages.
XX
KW   Oligomeric compound; 2'-O-modified ribosyl nucleoside; 3' endo geometry;
KW   nuclease resistance; phosphorothioate; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .19
FT                   /*tag=  a
FT                   /note= "nucleosides linked by phosphodiester linkages"
FT   modified_base   16. .19
FT                   /*tag=  b
FT                   /note= "2'-O-[2-N,N-dimethylaminoethyl)oxyethyl-5- methyl
FT                   uridine"
XX
PN   WO200008044-A1.
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XX
PD 17-FEB-2000.
XX
PF 06-AUG-1999; 99WO-US017895.
XX
PR 07-AUG-1998; 98US-00130566.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Manoharan M, Cook PD;
XX
DR WPI; 2000-205668/18.
XX
PT Novel 2'-O-aminoethyloxyethyl modified nucleosides and oligonucleotides
PT used in diagnostic, therapeutic and research reagents.
XX
PS Disclosure; Page 51; 60pp; English.
XX
CC The present sequence represents an oligomeric compound containing 2'-O-
CC modified ribosyl nucleosides. The oligomeric compound contains
CC phosphodiester linkages. The 2'-O-modified nucleosides include ring
CC structures that position the sugar moiety of the nucleosides
CC preferentially in 3' endo geometries. The modified oligomeric compounds
CC have increased binding affinity and increased nuclease resistance. The
CC oligomeric compounds can be used in diagnostic, therapeutic and research
CC reagents
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 19 AAAAAAAAAAAAAAAAAAA 1

RESULT 845
AAC62422
ID AAC62422 standard; DNA; 19 BP.
XX
AC AAC62422;
XX
DT 07-FEB-2001 (first entry)
XX
DE T19 diester for use in nuclease stability assay.
XX
KW T19 diester; nuclease stability assay; polymerase chain reaction; PCR;
KW molecular cloning; disease diagnosis; disease treatment; ss.
XX
OS Synthetic.
XX
PN US6127124-A.
XX
PD 03-OCT-2000.
XX
PF 20-JAN-1999; 99US-00234237.
XX
PR 20-JAN-1999; 99US-00234237.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Leeds JM, Cummins LL;
XX
DR WPI; 2000-637737/61.
XX
PT Determining the nuclease stability and relative binding affinity of an
PT oligomeric compound comprises capillary gel electrophoresis using laser-
PT induced fluorescence.
XX
PS Example 3; Col 19-20; 14pp; English.
XX
CC The present invention is concerned with methods of determining the
CC nuclease stability of oligomeric compounds using capillary-gel
CC electrophoresis and laser-induced fluorescence. The methods are useful in
CC the polymerase chain reaction (PCR), molecular cloning and disease
CC diagnosis and treatment. The present sequence was used in a demonstration
CC of the methods of the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTT 2184
||||||||||||||||||||
Db 1 TTTTTTTTTTTTTTTTTTT 19

RESULT 846
AAC62422/c
ID AAC62422 standard; DNA; 19 BP.
XX
AC AAC62422;
XX
DT 07-FEB-2001 (first entry)
XX
DE T19 diester for use in nuclease stability assay.
XX
KW T19 diester; nuclease stability assay; polymerase chain reaction; PCR;
KW molecular cloning; disease diagnosis; disease treatment; ss.
XX
OS Synthetic.
XX
PN US6127124-A.
XX
PD 03-OCT-2000.
XX
PF 20-JAN-1999; 99US-00234237.
XX
PR 20-JAN-1999; 99US-00234237.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Leeds JM, Cummins LL;
XX
DR WPI; 2000-637737/61.
XX
PT Determining the nuclease stability and relative binding affinity of an
PT oligomeric compound comprises capillary gel electrophoresis using laser-
PT induced fluorescence.
XX
PS Example 3; Col 19-20; 14pp; English.
XX
CC The present invention is concerned with methods of determining the
CC nuclease stability of oligomeric compounds using capillary-gel
CC electrophoresis and laser-induced fluorescence. The methods are useful in
CC the polymerase chain reaction (PCR), molecular cloning and disease
CC diagnosis and treatment. The present sequence was used in a demonstration
CC of the methods of the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 19 AAAAAAAAAAAAAAAAAAA 1

RESULT 847
AAZ95241

```
ID   AAZ95241 standard; DNA; 19 BP.
XX
AC   AAZ95241;
XX
DT   05-JUN-2000  (first entry)
XX
DE   Modified oligonucleotide #3 ISIS # 22111.
XX
KW   Antisense oligonucleotide; phosphorothioate; gene therapy; ISIS # 22111;
KW   research reagent; therapeutic; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .15
FT                   /*tag=  a
FT                   /note= "Phosphorothioate internucleotide linkage"
FT   misc_feature    15. .19
FT                   /*tag=  d
FT                   /note= "Optionally all phosphorothioate internucleotide
FT                   linkages"
FT   modified_base   16. .19
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "Optionally all 3'-O-(2-methoxyhexyl) or all 2'-O-
FT                   (2-methoxyethyl)"
FT   misc_RNA        19
FT                   /*tag=  d
XX
PN   WO200004189-A1.
XX
PD   27-JAN-2000.
XX
PF   13-JUL-1999;   99WO-US015886.
XX
PR   14-JUL-1998;   98US-00115043.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Manoharan M,  Cook PD;
XX
DR   WPI; 2000-182445/16.
XX
PT   Novel modified oligonucleotides, useful in antisense methodologies,
PT   diagnostics, therapeutics and as research reagents.
XX
PS   Example 54; Page 59; 75pp; English.
XX
CC   This sequence represents a modified oligonucleotide used in the course of
CC   the invention. The invention relates to oligonucleotides comprising
CC   nucleotides covalently linked together by internucleotide linkages where
CC   at least 1 nucleotide is linked to adjacent nucleotide by a 2',5'-
CC   internucleotide linkage and bears a 3'-substituent. The oligonucleotides
CC   can be used in gene therapy and are also useful in antisense
CC   methodologies, diagnostics, therapeutics and as research reagents
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 5.5e+02;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2184
              ||||||||||||||||||:
Db          1 TTTTTTTTTTTTTTTTTU 19


RESULT 848
AAZ95241/c
ID   AAZ95241 standard; DNA; 19 BP.
XX
AC   AAZ95241;
XX
DT   05-JUN-2000  (first entry)
XX
DE   Modified oligonucleotide #3 ISIS # 22111.
XX
KW   Antisense oligonucleotide; phosphorothioate; gene therapy; ISIS # 22111;
KW   research reagent; therapeutic; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .15
FT                   /*tag=  a
FT                   /note= "Phosphorothioate internucleotide linkage"
FT   misc_feature    15. .19
FT                   /*tag=  d
FT                   /note= "Optionally all phosphorothioate internucleotide
FT                   linkages"
FT   modified_base   16. .19
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "Optionally all 3'-O-(2-methoxyhexyl) or all 2'-O-
FT                   (2-methoxyethyl)"
FT   misc_RNA        19
FT                   /*tag=  d
XX
PN   WO200004189-A1.
XX
PD   27-JAN-2000.
XX
PF   13-JUL-1999;   99WO-US015886.
XX
PR   14-JUL-1998;   98US-00115043.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Manoharan M,  Cook PD;
XX
DR   WPI; 2000-182445/16.
XX
PT   Novel modified oligonucleotides, useful in antisense methodologies,
PT   diagnostics, therapeutics and as research reagents.
XX
PS   Example 54; Page 59; 75pp; English.
XX
CC   This sequence represents a modified oligonucleotide used in the course of
CC   the invention. The invention relates to oligonucleotides comprising
CC   nucleotides covalently linked together by internucleotide linkages where
CC   at least 1 nucleotide is linked to adjacent nucleotide by a 2',5'-
CC   internucleotide linkage and bears a 3'-substituent. The oligonucleotides
CC   can be used in gene therapy and are also useful in antisense
CC   methodologies, diagnostics, therapeutics and as research reagents
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 849
AAZ95240
ID   AAZ95240 standard; DNA; 19 BP.
XX
AC   AAZ95240;
XX
DT   05-JUN-2000  (first entry)
XX
DE   Modified oligonucleotide #3 ISIS # 22110.
XX
```

```
KW   Antisense oligonucleotide; phosphorothioate; gene therapy; ISIS # 22110;
KW   research reagent; therapeutic; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .15
FT                   /*tag=  a
FT                   /note= "Phosphorothioate internucleotide linkage"
FT   misc_feature    15. .19
FT                   /*tag=  d
FT                   /note= "Optionally all phosphorothioate internucleotide
FT                   linkages"
FT   modified_base   16. .19
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "Optionally all 3'-O-(2-methoxyhexyl) or all 2'-O-
FT                   (2-methoxyethyl)"
XX
PN   WO200004189-A1.
XX
PD   27-JAN-2000.
XX
PF   13-JUL-1999;   99WO-US015886.
XX
PR   14-JUL-1998;   98US-00115043.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Manoharan M,  Cook PD;
XX
DR   WPI; 2000-182445/16.
XX
PT   Novel modified oligonucleotides, useful in antisense methodologies,
PT   diagnostics, therapeutics and as research reagents.
XX
PS   Example 54; Page 59; 75pp; English.
XX
CC   This sequence represents a modified oligonucleotide used in the course of
CC   the invention. The invention relates to oligonucleotides comprising
CC   nucleotides covalently linked together by internucleotide linkages where
CC   at least 1 nucleotide is linked to adjacent nucleotide by a 2',5'-
CC   internucleotide linkage and bears a 3'-substituent. The oligonucleotides
CC   can be used in gene therapy and are also useful in antisense
CC   methodologies, diagnostics, therapeutics and as research reagents
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 850
AAZ95240/c
ID   AAZ95240 standard; DNA; 19 BP.
XX
AC   AAZ95240;
XX
DT   05-JUN-2000  (first entry)
XX
DE   Modified oligonucleotide #3 ISIS # 22110.
XX
KW   Antisense oligonucleotide; phosphorothioate; gene therapy; ISIS # 22110;
KW   research reagent; therapeutic; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .15
FT                   /*tag=  a
FT                   /note= "Phosphorothioate internucleotide linkage"
FT   misc_feature    15. .19
FT                   /*tag=  d
FT                   /note= "Optionally all phosphorothioate internucleotide
FT                   linkages"
FT   modified_base   16. .19
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "Optionally all 3'-O-(2-methoxyhexyl) or all 2'-O-
FT                   (2-methoxyethyl)"
XX
PN   WO200004189-A1.
XX
PD   27-JAN-2000.
XX
PF   13-JUL-1999;   99WO-US015886.
XX
PR   14-JUL-1998;   98US-00115043.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Manoharan M,  Cook PD;
XX
DR   WPI; 2000-182445/16.
XX
PT   Novel modified oligonucleotides, useful in antisense methodologies,
PT   diagnostics, therapeutics and as research reagents.
XX
PS   Example 54; Page 59; 75pp; English.
XX
CC   This sequence represents a modified oligonucleotide used in the course of
CC   the invention. The invention relates to oligonucleotides comprising
CC   nucleotides covalently linked together by internucleotide linkages where
CC   at least 1 nucleotide is linked to adjacent nucleotide by a 2',5'-
CC   internucleotide linkage and bears a 3'-substituent. The oligonucleotides
CC   can be used in gene therapy and are also useful in antisense
CC   methodologies, diagnostics, therapeutics and as research reagents
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 851
AAA06839
ID   AAA06839 standard; DNA; 19 BP.
XX
AC   AAA06839;
XX
DT   19-JUN-2000  (first entry)
XX
DE   Modified T-containing oligonucleotide, SEQ ID NO:14.
XX
KW   Modified nucleoside; aminooxy group;
KW   2'-deoxy-erythro-pentofuranosyl sugar moiety; nuclease resistant;
KW   hybridisation; binding affinity; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   16. .19
FT                   /*tag=  a
FT                   /note= "These nucleotides are substituted with 2'-O-(2-
FT                   [N-(2-amino)ethyl-N-(methyl)]aminooxyethyl) group"
XX
```

```
PN   WO200008042-A1.
XX
PD   17-FEB-2000.
XX
PF   09-AUG-1999;   99WO-US017988.
XX
PR   07-AUG-1998;   98US-00130973.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Manoharan M,  Cook PD,  Prakash TP,  Kawasaki AM;
XX
DR   WPI; 2000-224020/19.
XX
PT   Aminooxy-modified nucleosides and oligonucleotides useful in diagnostic,
PT   therapeutic and research reagents and for modulating the expression of
PT   protein in organisms.
XX
PS   Example 99; Page 120; 195pp; English.
XX
CC   The invention relates to aminooxy-modified nucleosides and
CC   oligonucleotides and to oligonucleotides that elicit RNase H for cleavage
CC   in a complementary nucleic acid strand. It also relates to
CC   oligonucleotides wherein at least some of the nucleotides are
CC   functionalised to be nuclease resistant, at least some of the nucleotides
CC   include a substituent that potentiates hybridisation of the
CC   oligonucleotide to a complementary strand, and at least some of the
CC   nucleotides include a 2'-deoxy-erythro-pentofuranosyl sugar moiety. The
CC   inclusion of one or more aminooxy moieties in such oligonucleotides
CC   provides for improved binding of such oligonucleotides to a complementary
CC   strand. The oligonucleotides of the invention aare used as diagnostic,
CC   therapeutic or research reagents, and can be used to modulate gene
CC   expression in organisms. The oligonucleotides containing the modified
CC   nucleosides have increased nuclease resistance and increased binding
CC   affinity to a complementary strand. The present sequence represents an
CC   oligonucleotide containing nucleotides substituted with a 2'-O-{2- [N-(2-
CC   amino)ethyl-N-(methyl)]aminooxyethyl} group
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 852
AAA06839/c
ID   AAA06839 standard; DNA; 19 BP.
XX
AC   AAA06839;
XX
DT   19-JUN-2000  (first entry)
XX
DE   Modified T-containing oligonucleotide, SEQ ID NO:14.
XX
KW   Modified nucleoside; aminooxy group;
KW   2'-deoxy-erythro-pentofuranosyl sugar moiety; nuclease resistant;
KW   hybridisation; binding affinity; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   16. .19
FT                   /*tag=  a
FT                   /note= "These nucleotides are substituted with 2'-O-{2-
FT                   [N-(2-amino)ethyl-N-(methyl)]aminooxyethyl} group"
XX
PN   WO200008042-A1.
XX
PD   17-FEB-2000.
XX
PF   09-AUG-1999;   99WO-US017988.
XX
PR   07-AUG-1998;   98US-00130973.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Manoharan M,  Cook PD,  Prakash TP,  Kawasaki AM;
XX
DR   WPI; 2000-224020/19.
XX
PT   Aminooxy-modified nucleosides and oligonucleotides useful in diagnostic,
PT   therapeutic and research reagents and for modulating the expression of
PT   protein in organisms.
XX
PS   Example 99; Page 120; 195pp; English.
XX
CC   The invention relates to aminooxy-modified nucleosides and
CC   oligonucleotides and to oligonucleotides that elicit RNase H for cleavage
CC   in a complementary nucleic acid strand. It also relates to
CC   oligonucleotides wherein at least some of the nucleotides are
CC   functionalised to be nuclease resistant, at least some of the nucleotides
CC   include a substituent that potentiates hybridisation of the
CC   oligonucleotide to a complementary strand, and at least some of the
CC   nucleotides include a 2'-deoxy-erythro-pentofuranosyl sugar moiety. The
CC   inclusion of one or more aminooxy moieties in such oligonucleotides
CC   provides for improved binding of such oligonucleotides to a complementary
CC   strand. The oligonucleotides of the invention aare used as diagnostic,
CC   therapeutic or research reagents, and can be used to modulate gene
CC   expression in organisms. The oligonucleotides containing the modified
CC   nucleosides have increased nuclease resistance and increased binding
CC   affinity to a complementary strand. The present sequence represents an
CC   oligonucleotide containing nucleotides substituted with a 2'-O-{2- [N-(2-
CC   amino)ethyl-N-(methyl)]aminooxyethyl} group
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 853
AAA88952
ID   AAA88952 standard; DNA; 19 BP.
XX
AC   AAA88952;
XX
DT   05-MAR-2001  (first entry)
XX
DE   Oligonucleotide ISIS 22115.
XX
KW   Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
KW   dermatological; cytostatic; virucide; antibacterial; fungicide; therapy;
KW   diagnosis; DNA-RNA hybrid; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .15
FT                   /*tag=  f
FT                   /note= "phosphorothioate linkage"
FT   modified_base   16
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-O-(2-methoxyethyl)thymidine"
FT   modified_base   17
FT                   /*tag=  b
```

```
FT                   /mod_base= OTHER
FT                   /note= "2'-O-(2-methoxyethyl)thymidine"
FT   modified_base   18
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-(2-methoxyethyl)thymidine"
FT   misc_RNA        19
FT                   /*tag=  e
FT                   /label= RNA
FT   modified_base   19
FT                   /*tag=  d
FT                   /mod_base= OTHER
FT                   /note= "2'-O-(2-methoxyethyl)uridine"
XX
PN   WO200066609-A1.
XX
PD   09-NOV-2000.
XX
PF   03-MAY-2000; 2000WO-US011913.
XX
PR   03-MAY-1999;   99US-00303586.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Manoharan M,  Mohan V;
XX
DR   WPI; 2000-672833/65.
XX
PT   New oligonucleotides containing sequences with A and B geometry, used to
PT   treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and
PT   bacterial infections, bind to single stranded RNA or DNA.
XX
PS   Example 54; Page 69; 132pp; English.
XX
CC   Oligonucleotide ISIS 22115 contains a mixed phosphodiester and
CC   phosphorothioate backbone and has 2'-O-(2-methoxyethyl) chemistry. It was
CC   used in experiments to determine the effects of snake venom
CC   phosphodiesterase and liver homogenate on the stability of
CC   oligonucleotides. Novel oligonucleotides of the invention have both A-
CC   and B-form conformational geometry. The A-form geometry modulates the
CC   binding affinity and nuclease resistance of the oligonucleotide. The B-
CC   form geometry allows the oligonucleotide to serve as substrate for RNase-
CC   H when bound to a target nucleic acid strand. The oligonucleotides can be
CC   used to treat psoriasis and other inflammatory skin conditions, skin
CC   cancers and viral, bacterial and fungal infections, and in various
CC   diagnostic applications
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 854
AAA88952/c
ID   AAA88952 standard; DNA; 19 BP.
XX
AC   AAA88952;
XX
DT   05-MAR-2001  (first entry)
XX
DE   Oligonucleotide ISIS 22115.
XX
KW   Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
KW   dermatological; cytostatic; virucide; antibacterial; fungicide; therapy;
KW   diagnosis; DNA-RNA hybrid; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .15
FT                   /*tag=  f
FT                   /note= "phosphorothioate linkage"
FT   modified_base   16
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-O-(2-methoxyethyl)thymidine"
FT   modified_base   17
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-O-(2-methoxyethyl)thymidine"
FT   modified_base   18
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-(2-methoxyethyl)thymidine"
FT   misc_RNA        19
FT                   /*tag=  e
FT                   /label= RNA
FT   modified_base   19
FT                   /*tag=  d
FT                   /mod_base= OTHER
FT                   /note= "2'-O-(2-methoxyethyl)uridine"
XX
PN   WO200066609-A1.
XX
PD   09-NOV-2000.
XX
PF   03-MAY-2000; 2000WO-US011913.
XX
PR   03-MAY-1999;   99US-00303586.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Manoharan M,  Mohan V;
XX
DR   WPI; 2000-672833/65.
XX
PT   New oligonucleotides containing sequences with A and B geometry, used to
PT   treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and
PT   bacterial infections, bind to single stranded RNA or DNA.
XX
PS   Example 54; Page 69; 132pp; English.
XX
CC   Oligonucleotide ISIS 22115 contains a mixed phosphodiester and
CC   phosphorothioate backbone and has 2'-O-(2-methoxyethyl) chemistry. It was
CC   used in experiments to determine the effects of snake venom
CC   phosphodiesterase and liver homogenate on the stability of
CC   oligonucleotides. Novel oligonucleotides of the invention have both A-
CC   and B-form conformational geometry. The A-form geometry modulates the
CC   binding affinity and nuclease resistance of the oligonucleotide. The B-
CC   form geometry allows the oligonucleotide to serve as substrate for RNase-
CC   H when bound to a target nucleic acid strand. The oligonucleotides can be
CC   used to treat psoriasis and other inflammatory skin conditions, skin
CC   cancers and viral, bacterial and fungal infections, and in various
CC   diagnostic applications
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 855
AAA88965
ID   AAA88965 standard; DNA; 19 BP.
XX
```

```
AC   AAA88965;
XX
DT   05-MAR-2001  (first entry)
XX
DE   2'-Modified chimeric oligonucleotide.
XX
KW   Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
KW   dermatological; cytostatic; virucide; antibacterial; fungicide; therapy;
KW   diagnosis; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   16
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-modified thymidine, i.e. -S-Me, -Me, 2'-ara-
FT                   (F), 2'-ara-(OH), -2'-ara-(OMe)"
FT   modified_base   17
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-modified thymidine, i.e. -S-Me, -Me, 2'-ara-
FT                   (F), 2'-ara-(OH), -2'-ara-(OMe)"
FT   modified_base   18
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-modified thymidine, i.e. -S-Me, -Me, 2'-ara-
FT                   (F), 2'-ara-(OH), -2'-ara-(OMe)"
FT   modified_base   19
FT                   /*tag=  d
FT                   /mod_base= OTHER
FT                   /note= "2'-modified thymidine, i.e. -S-Me, -Me, 2'-ara-
FT                   (F), 2'-ara-(OH), -2'-ara-(OMe)"
XX
PN   WO200066609-A1.
XX
PD   09-NOV-2000.
XX
PF   03-MAY-2000; 2000WO-US011913.
XX
PR   03-MAY-1999;   99US-00303586.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Manoharan M,  Mohan V;
XX
DR   WPI; 2000-672833/65.
XX
PT   New oligonucleotides containing sequences with A and B geometry, used to
PT   treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and
PT   bacterial infections, bind to single stranded RNA or DNA.
XX
PS   Example 86; Page 102; 132pp; English.
XX
CC   This sequence represents 2'-modified chimeric oligonucleotides containing
CC   2'-modified T. The nucleotides were used to examine the effects of the
CC   modifications on nuclease resistance. Novel oligonucleotides of the
CC   invention have both A- and B-form conformational geometry. The A-form
CC   geometry modulates the binding affinity and nuclease resistance of the
CC   oligonucleotide. The B-form geometry allows the oligonucleotide to serve
CC   as substrate for RNase-H when bound to a target nucleic acid strand. The
CC   oligonucleotides can be used to treat psoriasis and other inflammatory
CC   skin conditions, skin cancers and viral, bacterial and fungal infections,
CC   and in various diagnostic applications
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 856
AAA88965/c
ID   AAA88965 standard; DNA; 19 BP.
XX
AC   AAA88965;
XX
DT   05-MAR-2001  (first entry)
XX
DE   2'-Modified chimeric oligonucleotide.
XX
KW   Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
KW   dermatological; cytostatic; virucide; antibacterial; fungicide; therapy;
KW   diagnosis; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   16
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-modified thymidine, i.e. -S-Me, -Me, 2'-ara-
FT                   (F), 2'-ara-(OH), -2'-ara-(OMe)"
FT   modified_base   17
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-modified thymidine, i.e. -S-Me, -Me, 2'-ara-
FT                   (F), 2'-ara-(OH), -2'-ara-(OMe)"
FT   modified_base   18
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-modified thymidine, i.e. -S-Me, -Me, 2'-ara-
FT                   (F), 2'-ara-(OH), -2'-ara-(OMe)"
FT   modified_base   19
FT                   /*tag=  d
FT                   /mod_base= OTHER
FT                   /note= "2'-modified thymidine, i.e. -S-Me, -Me, 2'-ara-
FT                   (F), 2'-ara-(OH), -2'-ara-(OMe)"
XX
PN   WO200066609-A1.
XX
PD   09-NOV-2000.
XX
PF   03-MAY-2000; 2000WO-US011913.
XX
PR   03-MAY-1999;   99US-00303586.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Manoharan M,  Mohan V;
XX
DR   WPI; 2000-672833/65.
XX
PT   New oligonucleotides containing sequences with A and B geometry, used to
PT   treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and
PT   bacterial infections, bind to single stranded RNA or DNA.
XX
PS   Example 86; Page 102; 132pp; English.
XX
CC   This sequence represents 2'-modified chimeric oligonucleotides containing
CC   2'-modified T. The nucleotides were used to examine the effects of the
CC   modifications on nuclease resistance. Novel oligonucleotides of the
CC   invention have both A- and B-form conformational geometry. The A-form
CC   geometry modulates the binding affinity and nuclease resistance of the
CC   oligonucleotide. The B-form geometry allows the oligonucleotide to serve
CC   as substrate for RNase-H when bound to a target nucleic acid strand. The
CC   oligonucleotides can be used to treat psoriasis and other inflammatory
CC   skin conditions, skin cancers and viral, bacterial and fungal infections,
CC   and in various diagnostic applications
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
```

```
  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 857
AAA88949
ID   AAA88949 standard; DNA; 19 BP.
XX
AC   AAA88949;
XX
DT   05-MAR-2001  (first entry)
XX
DE   Oligonucleotide ISIS 22112.
XX
KW   Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
KW   dermatological; cytostatic; virucide; antibacterial; fungicide; therapy;
KW   diagnosis; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .19
FT                    /*tag=  e
FT                    /note= "phosphorothioate linkage"
FT   modified_base    16
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "3'-O-(2-methoxyethyl)thymidine"
FT   modified_base    17
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "3'-O-(2-methoxyethyl)thymidine"
FT   modified_base    18
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "3'-O-(2-methoxyethyl)thymidine"
FT   modified_base    19
FT                    /*tag=  d
FT                    /mod_base= OTHER
FT                    /note= "3'-O-(2-methoxyethyl)thymidine"
XX
PN   WO200066609-A1.
XX
PD   09-NOV-2000.
XX
PF   03-MAY-2000; 2000WO-US011913.
XX
PR   03-MAY-1999;   99US-00303586.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Manoharan M,  Mohan V;
XX
DR   WPI; 2000-672833/65.
XX
PT   New oligonucleotides containing sequences with A and B geometry, used to
PT   treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and
PT   bacterial infections, bind to single stranded RNA or DNA.
XX
PS   Example 54; Page 69; 132pp; English.
XX
CC   Oligonucleotide ISIS 22112 contains a phosphorothioate backbone and has
CC   3'-O-(2-methoxyethyl) chemistry. It was used in experiments to determine
CC   the effects of snake venom phosphodiesterase and liver homogenate on the
CC   stability of oligonucleotides. Novel oligonucleotides of the invention
CC   have both A- and B-form conformational geometry. The A-form geometry
CC   modulates the binding affinity and nuclease resistance of the
CC   oligonucleotide. The B-form geometry allows the oligonucleotide to serve
CC   as substrate for RNase-H when bound to a target nucleic acid strand. The
CC   oligonucleotides can be used to treat psoriasis and other inflammatory
CC   skin conditions, skin cancers and viral, bacterial and fungal infections,
CC   and in various diagnostic applications
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 858
AAA88949/c
ID   AAA88949 standard; DNA; 19 BP.
XX
AC   AAA88949;
XX
DT   05-MAR-2001  (first entry)
XX
DE   Oligonucleotide ISIS 22112.
XX
KW   Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
KW   dermatological; cytostatic; virucide; antibacterial; fungicide; therapy;
KW   diagnosis; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .19
FT                    /*tag=  e
FT                    /note= "phosphorothioate linkage"
FT   modified_base    16
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "3'-O-(2-methoxyethyl)thymidine"
FT   modified_base    17
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "3'-O-(2-methoxyethyl)thymidine"
FT   modified_base    18
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "3'-O-(2-methoxyethyl)thymidine"
FT   modified_base    19
FT                    /*tag=  d
FT                    /mod_base= OTHER
FT                    /note= "3'-O-(2-methoxyethyl)thymidine"
XX
PN   WO200066609-A1.
XX
PD   09-NOV-2000.
XX
PF   03-MAY-2000; 2000WO-US011913.
XX
PR   03-MAY-1999;   99US-00303586.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Manoharan M,  Mohan V;
XX
DR   WPI; 2000-672833/65.
XX
PT   New oligonucleotides containing sequences with A and B geometry, used to
PT   treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and
PT   bacterial infections, bind to single stranded RNA or DNA.
XX
PS   Example 54; Page 69; 132pp; English.
```

```
XX
CC   Oligonucleotide ISIS 22112 contains a phosphorothioate backbone and has
CC   3'-O-(2-methoxyethyl) chemistry. It was used in experiments to determine
CC   the effects of snake venom phosphodiesterase and liver homogenate on the
CC   stability of oligonucleotides. Novel oligonucleotides of the invention
CC   have both A- and B-form conformational geometry. The A-form geometry
CC   modulates the binding affinity and nuclease resistance of the
CC   oligonucleotide. The B-form geometry allows the oligonucleotide to serve
CC   as substrate for RNase-H when bound to a target nucleic acid strand. The
CC   oligonucleotides can be used to treat psoriasis and other inflammatory
CC   skin conditions, skin cancers and viral, bacterial and fungal infections,
CC   and in various diagnostic applications
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 859
AAA88950
ID   AAA88950 standard; DNA; 19 BP.
XX
AC   AAA88950;
XX
DT   05-MAR-2001  (first entry)
XX
DE   Oligonucleotide ISIS 22113.
XX
KW   Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
KW   dermatological; cytostatic; virucide; antibacterial; fungicide; therapy;
KW   diagnosis; DNA-RNA hybrid; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .19
FT                   /*tag=  f
FT                   /note= "phosphorothioate linkage"
FT   modified_base   16
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-O-(2-methoxyethyl)thymidine"
FT   modified_base   17
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-O-(2-methoxyethyl)thymidine"
FT   modified_base   18
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-(2-methoxyethyl)thymidine"
FT   misc_RNA        19
FT                   /*tag=  e
FT                   /label= RNA
FT   modified_base   19
FT                   /*tag=  d
FT                   /mod_base= OTHER
FT                   /note= "2'-O-(2-methoxyethyl)uridine"
XX
PN   WO200066609-A1.
XX
PD   09-NOV-2000.
XX
PF   03-MAY-2000; 2000WO-US011913.
XX
PR   03-MAY-1999;   99US-00303586.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Manoharan M,  Mohan V;
XX
DR   WPI; 2000-672833/65.
XX
PT   New oligonucleotides containing sequences with A and B geometry, used to
PT   treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and
PT   bacterial infections, bind to single stranded RNA or DNA.
XX
PS   Example 54; Page 69; 132pp; English.
XX
CC   Oligonucleotide ISIS 22113 contains a phosphorothioate backbone and has
CC   2'-O-(2-methoxyethyl) chemistry. It was used in experiments to determine
CC   the effects of snake venom phosphodiesterase and liver homogenate on the
CC   stability of oligonucleotides. Novel oligonucleotides of the invention
CC   have both A- and B-form conformational geometry. The A-form geometry
CC   modulates the binding affinity and nuclease resistance of the
CC   oligonucleotide. The B-form geometry allows the oligonucleotide to serve
CC   as substrate for RNase-H when bound to a target nucleic acid strand. The
CC   oligonucleotides can be used to treat psoriasis and other inflammatory
CC   skin conditions, skin cancers and viral, bacterial and fungal infections,
CC   and in various diagnostic applications
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 860
AAA88950/c
ID   AAA88950 standard; DNA; 19 BP.
XX
AC   AAA88950;
XX
DT   05-MAR-2001  (first entry)
XX
DE   Oligonucleotide ISIS 22113.
XX
KW   Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
KW   dermatological; cytostatic; virucide; antibacterial; fungicide; therapy;
KW   diagnosis; DNA-RNA hybrid; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .19
FT                   /*tag=  f
FT                   /note= "phosphorothioate linkage"
FT   modified_base   16
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-O-(2-methoxyethyl)thymidine"
FT   modified_base   17
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-O-(2-methoxyethyl)thymidine"
FT   modified_base   18
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-(2-methoxyethyl)thymidine"
FT   misc_RNA        19
FT                   /*tag=  e
FT                   /label= RNA
FT   modified_base   19
FT                   /*tag=  d
FT                   /mod_base= OTHER
FT                   /note= "2'-O-(2-methoxyethyl)uridine"
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XX
PN   WO200066609-A1.
XX
PD   09-NOV-2000.
XX
PF   03-MAY-2000; 2000WO-US011913.
XX
PR   03-MAY-1999;   99US-00303586.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Manoharan M,  Mohan V;
XX
DR   WPI; 2000-672833/65.
XX
PT   New oligonucleotides containing sequences with A and B geometry, used to
PT   treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and
PT   bacterial infections, bind to single stranded RNA or DNA.
XX
PS   Example 54; Page 69; 132pp; English.
XX
CC   Oligonucleotide ISIS 22113 contains a phosphorothioate backbone and has
CC   2'-O-(2-methoxyethyl) chemistry. It was used in experiments to determine
CC   the effects of snake venom phosphodiesterase and liver homogenate on the
CC   stability of oligonucleotides. Novel oligonucleotides of the invention
CC   have both A- and B-form conformational geometry. The A-form geometry
CC   modulates the binding affinity and nuclease resistance of the
CC   oligonucleotide. The B-form geometry allows the oligonucleotide to serve
CC   as substrate for RNase-H when bound to a target nucleic acid strand. The
CC   oligonucleotides can be used to treat psoriasis and other inflammatory
CC   skin conditions, skin cancers and viral, bacterial and fungal infections,
CC   and in various diagnostic applications
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 861
AAA88951
ID   AAA88951 standard; DNA; 19 BP.
XX
AC   AAA88951;
XX
DT   05-MAR-2001  (first entry)
XX
DE   Oligonucleotide ISIS 22114.
XX
KW   Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
KW   dermatological; cytostatic; virucide; antibacterial; fungicide; therapy;
KW   diagnosis; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .15
FT                    /*tag=  e
FT                    /note= "phosphorothioate linkage"
FT   modified_base    16
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "3'-O-(2-methoxyethyl)thymidine"
FT   modified_base    17
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "3'-O-(2-methoxyethyl)thymidine"
FT   modified_base    18
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "3'-O-(2-methoxyethyl)thymidine"
FT   modified_base    19
FT                    /*tag=  d
FT                    /mod_base= OTHER
FT                    /note= "3'-O-(2-methoxyethyl)thymidine"
XX
PN   WO200066609-A1.
XX
PD   09-NOV-2000.
XX
PF   03-MAY-2000; 2000WO-US011913.
XX
PR   03-MAY-1999;   99US-00303586.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Manoharan M,  Mohan V;
XX
DR   WPI; 2000-672833/65.
XX
PT   New oligonucleotides containing sequences with A and B geometry, used to
PT   treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and
PT   bacterial infections, bind to single stranded RNA or DNA.
XX
PS   Example 54; Page 69; 132pp; English.
XX
CC   Oligonucleotide ISIS 22114 contains a mixed phosphodiester and
CC   phosphorothioate backbone and has 3'-O-(2-methoxyethyl) chemistry. It was
CC   used in experiments to determine the effects of snake venom
CC   phosphodiesterase and liver homogenate on the stability of
CC   oligonucleotides. Novel oligonucleotides of the invention have both A-
CC   and B-form conformational geometry. The A-form geometry modulates the
CC   binding affinity and nuclease resistance of the oligonucleotide. The B-
CC   form geometry allows the oligonucleotide to serve as substrate for RNase-
CC   H when bound to a target nucleic acid strand. The oligonucleotides can be
CC   used to treat psoriasis and other inflammatory skin conditions, skin
CC   cancers and viral, bacterial and fungal infections, and in various
CC   diagnostic applications
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 862
AAA88951/c
ID   AAA88951 standard; DNA; 19 BP.
XX
AC   AAA88951;
XX
DT   05-MAR-2001  (first entry)
XX
DE   Oligonucleotide ISIS 22114.
XX
KW   Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
KW   dermatological; cytostatic; virucide; antibacterial; fungicide; therapy;
KW   diagnosis; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .15
FT                    /*tag=  e
FT                    /note= "phosphorothioate linkage"
FT   modified_base    16
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```
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "3'-O-(2-methoxyethyl)thymidine"
FT   modified_base   17
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "3'-O-(2-methoxyethyl)thymidine"
FT   modified_base   18
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "3'-O-(2-methoxyethyl)thymidine"
FT   modified_base   19
FT                   /*tag=  d
FT                   /mod_base= OTHER
FT                   /note= "3'-O-(2-methoxyethyl)thymidine"
XX
PN   WO200066609-A1.
XX
PD   09-NOV-2000.
XX
PF   03-MAY-2000; 2000WO-US011913.
XX
PR   03-MAY-1999;   99US-00303586.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Manoharan M,  Mohan V;
XX
DR   WPI; 2000-672833/65.
XX
PT   New oligonucleotides containing sequences with A and B geometry, used to
PT   treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and
PT   bacterial infections, bind to single stranded RNA or DNA.
XX
PS   Example 54; Page 69; 132pp; English.
XX
CC   Oligonucleotide ISIS 22114 contains a mixed phosphodiester and
CC   phosphorothioate backbone and has 3'-O-(2-methoxyethyl) chemistry. It was
CC   used in experiments to determine the effects of snake venom
CC   phosphodiesterase and liver homogenate on the stability of
CC   oligonucleotides. Novel oligonucleotides of the invention have both A-
CC   and B-form conformational geometry. The A-form geometry modulates the
CC   binding affinity and nuclease resistance of the oligonucleotide. The B-
CC   form geometry allows the oligonucleotide to serve as substrate for RNase-
CC   H when bound to a target nucleic acid strand. The oligonucleotides can be
CC   used to treat psoriasis and other inflammatory skin conditions, skin
CC   cancers and viral, bacterial and fungal infections, and in various
CC   diagnostic applications
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 863
AAA88947
ID   AAA88947 standard; DNA; 19 BP.
XX
AC   AAA88947;
XX
DT   05-MAR-2001  (first entry)
XX
DE   Oligonucleotide ISIS 22110.
XX
KW   Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
KW   dermatological; cytostatic; virucide; antibacterial; fungicide; therapy;
KW   diagnosis; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   16
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "3'-O-(2-methoxyethyl)thymidine"
FT   modified_base   17
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "3'-O-(2-methoxyethyl)thymidine"
FT   modified_base   18
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "3'-O-(2-methoxyethyl)thymidine"
FT   modified_base   19
FT                   /*tag=  d
FT                   /mod_base= OTHER
FT                   /note= "3'-O-(2-methoxyethyl)thymidine"
XX
PN   WO200066609-A1.
XX
PD   09-NOV-2000.
XX
PF   03-MAY-2000; 2000WO-US011913.
XX
PR   03-MAY-1999;   99US-00303586.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Manoharan M,  Mohan V;
XX
DR   WPI; 2000-672833/65.
XX
PT   New oligonucleotides containing sequences with A and B geometry, used to
PT   treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and
PT   bacterial infections, bind to single stranded RNA or DNA.
XX
PS   Example 54; Page 69; 132pp; English.
XX
CC   Oligonucleotide ISIS 22110 contains a phosphodiester backbone and has 3'-
CC   O-(2-methoxyethyl) chemistry. It was used in experiments to determine the
CC   effects of snake venom phosphodiesterase and liver homogenate on the
CC   stability of oligonucleotides. Novel oligonucleotides of the invention
CC   have both A- and B-form conformational geometry. The A-form geometry
CC   modulates the binding affinity and nuclease resistance of the
CC   oligonucleotide. The B-form geometry allows the oligonucleotide to serve
CC   as substrate for RNase-H when bound to a target nucleic acid strand. The
CC   oligonucleotides can be used to treat psoriasis and other inflammatory
CC   skin conditions, skin cancers and viral, bacterial and fungal infections,
CC   and in various diagnostic applications
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 864
AAA88947/c
ID   AAA88947 standard; DNA; 19 BP.
XX
AC   AAA88947;
XX
DT   05-MAR-2001  (first entry)
XX
DE   Oligonucleotide ISIS 22110.
```

```
XX
KW   Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
KW   dermatological; cytostatic; virucide; antibacterial; fungicide; therapy;
KW   diagnosis; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   16
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "3'-O-(2-methoxyethyl)thymidine"
FT   modified_base   17
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "3'-O-(2-methoxyethyl)thymidine"
FT   modified_base   18
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "3'-O-(2-methoxyethyl)thymidine"
FT   modified_base   19
FT                   /*tag=  d
FT                   /mod_base= OTHER
FT                   /note= "3'-O-(2-methoxyethyl)thymidine"
XX
PN   WO200066609-A1.
XX
PD   09-NOV-2000.
XX
PF   03-MAY-2000; 2000WO-US011913.
XX
PR   03-MAY-1999;   99US-00303586.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Manoharan M,  Mohan V;
XX
DR   WPI; 2000-672833/65.
XX
PT   New oligonucleotides containing sequences with A and B geometry, used to
PT   treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and
PT   bacterial infections, bind to single stranded RNA or DNA.
XX
PS   Example 54; Page 69; 132pp; English.
XX
CC   Oligonucleotide ISIS 22110 contains a phosphodiester backbone and has 3'-
CC   O-(2-methoxyethyl) chemistry. It was used in experiments to determine the
CC   effects of snake venom phosphodiesterase and liver homogenate on the
CC   stability of oligonucleotides. Novel oligonucleotides of the invention
CC   have both A- and B-form conformational geometry. The A-form geometry
CC   modulates the binding affinity and nuclease resistance of the
CC   oligonucleotide. The B-form geometry allows the oligonucleotide to serve
CC   as substrate for RNase-H when bound to a target nucleic acid strand. The
CC   oligonucleotides can be used to treat psoriasis and other inflammatory
CC   skin conditions, skin cancers and viral, bacterial and fungal infections,
CC   and in various diagnostic applications
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 865
AAA88948
ID   AAA88948 standard; DNA; 19 BP.
XX
AC   AAA88948;
XX
DT   05-MAR-2001  (first entry)
XX
DE   Oligonucleotide ISIS 22111.
XX
KW   Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
KW   dermatological; cytostatic; virucide; antibacterial; fungicide; therapy;
KW   diagnosis; DNA-RNA hybrid; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   16
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-O-(2-methoxyethyl)thymidine"
FT   modified_base   17
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-O-(2-methoxyethyl)thymidine"
FT   modified_base   18
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-(2-methoxyethyl)thymidine"
FT   misc_RNA        19
FT                   /*tag=  e
FT                   /label= RNA
FT   modified_base   19
FT                   /*tag=  d
FT                   /mod_base= OTHER
FT                   /note= "2'-O-(2-methoxyethyl)uridine"
XX
PN   WO200066609-A1.
XX
PD   09-NOV-2000.
XX
PF   03-MAY-2000; 2000WO-US011913.
XX
PR   03-MAY-1999;   99US-00303586.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Manoharan M,  Mohan V;
XX
DR   WPI; 2000-672833/65.
XX
PT   New oligonucleotides containing sequences with A and B geometry, used to
PT   treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and
PT   bacterial infections, bind to single stranded RNA or DNA.
XX
PS   Example 54; Page 69; 132pp; English.
XX
CC   Oligonucleotide ISIS 22111 contains a phosphodiester backbone and has 2'-
CC   O-(2-methoxyethyl) chemistry. It was used in experiments to determine the
CC   effects of snake venom phosphodiesterase and liver homogenate on the
CC   stability of oligonucleotides. Novel oligonucleotides of the invention
CC   have both A- and B-form conformational geometry. The A-form geometry
CC   modulates the binding affinity and nuclease resistance of the
CC   oligonucleotide. The B-form geometry allows the oligonucleotide to serve
CC   as substrate for RNase-H when bound to a target nucleic acid strand. The
CC   oligonucleotides can be used to treat psoriasis and other inflammatory
CC   skin conditions, skin cancers and viral, bacterial and fungal infections,
CC   and in various diagnostic applications
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19
```

```
RESULT 866
AAA88948/c
ID   AAA88948 standard; DNA; 19 BP.
XX
AC   AAA88948;
XX
DT   05-MAR-2001  (first entry)
XX
DE   Oligonucleotide ISIS 22111.
XX
KW   Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
KW   dermatological; cytostatic; virucide; antibacterial; fungicide; therapy;
KW   diagnosis; DNA-RNA hybrid; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   16
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-O-(2-methoxyethyl)thymidine"
FT   modified_base   17
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-O-(2-methoxyethyl)thymidine"
FT   modified_base   18
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-(2-methoxyethyl)thymidine"
FT   misc_RNA        19
FT                   /*tag=  e
FT                   /label= RNA
FT   modified_base   19
FT                   /*tag=  d
FT                   /mod_base= OTHER
FT                   /note= "2'-O-(2-methoxyethyl)uridine"
XX
PN   WO200066609-A1.
XX
PD   09-NOV-2000.
XX
PF   03-MAY-2000; 2000WO-US011913.
XX
PR   03-MAY-1999;   99US-00303586.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Manoharan M,  Mohan V;
XX
DR   WPI; 2000-672833/65.
XX
PT   New oligonucleotides containing sequences with A and B geometry, used to
PT   treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and
PT   bacterial infections, bind to single stranded RNA or DNA.
XX
PS   Example 54; Page 69; 132pp; English.
XX
CC   Oligonucleotide ISIS 22111 contains a phosphodiester backbone and has 2'-
CC   O-(2-methoxyethyl) chemistry. It was used in experiments to determine the
CC   effects of snake venom phosphodiesterase and liver homogenate on the
CC   stability of oligonucleotides. Novel oligonucleotides of the invention
CC   have both A- and B-form conformational geometry. The A-form geometry
CC   modulates the binding affinity and nuclease resistance of the
CC   oligonucleotide. The B-form geometry allows the oligonucleotide to serve
CC   as substrate for RNase-H when bound to a target nucleic acid strand. The
CC   oligonucleotides can be used to treat psoriasis and other inflammatory
CC   skin conditions, skin cancers and viral, bacterial and fungal infections,
CC   and in various diagnostic applications
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 867
AAA71630
ID   AAA71630 standard; DNA; 19 BP.
XX
AC   AAA71630;
XX
DT   14-DEC-2000  (first entry)
XX
DE   Phosphorothioate 20-mer primer DNA #1.
XX
KW   Phosphorothioate; primer; oligomer synthesis; antisense therapy; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkage"
XX
PN   EP1028124-A2.
XX
PD   16-AUG-2000.
XX
PF   06-SEP-1999;   99EP-00307066.
XX
PR   04-FEB-1999;   99US-0118564P.
PR   09-APR-1999;   99US-00288679.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Ravikumar VT,  Manoharan M,  Capaldi DC,  Krotz A,  Cole DL;
PI   Guzaev A;
XX
DR   WPI; 2000-500332/45.
XX
PT   Novel method for the production of oligomers with reduced exocyclic
PT   adducts comprises treatment with deprotecting and cleaving reagents.
XX
PS   Example 2; Page 17; 33pp; English.
XX
CC   This invention describes a novel synthetic method (M) comprising: (a)
CC   providing a sample comprising a number of oligomers of formula (I); (b)
CC   contacting the sample with a deprotecting agent to remove R_t groups from
CC   the oligomers; and (c) reacting the oligomer with a cleaving reagent. The
CC   method is used to produce oligomeric compounds for use in antisense and
CC   oligonucleotide therapies. The method enables the synthesis of oligomers
CC   with a reduction in the number acrylonitrile groups attached.
CC   Acrylonitrile has been demonstrated to be a potent carcinogen in rats.
CC   This sequence represents a phosphorothioate 20-mer primer which is used
CC   in the method of the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 868
```

```
AAA71630/c
ID   AAA71630 standard; DNA; 19 BP.
XX
AC   AAA71630;
XX
DT   14-DEC-2000  (first entry)
XX
DE   Phosphorothioate 20-mer primer DNA #1.
XX
KW   Phosphorothioate; primer; oligomer synthesis; antisense therapy; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkage"
XX
PN   EP1028124-A2.
XX
PD   16-AUG-2000.
XX
PF   06-SEP-1999;   99EP-00307066.
XX
PR   04-FEB-1999;   99US-0118564P.
PR   09-APR-1999;   99US-00288679.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Ravikumar VT,  Manoharan M,  Capaldi DC,  Krotz A,  Cole DL;
PI   Guzaev A;
XX
DR   WPI; 2000-500332/45.
XX
PT   Novel method for the production of oligomers with reduced exocyclic
PT   adducts comprises treatment with deprotecting and cleaving reagents.
XX
PS   Example 2; Page 17; 33pp; English.
XX
CC   This invention describes a novel synthetic method (M) comprising: (a)
CC   providing a sample comprising a number of oligomers of formula (I); (b)
CC   contacting the sample with a deprotecting agent to remove R_t groups from
CC   the oligomers; and (c) reacting the oligomer with a cleaving reagent. The
CC   method is used to produce oligomeric compounds for use in antisense and
CC   oligonucleotide therapies. The method enables the synthesis of oligomers
CC   with a reduction in the number acrylonitrile groups attached.
CC   Acrylonitrile has been demonstrated to be a potent carcinogen in rats.
CC   This sequence represents a phosphorothioate 20-mer primer which is used
CC   in the method of the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 869
AAC62454
ID   AAC62454 standard; DNA; 19 BP.
XX
AC   AAC62454;
XX
DT   07-FEB-2001  (first entry)
XX
DE   Cleavage of nucleic acids from solid supports assay oligonucleotide #3.
XX
KW   Nucleic acid cleavage; solid support; DNA-RNA hybrid;
KW   affinity chromatography; sequencing; mutagenesis; DNA preparation;
KW   nucleic acid purification; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        10
FT                   /*tag=  a
XX
PN   WO200058329-A1.
XX
PD   05-OCT-2000.
XX
PF   28-MAR-2000; 2000WO-GB001190.
XX
PR   29-MAR-1999;   99GB-00007245.
XX
PA   (GOLD/) GOLDSBOROUGH A.
XX
DR   WPI; 2000-664908/64.
XX
PT   Detaching nucleic acid molecule comprising unconventional nucleotide
PT   incorporated at predetermined site from a solid support involves cleaving
PT   the nucleic acid molecule at the site of unconventional nucleotide.
XX
PS   Example 3; Page 34; 47pp; English.
XX
CC   The present invention is concerned with the cleavage of nucleic acids
CC   from solid supports. This is carried out by adding a non-conventional
CC   nucleotide into the nucleic acid attached to the support, so that it is
CC   recognised and cleaved by a specific DNA glycosylase and the sequence is
CC   released. This is useful in many molecular biological procedures such as
CC   sequencing, in vitro amplifications, cDNA and template preparation, DNA-
CC   based assays, mutagenesis procedures, nucleic acid purification and
CC   affinity chromatography. The present sequence is an oligonucleotide used
CC   in assays to demonstrate the methods of the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 5.5e+02;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||:|||||||||
Db          1 TTTTTTTTTUTTTTTTTTT 19


RESULT 870
AAC62454/c
ID   AAC62454 standard; DNA; 19 BP.
XX
AC   AAC62454;
XX
DT   07-FEB-2001  (first entry)
XX
DE   Cleavage of nucleic acids from solid supports assay oligonucleotide #3.
XX
KW   Nucleic acid cleavage; solid support; DNA-RNA hybrid;
KW   affinity chromatography; sequencing; mutagenesis; DNA preparation;
KW   nucleic acid purification; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        10
FT                   /*tag=  a
XX
PN   WO200058329-A1.
XX
PD   05-OCT-2000.
XX
PF   28-MAR-2000; 2000WO-GB001190.
```

```
XX
PR   29-MAR-1999;   99GB-00007245.
XX
PA   (GOLD/) GOLDSBOROUGH A.
XX
DR   WPI; 2000-664908/64.
XX
PT   Detaching nucleic acid molecule comprising unconventional nucleotide
PT   incorporated at predetermined site from a solid support involves cleaving
PT   the nucleic acid molecule at the site of unconventional nucleotide.
XX
PS   Example 3; Page 34; 47pp; English.
XX
CC   The present invention is concerned with the cleavage of nucleic acids
CC   from solid supports. This is carried out by adding a non-conventional
CC   nucleotide into the nucleic acid attached to the support, so that it is
CC   recognised and cleaved by a specific DNA glycosylase and the sequence is
CC   released. This is useful in many molecular biological procedures such as
CC   sequencing, in vitro amplifications, cDNA and template preparation, DNA-
CC   based assays, mutagenesis procedures, nucleic acid purification and
CC   affinity chromatography. The present sequence is an oligonucleotide used
CC   in assays to demonstrate the methods of the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
             |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 871
AAF31458
ID   AAF31458 standard; DNA; 19 BP.
XX
AC   AAF31458;
XX
DT   10-APR-2001  (first entry)
XX
DE   Oligonucleotide ISIS 109989.
XX
KW   Gene expression; gene therapy; diagnosis; ss.
XX
OS   Synthetic.
XX
PN   WO200102423-A2.
XX
PD   11-JAN-2001.
XX
PF   07-JUL-2000; 2000WO-US018609.
XX
PR   07-JUL-1999;   99US-00349040.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Manoharan M,  Cook PD,  Prakash TP,  Mohan V;
XX
DR   WPI; 2001-138119/14.
XX
PT   Guanidinium functionalized oligomers prepared from corresponding monomer
PT   units, are hybridizable with a specific RNA or DNA sequence, useful for
PT   diagnostic and therapeutic purposes.
XX
PS   Example 26; Page 54; 108pp; English.
XX
CC   The present invention relates to nucleotide oligomers comprising monomer
CC   units. Oligomers modulate gene expression when hybridized by a single- or
CC   double-stranded nucleic acid. They are useful for gene therapy,
CC   diagnostic and investigative purposes
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
             |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 872
AAF31458/c
ID   AAF31458 standard; DNA; 19 BP.
XX
AC   AAF31458;
XX
DT   10-APR-2001  (first entry)
XX
DE   Oligonucleotide ISIS 109989.
XX
KW   Gene expression; gene therapy; diagnosis; ss.
XX
OS   Synthetic.
XX
PN   WO200102423-A2.
XX
PD   11-JAN-2001.
XX
PF   07-JUL-2000; 2000WO-US018609.
XX
PR   07-JUL-1999;   99US-00349040.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Manoharan M,  Cook PD,  Prakash TP,  Mohan V;
XX
DR   WPI; 2001-138119/14.
XX
PT   Guanidinium functionalized oligomers prepared from corresponding monomer
PT   units, are hybridizable with a specific RNA or DNA sequence, useful for
PT   diagnostic and therapeutic purposes.
XX
PS   Example 26; Page 54; 108pp; English.
XX
CC   The present invention relates to nucleotide oligomers comprising monomer
CC   units. Oligomers modulate gene expression when hybridized by a single- or
CC   double-stranded nucleic acid. They are useful for gene therapy,
CC   diagnostic and investigative purposes
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
             |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 873
AAF31564
ID   AAF31564 standard; DNA; 19 BP.
XX
AC   AAF31564;
XX
DT   09-APR-2001  (first entry)
XX
DE   ISIS sequence 32327.
XX
KW   DNA/RNA hybrid; oligomer; C3' methylene hydrogen phosphate; AIDS;
KW   atherosclerosis; ss.
```

```
XX
OS   Synthetic.
XX
PN   WO200102419-A1.
XX
PD   11-JAN-2001.
XX
PF   05-JUL-2000; 2000WO-US040304.
XX
PR   07-JUL-1999;   99US-00349033.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cook PD,  Manoharan M,  Maier M,  An H;
XX
DR   WPI; 2001-138117/14.
XX
PT   New oligomers for use as research reagent, for treating disease caused by
PT   undesired production of proteins, and for diagnosing and treating AIDS,
PT   atherosclerosis.
XX
PS   Example 46; Page 74; 110pp; English.
XX
CC   The present invention relates to C3' methylene hydrogen phosphate
CC   oligomers. The oligomers may be used as research reagents, for treating
CC   disease caused by undesired production of proteins and for diagnosing and
CC   treating AIDS and atherosclerosis
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 15 T; 4 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 5.5e+02;
  Matches   15;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              ||||||||||||||::::
Db          1 TTTTTTTTTTTTTTTUUUU 19


RESULT 874
AAF31564/c
ID   AAF31564 standard; DNA; 19 BP.
XX
AC   AAF31564;
XX
DT   09-APR-2001  (first entry)
XX
DE   ISIS sequence 32327.
XX
KW   DNA/RNA hybrid; oligomer; C3' methylene hydrogen phosphate; AIDS;
KW   atherosclerosis; ss.
XX
OS   Synthetic.
XX
PN   WO200102419-A1.
XX
PD   11-JAN-2001.
XX
PF   05-JUL-2000; 2000WO-US040304.
XX
PR   07-JUL-1999;   99US-00349033.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cook PD,  Manoharan M,  Maier M,  An H;
XX
DR   WPI; 2001-138117/14.
XX
PT   New oligomers for use as research reagent, for treating disease caused by
PT   undesired production of proteins, and for diagnosing and treating AIDS,
PT   atherosclerosis.
XX
PS   Example 46; Page 74; 110pp; English.
XX
CC   The present invention relates to C3' methylene hydrogen phosphate
CC   oligomers. The oligomers may be used as research reagents, for treating
CC   disease caused by undesired production of proteins and for diagnosing and
CC   treating AIDS and atherosclerosis
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 15 T; 4 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 875
AAH46460
ID   AAH46460 standard; DNA; 19 BP.
XX
AC   AAH46460;
XX
DT   14-SEP-2001  (first entry)
XX
DE   Oligonucleotide #8.
XX
KW   Phosphorothioate; anti-viral therapy; stereochemical pathway; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .19
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "All bases are phosphorothioate"
FT   modified_base    1
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "Modified with 2'-O-methoxyethyl"
XX
PN   US6242591-B1.
XX
PD   05-JUN-2001.
XX
PF   11-JAN-2000; 2000US-00481486.
XX
PR   15-OCT-1997;   97US-00950779.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cole DL,  Ravikumar VT,  Cheruvallath ZS;
XX
DR   WPI; 2001-407218/43.
XX
PT   Preparing sulfurized 2' substituted phosphorothioate oligonucleotides
PT   useful in biological research, comprises phosphitylating the 5'-hydroxyl
PT   of a nucleic acid having a nucleoside with a 2' modification.
XX
PS   Example 12; Col 7; 7pp; English.
XX
CC   The present invention relates to a method for preparing phosphorothioate
CC   oligonucleotides having at least one nucleoside with a 2' modification.
CC   The method comprises phosphitylating the 5'-hydroxyl of a nucleic acid
CC   group having at least one nucleoside with a 2' modification in an
CC   acetonitrile. The present sequence was used to illustrate the method of
CC   the present invention. The method is useful for synthesising sulphurised
CC   2' substituted phosphorothioate oligonucleotides, which may be used in
CC   molecular biological research, in applications such as anti-viral
CC   therapy, and for determining the stereochemical pathways of certain
CC   enzymes which recognise nucleic acids
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
```

```
  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 876
AAH46460/c
ID   AAH46460 standard; DNA; 19 BP.
XX
AC   AAH46460;
XX
DT   14-SEP-2001  (first entry)
XX
DE   Oligonucleotide #8.
XX
KW   Phosphorothioate; anti-viral therapy; stereochemical pathway; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .19
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "All bases are phosphorothioate"
FT   modified_base   1
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "Modified with 2'-O-methoxyethyl"
XX
PN   US6242591-B1.
XX
PD   05-JUN-2001.
XX
PF   11-JAN-2000; 2000US-00481486.
XX
PR   15-OCT-1997;   97US-00950779.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cole DL,  Ravikumar VT,  Cheruvallath ZS;
XX
DR   WPI; 2001-407218/43.
XX
PT   Preparing sulfurized 2' substituted phosphorothioate oligonucleotides
PT   useful in biological research, comprises phosphitylating the 5'-hydroxyl
PT   of a nucleic acid having a nucleoside with a 2' modification.
XX
PS   Example 12; Col 7; 7pp; English.
XX
CC   The present invention relates to a method for preparing phosphorothioate
CC   oligonucleotides having at least one nucleoside with a 2' modification.
CC   The method comprises phosphitylating the 5'-hydroxyl of a nucleic acid
CC   group having at least one nucleoside with a 2' modification in an
CC   acetonitrile. The present sequence was used to illustrate the method of
CC   the present invention. The method is useful for synthesising sulphurised
CC   2' substituted phosphorothioate oligonucleotides, which may be used in
CC   molecular biological research, in applications such as anti-viral
CC   therapy, and for determining the stereochemical pathways of certain
CC   enzymes which recognise nucleic acids
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          19 AAAAAAAAAAAAAAAAAAA 1


RESULT 877
AAH25737
ID   AAH25737 standard; DNA; 19 BP.
XX
AC   AAH25737;
XX
DT   14-AUG-2001  (first entry)
XX
DE   Human type II RNase H substrate oligonucleotide #4.
XX
KW   Human; RNase H type II; RNase H1 cleavage substrate; antisense therapy;
KW   gene therapy; primer; phosphorothioate backbone; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .19
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "optionally phosphorothioate backbone"
FT   modified_base   16. .19
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "optionally 3'-O-(2-methoxyethyl) or 2'-O-(2-
FT                   methoxyethyl)"
XX
PN   WO200123613-A1.
XX
PD   05-APR-2001.
XX
PF   29-SEP-2000; 2000WO-US026729.
XX
PR   30-SEP-1999;   99US-00409926.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke ST,  Lima WF,  Wu H,  Manoharan M;
XX
DR   WPI; 2001-343164/36.
XX
PT   Chimeric oligonucleotides that can serve as substrates for human RNase
PT   H1, useful for enhancing the effectiveness of antisense gene therapies.
XX
PS   Example 54; Page 88; 178pp; English.
XX
CC   The present invention provides a number of DNA-RNA oligonucleotides which
CC   can act as substrates for human RNase HI (a type II RNase). The sequence
CC   consists of two portions, one of which is capable of supporting cleavage
CC   of a complementary target RNA and the other of which is incapable of
CC   supporting such cleavage. These can be used to enhance the effectiveness
CC   of antisense therapies. The present sequence is an RNase H substrate used
CC   in the exemplification of the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 878
AAH25737/c
ID   AAH25737 standard; DNA; 19 BP.
XX
AC   AAH25737;
XX
```

```
DT   14-AUG-2001  (first entry)
XX
DE   Human type II RNase H substrate oligonucleotide #4.
XX
KW   Human; RNase H type II; RNase H1 cleavage substrate; antisense therapy;
KW   gene therapy; primer; phosphorothioate backbone; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .19
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "optionally phosphorothioate backbone"
FT   modified_base   16. .19
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "optionally 3'-O-(2-methoxyethyl) or 2'-O-(2-
FT                   methoxyethyl)"
XX
PN   WO200123613-A1.
XX
PD   05-APR-2001.
XX
PF   29-SEP-2000; 2000WO-US026729.
XX
PR   30-SEP-1999;   99US-00409926.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke ST,  Lima WF,  Wu H,  Manoharan M;
XX
DR   WPI; 2001-343164/36.
XX
PT   Chimeric oligonucleotides that can serve as substrates for human RNase
PT   H1, useful for enhancing the effectiveness of antisense gene therapies.
XX
PS   Example 54; Page 88; 178pp; English.
XX
CC   The present invention provides a number of DNA-RNA oligonucleotides which
CC   can act as substrates for human RNase HI (a type II RNase). The sequence
CC   consists of two portions, one of which is capable of supporting cleavage
CC   of a complementary target RNA and the other of which is incapable of
CC   supporting such cleavage. These can be used to enhance the effectiveness
CC   of antisense therapies. The present sequence is an RNase H substrate used
CC   in the exemplification of the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 879
AAH25738
ID   AAH25738 standard; DNA; 19 BP.
XX
AC   AAH25738;
XX
DT   14-AUG-2001  (first entry)
XX
DE   Human type II RNase H substrate oligonucleotide #5.
XX
KW   Human; RNase H type II; RNase H1 cleavage substrate; antisense therapy;
KW   gene therapy; primer; phosphorothioate backbone; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .19
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "optionally phosphorothioate backbone"
FT   modified_base   16. .19
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "optionally 3'-O-(2-methoxyethyl) or 2'-O-(2-
FT                   methoxyethyl)"
FT   misc_RNA        19
FT                   /*tag=  c
XX
PN   WO200123613-A1.
XX
PD   05-APR-2001.
XX
PF   29-SEP-2000; 2000WO-US026729.
XX
PR   30-SEP-1999;   99US-00409926.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke ST,  Lima WF,  Wu H,  Manoharan M;
XX
DR   WPI; 2001-343164/36.
XX
PT   Chimeric oligonucleotides that can serve as substrates for human RNase
PT   H1, useful for enhancing the effectiveness of antisense gene therapies.
XX
PS   Example 54; Page 88; 178pp; English.
XX
CC   The present invention provides a number of DNA-RNA oligonucleotides which
CC   can act as substrates for human RNase HI (a type II RNase). The sequence
CC   consists of two portions, one of which is capable of supporting cleavage
CC   of a complementary target RNA and the other of which is incapable of
CC   supporting such cleavage. These can be used to enhance the effectiveness
CC   of antisense therapies. The present sequence is an RNase H substrate used
CC   in the exemplification of the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 5.5e+02;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2184
              ||||||||||||||||||:
Db          1 TTTTTTTTTTTTTTTTTTU 19


RESULT 880
AAH25738/c
ID   AAH25738 standard; DNA; 19 BP.
XX
AC   AAH25738;
XX
DT   14-AUG-2001  (first entry)
XX
DE   Human type II RNase H substrate oligonucleotide #5.
XX
KW   Human; RNase H type II; RNase H1 cleavage substrate; antisense therapy;
KW   gene therapy; primer; phosphorothioate backbone; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .19
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "optionally phosphorothioate backbone"
FT   modified_base   16. .19
FT                   /*tag=  b
```

```
FT                   /mod_base= OTHER
FT                   /note= "optionally 3'-O-(2-methoxyethyl) or 2'-O-(2-
FT                   methoxyethyl)"
FT   misc_RNA        19
FT                   /*tag=  c
XX
PN   WO200123613-A1.
XX
PD   05-APR-2001.
XX
PF   29-SEP-2000; 2000WO-US026729.
XX
PR   30-SEP-1999;   99US-00409926.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke ST,  Lima WF,  Wu H,  Manoharan M;
XX
DR   WPI; 2001-343164/36.
XX
PT   Chimeric oligonucleotides that can serve as substrates for human RNase
PT   H1, useful for enhancing the effectiveness of antisense gene therapies.
XX
PS   Example 54; Page 88; 178pp; English.
XX
CC   The present invention provides a number of DNA-RNA oligonucleotides which
CC   can act as substrates for human RNase HI (a type II RNase). The sequence
CC   consists of two portions, one of which is capable of supporting cleavage
CC   of a complementary target RNA and the other of which is incapable of
CC   supporting such cleavage. These can be used to enhance the effectiveness
CC   of antisense therapies. The present sequence is an RNase H substrate used
CC   in the exemplification of the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 881
AAC83664
ID   AAC83664 standard; DNA; 19 BP.
XX
AC   AAC83664;
XX
DT   02-MAR-2001  (first entry)
XX
DE   2'-O-N-[2-(dimethylamino)ethylacetamido]-modified oligo ISIS #32335.
XX
KW   2'-O-acetamido; diagnostic; kinase modulator; nuclease resistance;
KW   tumour formation; cancer; protein kinase C expression;
KW   cell adhesion molecule expression; multidrug resistance; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   16. .19
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-O-N-[2-(dimethylamino)ethylacetamido]5MeU"
XX
PN   US6147200-A.
XX
PD   14-NOV-2000.
XX
PF   19-AUG-1999;   99US-00378568.
XX
PR   19-AUG-1999;   99US-00378568.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Manoharan M,  Cook PD,  Fraser AS,  Prakash TP,  Kawasaki AM;
XX
DR   WPI; 2001-069824/08.
XX
PT   New 2'-O-acetamido modified nucleosides (I) used to produce
PT   oligonucleotides which have enhanced nuclease resistance and superior
PT   hybridization properties than prior art.
XX
PS   Example 12; Col 28; 29pp; English.
XX
CC   The present sequence is a modified oligonucleotide. 2'-O-acetamido-
CC   modified nucleosides were used to produce oligonucleotides which have
CC   enhanced nuclease resistance and superior hybridisation properties than
CC   prior art. The oligomeric compounds are useful for identification or
CC   quantification of ribonucleic acid and deoxyribonucleic acid or for
CC   modulating the activity of an ribonucleic acid or deoxyribonucleic acid
CC   molecule. They have a modified nucleoside monomer and are specifically
CC   hybridisable with a preselected nucleotide sequence of a single-stranded
CC   or double-stranded target deoxyribonucleic acid or ribonucleic acid
CC   molecule. The oligomers are further useful in a ras-luciferase fusion
CC   system using ras-luciferase transactivation. They are useful in abnormal
CC   cell proliferation and tumour formation and modulation of expression of
CC   protein kinase C and cell adhesion molecules such as ICAM. They are
CC   useful in the modulation of proteins related to multidrug resistance and
CC   viral genomic nucleic acids such as HOV, herpes viruses, Epstein-Barr
CC   virus, cytomegalovirus, papillomavirus, hepatitis C virus and influenza
CC   virus
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 882
AAC83664/c
ID   AAC83664 standard; DNA; 19 BP.
XX
AC   AAC83664;
XX
DT   02-MAR-2001  (first entry)
XX
DE   2'-O-N-[2-(dimethylamino)ethylacetamido]-modified oligo ISIS #32335.
XX
KW   2'-O-acetamido; diagnostic; kinase modulator; nuclease resistance;
KW   tumour formation; cancer; protein kinase C expression;
KW   cell adhesion molecule expression; multidrug resistance; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   16. .19
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-O-N-[2-(dimethylamino)ethylacetamido]5MeU"
XX
PN   US6147200-A.
XX
PD   14-NOV-2000.
XX
PF   19-AUG-1999;   99US-00378568.
XX
PR   19-AUG-1999;   99US-00378568.
XX
PA   (ISIS-) ISIS PHARM INC.
```

```
XX
PI   Manoharan M,  Cook PD,  Fraser AS,  Prakash TP,  Kawasaki AM;
XX
DR   WPI; 2001-069824/08.
XX
PT   New 2'-O-acetamido modified nucleosides (I) used to produce
PT   oligonucleotides which have enhanced nuclease resistance and superior
PT   hybridization properties than prior art.
XX
PS   Example 12; Col 28; 29pp; English.
XX
CC   The present sequence is a modified oligonucleotide. 2'-O-acetamido-
CC   modified nucleosides were used to produce oligonucleotides which have
CC   enhanced nuclease resistance and superior hybridisation properties than
CC   prior art. The oligomeric compounds are useful for identification or
CC   quantification of ribonucleic acid and deoxyribonucleic acid or for
CC   modulating the activity of an ribonucleic acid or deoxyribonucleic acid
CC   molecule. They have a modified nucleoside monomer and are specifically
CC   hybridisable with a preselected nucleotide sequence of a single-stranded
CC   or double-stranded target deoxyribonucleic acid or ribonucleic acid
CC   molecule. The oligomers are further useful in a ras-luciferase fusion
CC   system using ras-luciferase transactivation. They are useful in abnormal
CC   cell proliferation and tumour formation and modulation of expression of
CC   protein kinase C and cell adhesion molecules such as ICAM. They are
CC   useful in the modulation of proteins related to multidrug resistance and
CC   viral genomic nucleic acids such as HOV, herpes viruses, Epstein-Barr
CC   virus, cytomegalovirus, papillomavirus, hepatitis C virus and influenza
CC   virus
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 883
AAK98526
ID   AAK98526 standard; DNA; 19 BP.
XX
AC   AAK98526;
XX
DT   16-APR-2002  (first entry)
XX
DE   Nucleic acid quantitative analysis related oligonucleotide #1.
XX
KW   Target detection; quantitative analysis; probe; medical diagnosis;
KW   forensics; bacterial screening; tissue typing; gene expression analysis;
KW   genotyping; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "modified by thiol"
XX
PN   WO200202810-A2.
XX
PD   10-JAN-2002.
XX
PF   02-JUL-2001; 2001WO-EP007575.
XX
PR   01-JUL-2000; 2000DE-01033334.
XX
PA   (CLON-) CLONDIAG CHIP TECHNOLOGIES GMBH.
XX
PI   Bickel R,  Ehricht R,  Ellinger T,  Ermantraut E,  Kaiser T;
PI   Schulz T,  Wagner G;
XX
DR   WPI; 2002-154760/20.
XX
PT   Determining targets by interaction with probe array, useful e.g. for
PT   diagnosis, based on detecting formation of precipitate at specific probe
PT   sites.
XX
PS   Example 5; Page 47; 92pp; German.
XX
CC   The present invention relates to a method for the qualitative and
CC   quantitative detection of targets in a sample by molecular interaction
CC   between the target and probes in an array. The method can be used to
CC   detect interactions between nucleic acids, antigens and antibodies or
CC   receptor and ligands, particularly in applications such as medical
CC   diagnosis, forensic science, bacterial screening, tissue typing for
CC   transplantation, monitoring gene expression, and genotyping. The present
CC   sequence is a modifying oligonucleotide used in the exemplification of
CC   the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 884
AAK98526/c
ID   AAK98526 standard; DNA; 19 BP.
XX
AC   AAK98526;
XX
DT   16-APR-2002  (first entry)
XX
DE   Nucleic acid quantitative analysis related oligonucleotide #1.
XX
KW   Target detection; quantitative analysis; probe; medical diagnosis;
KW   forensics; bacterial screening; tissue typing; gene expression analysis;
KW   genotyping; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "modified by thiol"
XX
PN   WO200202810-A2.
XX
PD   10-JAN-2002.
XX
PF   02-JUL-2001; 2001WO-EP007575.
XX
PR   01-JUL-2000; 2000DE-01033334.
XX
PA   (CLON-) CLONDIAG CHIP TECHNOLOGIES GMBH.
XX
PI   Bickel R,  Ehricht R,  Ellinger T,  Ermantraut E,  Kaiser T;
PI   Schulz T,  Wagner G;
XX
DR   WPI; 2002-154760/20.
XX
PT   Determining targets by interaction with probe array, useful e.g. for
PT   diagnosis, based on detecting formation of precipitate at specific probe
PT   sites.
XX
PS   Example 5; Page 47; 92pp; German.
```

```
XX
CC   The present invention relates to a method for the qualitative and
CC   quantitative detection of targets in a sample by molecular interaction
CC   between the target and probes in an array. The method can be used to
CC   detect interactions between nucleic acids, antigens and antibodies or
CC   receptor and ligands, particularly in applications such as medical
CC   diagnosis, forensic science, bacterial screening, tissue typing for
CC   transplantation, monitoring gene expression, and genotyping. The present
CC   sequence is a modifying oligonucleotide used in the exemplification of
CC   the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 885
ABA91949
ID   ABA91949 standard; DNA; 19 BP.
XX
AC   ABA91949;
XX
DT   23-MAY-2002  (first entry)
XX
DE   Methyl thioethyl modified oligonucleotide.
XX
KW   2'-O-alkyl oligonucleotide; nuclease resistance; diagnosis; therapy; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   16
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-methyl thioethyl thymidine"
FT   modified_base   17
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-methyl thioethyl thymidine"
FT   modified_base   18
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-methyl thioethyl thymidine"
FT   modified_base   19
FT                   /*tag=  d
FT                   /mod_base= OTHER
FT                   /note= "2'-methyl thioethyl thymidine"
XX
PN   US6277982-B1.
XX
PD   21-AUG-2001.
XX
PF   20-AUG-1999;   99US-00378665.
XX
PR   20-AUG-1999;   99US-00378665.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Fraser AS,  Manoharan M,  Cook PD,  Jung ME,  Kawasaki AM;
XX
DR   WPI; 2002-235143/29.
XX
PT   Alkylation of alcohols, amines, or thiols, useful for preparing
PT   nucleosides that are precursors for preparation of oligomeric compounds
PT   beneficial as therapeutics, involves use of cyclic sulfate intermediates.
XX
PS   Example 15; Col 35; 45pp; English.
XX
CC   The present sequence is that of a chimeric oligonucleotide having some 2'
CC   -methyl thioethyl modifications. This was compared with oligonucleotides
CC   with methoxyethoxy (see ABA91950) and dimethylaminopropyl (see ABA91951)
CC   modifications for resistance to snake venom phosphodiesterase. The assay
CC   revealed the nuclease resistance of the modified oligomers. The invention
CC   provides methods for the alkylation of alcohols, amines, thiols and their
CC   derivatives by cyclic sulfate intermediates. In particular, methods for
CC   the alkylation of the 2', 3' or 5'-hydroxy position of nucleosides and
CC   their analogues with cyclic sulfates to form the 2', 3' or 5'-O-alkyl
CC   sulfate modified compounds are disclosed. Displacement of the 2', 3' or
CC   5'-O-sulfate with a nucleophile provides 2', 3' or 5'-O-modified
CC   nucleosides and their analogues. The methods are especially useful for
CC   the preparation of 2'-O-alkyl nucleotides, nucleosides and nucleoside
CC   surrogates that are precursors for the preparation of oligomeric
CC   compounds useful as therapeutics, diagnostics and research reagents
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 886
ABA91949/c
ID   ABA91949 standard; DNA; 19 BP.
XX
AC   ABA91949;
XX
DT   23-MAY-2002  (first entry)
XX
DE   Methyl thioethyl modified oligonucleotide.
XX
KW   2'-O-alkyl oligonucleotide; nuclease resistance; diagnosis; therapy; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   16
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-methyl thioethyl thymidine"
FT   modified_base   17
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-methyl thioethyl thymidine"
FT   modified_base   18
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-methyl thioethyl thymidine"
FT   modified_base   19
FT                   /*tag=  d
FT                   /mod_base= OTHER
FT                   /note= "2'-methyl thioethyl thymidine"
XX
PN   US6277982-B1.
XX
PD   21-AUG-2001.
XX
PF   20-AUG-1999;   99US-00378665.
XX
PR   20-AUG-1999;   99US-00378665.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Fraser AS,  Manoharan M,  Cook PD,  Jung ME,  Kawasaki AM;
XX
DR   WPI; 2002-235143/29.
```

```
XX
PT   Alkylation of alcohols, amines, or thiols, useful for preparing
PT   nucleosides that are precursors for preparation of oligomeric compounds
PT   beneficial as therapeutics, involves use of cyclic sulfate intermediates.
XX
PS   Example 15; Col 35; 45pp; English.
XX
CC   The present sequence is that of a chimeric oligonucleotide having some 2'
CC   -methyl thioethyl modifications. This was compared with oligonucleotides
CC   with methoxyethoxy (see ABA91950) and dimethylaminopropyl (see ABA91951)
CC   modifications for resistance to snake venom phosphodiesterase. The assay
CC   revealed the nuclease resistance of the modified oligomers. The invention
CC   provides methods for the alkylation of alcohols, amines, thiols and their
CC   derivatives by cyclic sulfate intermediates. In particular, methods for
CC   the alkylation of the 2', 3' or 5'-hydroxy position of nucleosides and
CC   their analogues with cyclic sulfates to form the 2', 3' or 5'-O-alkyl
CC   sulfate modified compounds are disclosed. Displacement of the 2', 3' or
CC   5'-O-sulfate with a nucleophile provides 2', 3' or 5'-O-modified
CC   nucleosides and their analogues. The methods are especially useful for
CC   the preparation of 2'-O-alkyl nucleotides, nucleosides and nucleoside
CC   surrogates that are precursors for the preparation of oligomeric
CC   compounds useful as therapeutics, diagnostics and research reagents
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 887
ABA91951
ID   ABA91951 standard; DNA; 19 BP.
XX
AC   ABA91951;
XX
DT   23-MAY-2002  (first entry)
XX
DE   Dimethylaminopropyl modified oligonucleotide.
XX
KW   2'-O-alkyl oligonucleotide; nuclease resistance; diagnosis; therapy; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    16
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "2'-dimethylaminopropyl thymidine"
FT   modified_base    17
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'-dimethylaminopropyl thymidine"
FT   modified_base    18
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'-dimethylaminopropyl thymidine"
FT   modified_base    19
FT                    /*tag=  d
FT                    /mod_base= OTHER
FT                    /note= "2'-dimethylaminopropyl thymidine"
XX
PN   US6277982-B1.
XX
PD   21-AUG-2001.
XX
PF   20-AUG-1999;   99US-00378665.
XX
PR   20-AUG-1999;   99US-00378665.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Fraser AS,  Manoharan M,  Cook PD,  Jung ME,  Kawasaki AM;
XX
DR   WPI; 2002-235143/29.
XX
PT   Alkylation of alcohols, amines, or thiols, useful for preparing
PT   nucleosides that are precursors for preparation of oligomeric compounds
PT   beneficial as therapeutics, involves use of cyclic sulfate intermediates.
XX
PS   Example 15; Col 35; 45pp; English.
XX
CC   The present sequence is that of a chimeric oligonucleotide having some 2'
CC   -dimethylaminopropyl modifications. This was compared with
CC   oligonucleotides with methyl thioethyl (see ABA91949) and methoxyethoxy
CC   (see ABA91950) modifications for resistance to snake venom
CC   phosphodiesterase. The assay revealed the nuclease resistance of the
CC   modified oligomers. The invention provides methods for the alkylation of
CC   alcohols, amines, thiols and their derivatives by cyclic sulfate
CC   intermediates. In particular, methods for the alkylation of the 2', 3' or
CC   5'-hydroxy position of nucleosides and their analogues with cyclic
CC   sulfates to form the 2', 3' or 5'-O-alkyl sulfate modified compounds are
CC   disclosed. Displacement of the 2', 3' or 5'-O-sulfate with a nucleophile
CC   provides 2', 3' or 5'-O-modified nucleosides and their analogues. The
CC   methods are especially useful for the preparation of 2'-O-alkyl
CC   nucleotides, nucleosides and nucleoside surrogates that are precursors
CC   for the preparation of oligomeric compounds useful as therapeutics,
CC   diagnostics and research reagents
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 888
ABA91951/c
ID   ABA91951 standard; DNA; 19 BP.
XX
AC   ABA91951;
XX
DT   23-MAY-2002  (first entry)
XX
DE   Dimethylaminopropyl modified oligonucleotide.
XX
KW   2'-O-alkyl oligonucleotide; nuclease resistance; diagnosis; therapy; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    16
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "2'-dimethylaminopropyl thymidine"
FT   modified_base    17
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'-dimethylaminopropyl thymidine"
FT   modified_base    18
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'-dimethylaminopropyl thymidine"
FT   modified_base    19
FT                    /*tag=  d
FT                    /mod_base= OTHER
FT                    /note= "2'-dimethylaminopropyl thymidine"
XX
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PN   US6277982-B1.
XX
PD   21-AUG-2001.
XX
PF   20-AUG-1999;   99US-00378665.
XX
PR   20-AUG-1999;   99US-00378665.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Fraser AS,  Manoharan M,  Cook PD,  Jung ME,  Kawasaki AM;
XX
DR   WPI; 2002-235143/29.
XX
PT   Alkylation of alcohols, amines, or thiols, useful for preparing
PT   nucleosides that are precursors for preparation of oligomeric compounds
PT   beneficial as therapeutics, involves use of cyclic sulfate intermediates.
XX
PS   Example 15; Col 35; 45pp; English.
XX
CC   The present sequence is that of a chimeric oligonucleotide having some 2'
CC   -dimethylaminopropyl modifications. This was compared with
CC   oligonucleotides with methyl thioethyl (see ABA91949) and methoxyethoxy
CC   (see ABA91950) modifications for resistance to snake venom
CC   phosphodiesterase. The assay revealed the nuclease resistance of the
CC   modified oligomers. The invention provides methods for the alkylation of
CC   alcohols, amines, thiols and their derivatives by cyclic sulfate
CC   intermediates. In particular, methods for the alkylation of the 2', 3' or
CC   5'-hydroxy position of nucleosides and their analogues with cyclic
CC   sulfates to form the 2', 3' or 5'-O-alkyl sulfate modified compounds are
CC   disclosed. Displacement of the 2', 3' or 5'-O-sulfate with a nucleophile
CC   provides 2', 3' or 5'-O-modified nucleosides and their analogues. The
CC   methods are especially useful for the preparation of 2'-O-alkyl
CC   nucleotides, nucleosides and nucleoside surrogates that are precursors
CC   for the preparation of oligomeric compounds useful as therapeutics,
CC   diagnostics and research reagents
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 889
ABA91950
ID   ABA91950 standard; DNA; 19 BP.
XX
AC   ABA91950;
XX
DT   23-MAY-2002  (first entry)
XX
DE   Methoxyethoxy modified oligonucleotide.
XX
KW   2'-O-alkyl oligonucleotide; nuclease resistance; diagnosis; therapy; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    16
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "2'-methoxyethoxy thymidine"
FT   modified_base    17
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'-methoxyethoxy thymidine"
FT   modified_base    18
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'-methoxyethoxy thymidine"
FT   modified_base    19
FT                    /*tag=  d
FT                    /mod_base= OTHER
FT                    /note= "2'-methoxyethoxy thymidine"
XX
PN   US6277982-B1.
XX
PD   21-AUG-2001.
XX
PF   20-AUG-1999;   99US-00378665.
XX
PR   20-AUG-1999;   99US-00378665.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Fraser AS,  Manoharan M,  Cook PD,  Jung ME,  Kawasaki AM;
XX
DR   WPI; 2002-235143/29.
XX
PT   Alkylation of alcohols, amines, or thiols, useful for preparing
PT   nucleosides that are precursors for preparation of oligomeric compounds
PT   beneficial as therapeutics, involves use of cyclic sulfate intermediates.
XX
PS   Example 15; Col 35; 45pp; English.
XX
CC   The present sequence is that of a chimeric oligonucleotide having some 2'
CC   -methoxyethoxy modifications. This was compared with oligonucleotides
CC   with methyl thioethyl (see ABA91949) and dimethylaminopropyl (see
CC   ABA91951) modifications for resistance to snake venom phosphodiesterase.
CC   The assay revealed the nuclease resistance of the modified oligomers. The
CC   invention provides methods for the alkylation of alcohols, amines, thiols
CC   and their derivatives by cyclic sulfate intermediates. In particular,
CC   methods for the alkylation of the 2', 3' or 5'-hydroxy position of
CC   nucleosides and their analogues with cyclic sulfates to form the 2', 3'
CC   or 5'-O-alkyl sulfate modified compounds are disclosed. Displacement of
CC   the 2', 3' or 5'-O-sulfate with a nucleophile provides 2', 3' or 5'-O-
CC   modified nucleosides and their analogues. The methods are especially
CC   useful for the preparation of 2'-O-alkyl nucleotides, nucleosides and
CC   nucleoside surrogates that are precursors for the preparation of
CC   oligomeric compounds useful as therapeutics, diagnostics and research
CC   reagents
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 890
ABA91950/c
ID   ABA91950 standard; DNA; 19 BP.
XX
AC   ABA91950;
XX
DT   23-MAY-2002  (first entry)
XX
DE   Methoxyethoxy modified oligonucleotide.
XX
KW   2'-O-alkyl oligonucleotide; nuclease resistance; diagnosis; therapy; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    16
FT                    /*tag=  a
FT                    /mod_base= OTHER
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FT                   /note= "2'-methoxyethoxy thymidine"
FT   modified_base   17
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-methoxyethoxy thymidine"
FT   modified_base   18
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-methoxyethoxy thymidine"
FT   modified_base   19
FT                   /*tag=  d
FT                   /mod_base= OTHER
FT                   /note= "2'-methoxyethoxy thymidine"
XX
PN   US6277982-B1.
XX
PD   21-AUG-2001.
XX
PF   20-AUG-1999;   99US-00378665.
XX
PR   20-AUG-1999;   99US-00378665.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Fraser AS,  Manoharan M,  Cook PD,  Jung ME,  Kawasaki AM;
XX
DR   WPI; 2002-235143/29.
XX
PT   Alkylation of alcohols, amines, or thiols, useful for preparing
PT   nucleosides that are precursors for preparation of oligomeric compounds
PT   beneficial as therapeutics, involves use of cyclic sulfate intermediates.
XX
PS   Example 15; Col 35; 45pp; English.
XX
CC   The present sequence is that of a chimeric oligonucleotide having some 2'
CC   -methoxyethoxy modifications. This was compared with oligonucleotides
CC   with methyl thioethyl (see ABA91949) and dimethylaminopropyl (see
CC   ABA91951) modifications for resistance to snake venom phosphodiesterase.
CC   The assay revealed the nuclease resistance of the modified oligomers. The
CC   invention provides methods for the alkylation of alcohols, amines, thiols
CC   and their derivatives by cyclic sulfate intermediates. In particular,
CC   methods for the alkylation of the 2', 3' or 5'-hydroxy position of
CC   nucleosides and their analogues with cyclic sulfates to form the 2', 3'
CC   or 5'-O-alkyl sulfate modified compounds are disclosed. Displacement of
CC   the 2', 3' or 5'-O-sulfate with a nucleophile provides 2', 3' or 5'-O-
CC   modified nucleosides and their analogues. The methods are especially
CC   useful for the preparation of 2'-O-alkyl nucleotides, nucleosides and
CC   nucleoside surrogates that are precursors for the preparation of
CC   oligomeric compounds useful as therapeutics, diagnostics and research
CC   reagents
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 891
ABL51520
ID   ABL51520 standard; DNA; 19 BP.
XX
AC   ABL51520;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Tailing reaction related exemplary primer biotin-dT18U SEQ ID NO:1.
XX
KW   Tailing reaction; tailed primer; primer; probe; identification;
KW   detection; linear amplification scheme; chain extending enzyme;
KW   telomerase; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "biotinylated"
FT   misc_RNA        19
FT                   /*tag=  b
XX
PN   US2002031776-A1.
XX
PD   14-MAR-2002.
XX
PF   26-JUL-2001; 2001US-00917138.
XX
PR   28-MAY-1999;   99US-0136545P.
PR   25-MAY-2000; 2000US-00580358.
XX
PA   (TULL/) TULLIS R H.
PA   (STRE/) STREIFEL J A.
XX
PI   Tullis RH,  Streifel JA;
XX
DR   WPI; 2002-361176/39.
XX
PT   Identifying and detecting nucleic acids, particularly DNA hybridization
PT   probes, involves employing chain extending enzymes (e.g. telomerase) to
PT   elongate probes to render them readily detectable.
XX
PS   Example 1; Page 5; 10pp; English.
XX
CC   The present invention describes a method for detecting a nucleic acid
CC   probe, which comprises using chain extending enzymes to elongate probes.
CC   The method comprises: (a) treating the sample with a chain terminating
CC   reagent to prevent polynucleotide chain growth from the nucleic acid in
CC   the sample; (b) contacting the sample with the probe containing a
CC   terminus capable of elongation by a chain extending enzyme, where the
CC   probe hybridises to the nucleic acid in the sample; (c) contacting the
CC   sample with a chain extending enzyme and its substrates, which elongates
CC   the probe; and (d) detecting the elongated hybridised probe. Also
CC   described is a method comprising: (a) treating nucleic acid molecules or
CC   modified nucleic acids in a sample with a reagent or reagents that render
CC   the nucleic acid chains unextendable by a non-template-dependent enzyme;
CC   (b) hybridising the treated molecules with a nucleic acid probe that
CC   includes an extendable terminus, under conditions where hybrids form; and
CC   (c) treating any hybrids formed with a non-template dependent chain
CC   elongating enzyme and its substrates, where any hybridised probe is
CC   extended. The method is useful for identifying and detecting nucleic
CC   acids, particularly DNA hybridisation probes. The present sequence
CC   represents a tailing reaction exemplary primer, which is used in an
CC   example from the present invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 5.5e+02;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2184
              ||||||||||||||||||:
Db          1 TTTTTTTTTTTTTTTTTTU 19


RESULT 892
ABL51520/c
ID   ABL51520 standard; DNA; 19 BP.
XX
AC   ABL51520;
XX
```

```
DT   01-JUL-2002  (first entry)
XX
DE   Tailing reaction related exemplary primer biotin-dT18U SEQ ID NO:1.
XX
KW   Tailing reaction; tailed primer; primer; probe; identification;
KW   detection; linear amplification scheme; chain extending enzyme;
KW   telomerase; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "biotinylated"
FT   misc_RNA        19
FT                   /*tag=  b
XX
PN   US2002031776-A1.
XX
PD   14-MAR-2002.
XX
PF   26-JUL-2001; 2001US-00917138.
XX
PR   28-MAY-1999;   99US-0136545P.
PR   25-MAY-2000; 2000US-00580358.
XX
PA   (TULL/) TULLIS R H.
PA   (STRE/) STREIFEL J A.
XX
PI   Tullis RH,  Streifel JA;
XX
DR   WPI; 2002-361176/39.
XX
PT   Identifying and detecting nucleic acids, particularly DNA hybridization
PT   probes, involves employing chain extending enzymes (e.g. telomerase) to
PT   elongate probes to render them readily detectable.
XX
PS   Example 1; Page 5; 10pp; English.
XX
CC   The present invention describes a method for detecting a nucleic acid
CC   probe, which comprises using chain extending enzymes to elongate probes.
CC   The method comprises: (a) treating the sample with a chain terminating
CC   reagent to prevent polynucleotide chain growth from the nucleic acid in
CC   the sample; (b) contacting the sample with the probe containing a
CC   terminus capable of elongation by a chain extending enzyme, where the
CC   probe hybridises to the nucleic acid in the sample; (c) contacting the
CC   sample with a chain extending enzyme and its substrates, which elongates
CC   the probe; and (d) detecting the elongated hybridised probe. Also
CC   described is a method comprising: (a) treating nucleic acid molecules or
CC   modified nucleic acids in a sample with a reagent or reagents that render
CC   the nucleic acid chains unextendable by a non-template-dependent enzyme;
CC   (b) hybridising the treated molecules with a nucleic acid probe that
CC   includes an extendable terminus, under conditions where hybrids form; and
CC   (c) treating any hybrids formed with a non-template dependent chain
CC   elongating enzyme and its substrates, where any hybridised probe is
CC   extended. The method is useful for identifying and detecting nucleic
CC   acids, particularly DNA hybridisation probes. The present sequence
CC   represents a tailing reaction exemplary primer, which is used in an
CC   example from the present invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 893
```

```
AAD42000
ID   AAD42000 standard; DNA; 19 BP.
XX
AC   AAD42000;
XX
DT   04-NOV-2002  (first entry)
XX
DE   Oligonucleotide #3 used to illustrate the method of the invention.
XX
KW   Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW   nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   15. .18
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-methoxyethoxy (MOE) residues"
XX
PN   US6403779-B1.
XX
PD   11-JUN-2002.
XX
PF   08-JAN-1999;   99US-00227782.
XX
PR   08-JAN-1999;   99US-00227782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Kawasaki AM,  Fraser AS,  Manoharan M,  Cook PD,  Prakash TP;
XX
DR   WPI; 2002-546338/58.
XX
PT   Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
PT   for preparation of 2'-O-alkylated compounds comprises dissolving
PT   nucleoside in aprotic solvent, cooling, treating with base, warming,
PT   cooling and reacting with ester.
XX
PS   Example 46; Col 31; 24pp; English.
XX
CC   The present invention relates to a novel method of selective alkylation
CC   of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
CC   The method involves dissolving the nucleoside in at least one aprotic
CC   solvent, cooling, treating with base, warming, cooling and reacting with
CC   a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC   nucleotides, nucleosides and nucleoside surrogates used for preparation
CC   of oligomeric compounds having improved hybridisation affinity and
CC   nuclear resistance, which are useful as therapeutics, diagnostics and
CC   research reagents. The present sequence is a modified oligonucleotide
CC   used to illustrate the method of the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 894
AAD42000/c
ID   AAD42000 standard; DNA; 19 BP.
XX
AC   AAD42000;
XX
DT   04-NOV-2002  (first entry)
XX
DE   Oligonucleotide #3 used to illustrate the method of the invention.
XX
```

```
KW   Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW   nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   15. .18
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-methoxyethoxy (MOE) residues"
XX
PN   US6403779-B1.
XX
PD   11-JUN-2002.
XX
PF   08-JAN-1999;   99US-00227782.
XX
PR   08-JAN-1999;   99US-00227782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Kawasaki AM,  Fraser AS,  Manoharan M,  Cook PD,  Prakash TP;
XX
DR   WPI; 2002-546338/58.
XX
PT   Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
PT   for preparation of 2'-O-alkylated compounds comprises dissolving
PT   nucleoside in aprotic solvent, cooling, treating with base, warming,
PT   cooling and reacting with ester.
XX
PS   Example 46; Col 31; 24pp; English.
XX
CC   The present invention relates to a novel method of selective alkylation
CC   of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
CC   The method involves dissolving the nucleoside in at least one aprotic
CC   solvent, cooling, treating with base, warming, cooling and reacting with
CC   a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC   nucleotides, nucleosides and nucleoside surrogates used for preparation
CC   of oligomeric compounds having improved hybridisation affinity and
CC   nuclear resistance, which are useful as therapeutics, diagnostics and
CC   research reagents. The present sequence is a modified oligonucleotide
CC   used to illustrate the method of the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 895
AAD42002
ID   AAD42002 standard; DNA; 19 BP.
XX
AC   AAD42002;
XX
DT   04-NOV-2002  (first entry)
XX
DE   Oligonucleotide #5 used to illustrate the method of the invention.
XX
KW   Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW   nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   16. .19
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "5-methyl, 2'-methoxyethyl residues"
XX
PN   US6403779-B1.
XX
PD   11-JUN-2002.
XX
PF   08-JAN-1999;   99US-00227782.
XX
PR   08-JAN-1999;   99US-00227782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Kawasaki AM,  Fraser AS,  Manoharan M,  Cook PD,  Prakash TP;
XX
DR   WPI; 2002-546338/58.
XX
PT   Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
PT   for preparation of 2'-O-alkylated compounds comprises dissolving
PT   nucleoside in aprotic solvent, cooling, treating with base, warming,
PT   cooling and reacting with ester.
XX
PS   Example 46; Col 33; 24pp; English.
XX
CC   The present invention relates to a novel method of selective alkylation
CC   of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
CC   The method involves dissolving the nucleoside in at least one aprotic
CC   solvent, cooling, treating with base, warming, cooling and reacting with
CC   a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC   nucleotides, nucleosides and nucleoside surrogates used for preparation
CC   of oligomeric compounds having improved hybridisation affinity and
CC   nuclear resistance, which are useful as therapeutics, diagnostics and
CC   research reagents. The present sequence is a modified oligonucleotide
CC   used to illustrate the method of the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 896
AAD42002/c
ID   AAD42002 standard; DNA; 19 BP.
XX
AC   AAD42002;
XX
DT   04-NOV-2002  (first entry)
XX
DE   Oligonucleotide #5 used to illustrate the method of the invention.
XX
KW   Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW   nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   16. .19
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "5-methyl, 2'-methoxyethyl residues"
XX
PN   US6403779-B1.
XX
PD   11-JUN-2002.
XX
PF   08-JAN-1999;   99US-00227782.
XX
PR   08-JAN-1999;   99US-00227782.
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```
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Kawasaki AM,  Fraser AS,  Manoharan M,  Cook PD,  Prakash TP;
XX
DR   WPI; 2002-546338/58.
XX
PT   Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
PT   for preparation of 2'-O-alkylated compounds comprises dissolving
PT   nucleoside in aprotic solvent, cooling, treating with base, warming,
PT   cooling and reacting with ester.
XX
PS   Example 46; Col 33; 24pp; English.
XX
CC   The present invention relates to a novel method of selective alkylation
CC   of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
CC   The method involves dissolving the nucleoside in at least one aprotic
CC   solvent, cooling, treating with base, warming, cooling and reacting with
CC   a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC   nucleotides, nucleosides and nucleoside surrogates used for preparation
CC   of oligomeric compounds having improved hybridisation affinity and
CC   nuclear resistance, which are useful as therapeutics, diagnostics and
CC   research reagents. The present sequence is a modified oligonucleotide
CC   used to illustrate the method of the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 897
AAD42004
ID   AAD42004 standard; DNA; 19 BP.
XX
AC   AAD42004;
XX
DT   04-NOV-2002  (first entry)
XX
DE   Oligonucleotide #7 used to illustrate the method of the invention.
XX
KW   Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW   nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   18
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "5-methyl, 2'-dimethylaminooxyethyl residue"
XX
PN   US6403779-B1.
XX
PD   11-JUN-2002.
XX
PF   08-JAN-1999;   99US-00227782.
XX
PR   08-JAN-1999;   99US-00227782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Kawasaki AM,  Fraser AS,  Manoharan M,  Cook PD,  Prakash TP;
XX
DR   WPI; 2002-546338/58.
XX
PT   Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
PT   for preparation of 2'-O-alkylated compounds comprises dissolving
PT   nucleoside in aprotic solvent, cooling, treating with base, warming,
PT   cooling and reacting with ester.
XX
PS   Example 46; Col 33; 24pp; English.
XX
CC   The present invention relates to a novel method of selective alkylation
CC   of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
CC   The method involves dissolving the nucleoside in at least one aprotic
CC   solvent, cooling, treating with base, warming, cooling and reacting with
CC   a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC   nucleotides, nucleosides and nucleoside surrogates used for preparation
CC   of oligomeric compounds having improved hybridisation affinity and
CC   nuclear resistance, which are useful as therapeutics, diagnostics and
CC   research reagents. The present sequence is a modified oligonucleotide
CC   used to illustrate the method of the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 898
AAD42004/c
ID   AAD42004 standard; DNA; 19 BP.
XX
AC   AAD42004;
XX
DT   04-NOV-2002  (first entry)
XX
DE   Oligonucleotide #7 used to illustrate the method of the invention.
XX
KW   Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW   nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   18
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "5-methyl, 2'-dimethylaminooxyethyl residue"
XX
PN   US6403779-B1.
XX
PD   11-JUN-2002.
XX
PF   08-JAN-1999;   99US-00227782.
XX
PR   08-JAN-1999;   99US-00227782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Kawasaki AM,  Fraser AS,  Manoharan M,  Cook PD,  Prakash TP;
XX
DR   WPI; 2002-546338/58.
XX
PT   Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
PT   for preparation of 2'-O-alkylated compounds comprises dissolving
PT   nucleoside in aprotic solvent, cooling, treating with base, warming,
PT   cooling and reacting with ester.
XX
PS   Example 46; Col 33; 24pp; English.
XX
CC   The present invention relates to a novel method of selective alkylation
CC   of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
CC   The method involves dissolving the nucleoside in at least one aprotic
CC   solvent, cooling, treating with base, warming, cooling and reacting with
```

```
CC   a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC   nucleotides, nucleosides and nucleoside surrogates used for preparation
CC   of oligomeric compounds having improved hybridisation affinity and
CC   nuclear resistance, which are useful as therapeutics, diagnostics and
CC   research reagents. The present sequence is a modified oligonucleotide
CC   used to illustrate the method of the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 899
AAD42010
ID   AAD42010 standard; DNA; 19 BP.
XX
AC   AAD42010;
XX
DT   04-NOV-2002  (first entry)
XX
DE   Oligonucleotide #13 used to illustrate the method of the invention.
XX
KW   Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW   nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   16. .19
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-dimethylaminooxyethyl thymidine (T-2'DMAOE)"
FT   modified_base   18. .19
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone"
XX
PN   US6403779-B1.
XX
PD   11-JUN-2002.
XX
PF   08-JAN-1999;   99US-00227782.
XX
PR   08-JAN-1999;   99US-00227782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Kawasaki AM,  Fraser AS,  Manoharan M,  Cook PD,  Prakash TP;
XX
DR   WPI; 2002-546338/58.
XX
PT   Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
PT   for preparation of 2'-O-alkylated compounds comprises dissolving
PT   nucleoside in aprotic solvent, cooling, treating with base, warming,
PT   cooling and reacting with ester.
XX
PS   Example 46; Col 35; 24pp; English.
XX
CC   The present invention relates to a novel method of selective alkylation
CC   of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
CC   The method involves dissolving the nucleoside in at least one aprotic
CC   solvent, cooling, treating with base, warming, cooling and reacting with
CC   a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC   nucleotides, nucleosides and nucleoside surrogates used for preparation
CC   of oligomeric compounds having improved hybridisation affinity and
CC   nuclear resistance, which are useful as therapeutics, diagnostics and
CC   research reagents. The present sequence is a modified oligonucleotide
CC   used to illustrate the method of the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 900
AAD42010/c
ID   AAD42010 standard; DNA; 19 BP.
XX
AC   AAD42010;
XX
DT   04-NOV-2002  (first entry)
XX
DE   Oligonucleotide #13 used to illustrate the method of the invention.
XX
KW   Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW   nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   16. .19
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-dimethylaminooxyethyl thymidine (T-2'DMAOE)"
FT   modified_base   18. .19
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone"
XX
PN   US6403779-B1.
XX
PD   11-JUN-2002.
XX
PF   08-JAN-1999;   99US-00227782.
XX
PR   08-JAN-1999;   99US-00227782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Kawasaki AM,  Fraser AS,  Manoharan M,  Cook PD,  Prakash TP;
XX
DR   WPI; 2002-546338/58.
XX
PT   Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
PT   for preparation of 2'-O-alkylated compounds comprises dissolving
PT   nucleoside in aprotic solvent, cooling, treating with base, warming,
PT   cooling and reacting with ester.
XX
PS   Example 46; Col 35; 24pp; English.
XX
CC   The present invention relates to a novel method of selective alkylation
CC   of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
CC   The method involves dissolving the nucleoside in at least one aprotic
CC   solvent, cooling, treating with base, warming, cooling and reacting with
CC   a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC   nucleotides, nucleosides and nucleoside surrogates used for preparation
CC   of oligomeric compounds having improved hybridisation affinity and
CC   nuclear resistance, which are useful as therapeutics, diagnostics and
CC   research reagents. The present sequence is a modified oligonucleotide
CC   used to illustrate the method of the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
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  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 901
AAD42020
ID   AAD42020 standard; DNA; 19 BP.
XX
AC   AAD42020;
XX
DT   04-NOV-2002  (first entry)
XX
DE   Oligonucleotide #23 used to illustrate the method of the invention.
XX
KW   Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW   nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   15. .18
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methyleneiminooxyethyl thymidine"
XX
PN   US6403779-B1.
XX
PD   11-JUN-2002.
XX
PF   08-JAN-1999;   99US-00227782.
XX
PR   08-JAN-1999;   99US-00227782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Kawasaki AM,  Fraser AS,  Manoharan M,  Cook PD,  Prakash TP;
XX
DR   WPI; 2002-546338/58.
XX
PT   Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
PT   for preparation of 2'-O-alkylated compounds comprises dissolving
PT   nucleoside in aprotic solvent, cooling, treating with base, warming,
PT   cooling and reacting with ester.
XX
PS   Example 46; Col 41; 24pp; English.
XX
CC   The present invention relates to a novel method of selective alkylation
CC   of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
CC   The method involves dissolving the nucleoside in at least one aprotic
CC   solvent, cooling, treating with base, warming, cooling and reacting with
CC   a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC   nucleotides, nucleosides and nucleoside surrogates used for preparation
CC   of oligomeric compounds having improved hybridisation affinity and
CC   nuclear resistance, which are useful as therapeutics, diagnostics and
CC   research reagents. The present sequence is a modified oligonucleotide
CC   used to illustrate the method of the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 902
AAD42020/c
ID   AAD42020 standard; DNA; 19 BP.
XX
AC   AAD42020;
XX
DT   04-NOV-2002  (first entry)
XX
DE   Oligonucleotide #23 used to illustrate the method of the invention.
XX
KW   Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW   nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   15. .18
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methyleneiminooxyethyl thymidine"
XX
PN   US6403779-B1.
XX
PD   11-JUN-2002.
XX
PF   08-JAN-1999;   99US-00227782.
XX
PR   08-JAN-1999;   99US-00227782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Kawasaki AM,  Fraser AS,  Manoharan M,  Cook PD,  Prakash TP;
XX
DR   WPI; 2002-546338/58.
XX
PT   Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
PT   for preparation of 2'-O-alkylated compounds comprises dissolving
PT   nucleoside in aprotic solvent, cooling, treating with base, warming,
PT   cooling and reacting with ester.
XX
PS   Example 46; Col 41; 24pp; English.
XX
CC   The present invention relates to a novel method of selective alkylation
CC   of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
CC   The method involves dissolving the nucleoside in at least one aprotic
CC   solvent, cooling, treating with base, warming, cooling and reacting with
CC   a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC   nucleotides, nucleosides and nucleoside surrogates used for preparation
CC   of oligomeric compounds having improved hybridisation affinity and
CC   nuclear resistance, which are useful as therapeutics, diagnostics and
CC   research reagents. The present sequence is a modified oligonucleotide
CC   used to illustrate the method of the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 903
AAD42001
ID   AAD42001 standard; DNA; 19 BP.
XX
AC   AAD42001;
XX
DT   04-NOV-2002  (first entry)
XX
DE   Oligonucleotide #4 used to illustrate the method of the invention.
XX
```

```
KW   Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW   nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   16. .19
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "5-methyl, 2'-dimethylaminooxyethyl residues"
XX
PN   US6403779-B1.
XX
PD   11-JUN-2002.
XX
PF   08-JAN-1999;   99US-00227782.
XX
PR   08-JAN-1999;   99US-00227782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Kawasaki AM,  Fraser AS,  Manoharan M,  Cook PD,  Prakash TP;
XX
DR   WPI; 2002-546338/58.
XX
PT   Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
PT   for preparation of 2'-O-alkylated compounds comprises dissolving
PT   nucleoside in aprotic solvent, cooling, treating with base, warming,
PT   cooling and reacting with ester.
XX
PS   Example 46; Col 31; 24pp; English.
XX
CC   The present invention relates to a novel method of selective alkylation
CC   of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
CC   The method involves dissolving the nucleoside in at least one aprotic
CC   solvent, cooling, treating with base, warming, cooling and reacting with
CC   a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC   nucleotides, nucleosides and nucleoside surrogates used for preparation
CC   of oligomeric compounds having improved hybridisation affinity and
CC   nuclear resistance, which are useful as therapeutics, diagnostics and
CC   research reagents. The present sequence is a modified oligonucleotide
CC   used to illustrate the method of the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 904
AAD42001/c
ID   AAD42001 standard; DNA; 19 BP.
XX
AC   AAD42001;
XX
DT   04-NOV-2002  (first entry)
XX
DE   Oligonucleotide #4 used to illustrate the method of the invention.
XX
KW   Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW   nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   16. .19
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "5-methyl, 2'-dimethylaminooxyethyl residues"
XX
PN   US6403779-B1.
XX
PD   11-JUN-2002.
XX
PF   08-JAN-1999;   99US-00227782.
XX
PR   08-JAN-1999;   99US-00227782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Kawasaki AM,  Fraser AS,  Manoharan M,  Cook PD,  Prakash TP;
XX
DR   WPI; 2002-546338/58.
XX
PT   Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
PT   for preparation of 2'-O-alkylated compounds comprises dissolving
PT   nucleoside in aprotic solvent, cooling, treating with base, warming,
PT   cooling and reacting with ester.
XX
PS   Example 46; Col 31; 24pp; English.
XX
CC   The present invention relates to a novel method of selective alkylation
CC   of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
CC   The method involves dissolving the nucleoside in at least one aprotic
CC   solvent, cooling, treating with base, warming, cooling and reacting with
CC   a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC   nucleotides, nucleosides and nucleoside surrogates used for preparation
CC   of oligomeric compounds having improved hybridisation affinity and
CC   nuclear resistance, which are useful as therapeutics, diagnostics and
CC   research reagents. The present sequence is a modified oligonucleotide
CC   used to illustrate the method of the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 905
AAD42011
ID   AAD42011 standard; DNA; 19 BP.
XX
AC   AAD42011;
XX
DT   04-NOV-2002  (first entry)
XX
DE   Oligonucleotide #14 used to illustrate the method of the invention.
XX
KW   Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW   nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   16. .19
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-dimethylaminooxyethyl thymidine (T-2'DMAOE)"
XX
PN   US6403779-B1.
XX
PD   11-JUN-2002.
XX
PF   08-JAN-1999;   99US-00227782.
XX
PR   08-JAN-1999;   99US-00227782.
```

```
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Kawasaki AM,  Fraser AS,  Manoharan M,  Cook PD,  Prakash TP;
XX
DR   WPI; 2002-546338/58.
XX
PT   Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
PT   for preparation of 2'-O-alkylated compounds comprises dissolving
PT   nucleoside in aprotic solvent, cooling, treating with base, warming,
PT   cooling and reacting with ester.
XX
PS   Example 46; Col 37; 24pp; English.
XX
CC   The present invention relates to a novel method of selective alkylation
CC   of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
CC   The method involves dissolving the nucleoside in at least one aprotic
CC   solvent, cooling, treating with base, warming, cooling and reacting with
CC   a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC   nucleotides, nucleosides and nucleoside surrogates used for preparation
CC   of oligomeric compounds having improved hybridisation affinity and
CC   nuclear resistance, which are useful as therapeutics, diagnostics and
CC   research reagents. The present sequence is a modified oligonucleotide
CC   used to illustrate the method of the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 906
AAD42011/c
ID   AAD42011 standard; DNA; 19 BP.
XX
AC   AAD42011;
XX
DT   04-NOV-2002  (first entry)
XX
DE   Oligonucleotide #14 used to illustrate the method of the invention.
XX
KW   Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW   nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base    16. .19
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-dimethylaminooxyethyl thymidine (T-2'DMAOE)"
XX
PN   US6403779-B1.
XX
PD   11-JUN-2002.
XX
PF   08-JAN-1999;   99US-00227782.
XX
PR   08-JAN-1999;   99US-00227782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Kawasaki AM,  Fraser AS,  Manoharan M,  Cook PD,  Prakash TP;
XX
DR   WPI; 2002-546338/58.
XX
PT   Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
PT   for preparation of 2'-O-alkylated compounds comprises dissolving
PT   nucleoside in aprotic solvent, cooling, treating with base, warming,
PT   cooling and reacting with ester.
XX
PS   Example 46; Col 37; 24pp; English.
XX
CC   The present invention relates to a novel method of selective alkylation
CC   of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
CC   The method involves dissolving the nucleoside in at least one aprotic
CC   solvent, cooling, treating with base, warming, cooling and reacting with
CC   a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC   nucleotides, nucleosides and nucleoside surrogates used for preparation
CC   of oligomeric compounds having improved hybridisation affinity and
CC   nuclear resistance, which are useful as therapeutics, diagnostics and
CC   research reagents. The present sequence is a modified oligonucleotide
CC   used to illustrate the method of the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 907
AAD42005
ID   AAD42005 standard; DNA; 19 BP.
XX
AC   AAD42005;
XX
DT   04-NOV-2002  (first entry)
XX
DE   Oligonucleotide #8 used to illustrate the method of the invention.
XX
KW   Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW   nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base    18
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "5-methyl, 2'-methoxyethyl residues"
XX
PN   US6403779-B1.
XX
PD   11-JUN-2002.
XX
PF   08-JAN-1999;   99US-00227782.
XX
PR   08-JAN-1999;   99US-00227782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Kawasaki AM,  Fraser AS,  Manoharan M,  Cook PD,  Prakash TP;
XX
DR   WPI; 2002-546338/58.
XX
PT   Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
PT   for preparation of 2'-O-alkylated compounds comprises dissolving
PT   nucleoside in aprotic solvent, cooling, treating with base, warming,
PT   cooling and reacting with ester.
XX
PS   Example 46; Col 33; 24pp; English.
XX
CC   The present invention relates to a novel method of selective alkylation
CC   of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
CC   The method involves dissolving the nucleoside in at least one aprotic
CC   solvent, cooling, treating with base, warming, cooling and reacting with
```

```
CC   a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC   nucleotides, nucleosides and nucleoside surrogates used for preparation
CC   of oligomeric compounds having improved hybridisation affinity and
CC   nuclear resistance, which are useful as therapeutics, diagnostics and
CC   research reagents. The present sequence is a modified oligonucleotide
CC   used to illustrate the method of the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 908
AAD42005/c
ID   AAD42005 standard; DNA; 19 BP.
XX
AC   AAD42005;
XX
DT   04-NOV-2002  (first entry)
XX
DE   Oligonucleotide #8 used to illustrate the method of the invention.
XX
KW   Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW   nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   18
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "5-methyl, 2'-methoxyethyl residues"
XX
PN   US6403779-B1.
XX
PD   11-JUN-2002.
XX
PF   08-JAN-1999;   99US-00227782.
XX
PR   08-JAN-1999;   99US-00227782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Kawasaki AM,  Fraser AS,  Manoharan M,  Cook PD,  Prakash TP;
XX
DR   WPI; 2002-546338/58.
XX
PT   Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
PT   for preparation of 2'-O-alkylated compounds comprises dissolving
PT   nucleoside in aprotic solvent, cooling, treating with base, warming,
PT   cooling and reacting with ester.
XX
PS   Example 46; Col 33; 24pp; English.
XX
CC   The present invention relates to a novel method of selective alkylation
CC   of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
CC   The method involves dissolving the nucleoside in at least one aprotic
CC   solvent, cooling, treating with base, warming, cooling and reacting with
CC   a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC   nucleotides, nucleosides and nucleoside surrogates used for preparation
CC   of oligomeric compounds having improved hybridisation affinity and
CC   nuclear resistance, which are useful as therapeutics, diagnostics and
CC   research reagents. The present sequence is a modified oligonucleotide
CC   used to illustrate the method of the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 909
AAD42003
ID   AAD42003 standard; DNA; 19 BP.
XX
AC   AAD42003;
XX
DT   04-NOV-2002  (first entry)
XX
DE   Oligonucleotide #6 used to illustrate the method of the invention.
XX
KW   Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW   nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   16. .19
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "5-methyl, 2'-O-propyl residues"
XX
PN   US6403779-B1.
XX
PD   11-JUN-2002.
XX
PF   08-JAN-1999;   99US-00227782.
XX
PR   08-JAN-1999;   99US-00227782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Kawasaki AM,  Fraser AS,  Manoharan M,  Cook PD,  Prakash TP;
XX
DR   WPI; 2002-546338/58.
XX
PT   Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
PT   for preparation of 2'-O-alkylated compounds comprises dissolving
PT   nucleoside in aprotic solvent, cooling, treating with base, warming,
PT   cooling and reacting with ester.
XX
PS   Example 46; Col 33; 24pp; English.
XX
CC   The present invention relates to a novel method of selective alkylation
CC   of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
CC   The method involves dissolving the nucleoside in at least one aprotic
CC   solvent, cooling, treating with base, warming, cooling and reacting with
CC   a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC   nucleotides, nucleosides and nucleoside surrogates used for preparation
CC   of oligomeric compounds having improved hybridisation affinity and
CC   nuclear resistance, which are useful as therapeutics, diagnostics and
CC   research reagents. The present sequence is a modified oligonucleotide
CC   used to illustrate the method of the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19
```

```
RESULT 910
AAD42003/c
ID   AAD42003 standard; DNA; 19 BP.
XX
AC   AAD42003;
XX
DT   04-NOV-2002  (first entry)
XX
DE   Oligonucleotide #6 used to illustrate the method of the invention.
XX
KW   Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW   nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   16. .19
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "5-methyl, 2'-O-propyl residues"
XX
PN   US6403779-B1.
XX
PD   11-JUN-2002.
XX
PF   08-JAN-1999;   99US-00227782.
XX
PR   08-JAN-1999;   99US-00227782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Kawasaki AM,  Fraser AS,  Manoharan M,  Cook PD,  Prakash TP;
XX
DR   WPI; 2002-546338/58.
XX
PT   Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
PT   for preparation of 2'-O-alkylated compounds comprises dissolving
PT   nucleoside in aprotic solvent, cooling, treating with base, warming,
PT   cooling and reacting with ester.
XX
PS   Example 46; Col 33; 24pp; English.
XX
CC   The present invention relates to a novel method of selective alkylation
CC   of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
CC   The method involves dissolving the nucleoside in at least one aprotic
CC   solvent, cooling, treating with base, warming, cooling and reacting with
CC   a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC   nucleotides, nucleosides and nucleoside surrogates used for preparation
CC   of oligomeric compounds having improved hybridisation affinity and
CC   nuclear resistance, which are useful as therapeutics, diagnostics and
CC   research reagents. The present sequence is a modified oligonucleotide
CC   used to illustrate the method of the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 911
AAD41998
ID   AAD41998 standard; DNA; 19 BP.
XX
AC   AAD41998;
XX
DT   04-NOV-2002  (first entry)
XX
DE   Oligonucleotide #1 used to illustrate the method of the invention.
XX
KW   Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW   nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   15. .18
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "5-methyl, 2'-aminooxyethoxy (2'-AOE) residues"
XX
PN   US6403779-B1.
XX
PD   11-JUN-2002.
XX
PF   08-JAN-1999;   99US-00227782.
XX
PR   08-JAN-1999;   99US-00227782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Kawasaki AM,  Fraser AS,  Manoharan M,  Cook PD,  Prakash TP;
XX
DR   WPI; 2002-546338/58.
XX
PT   Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
PT   for preparation of 2'-O-alkylated compounds comprises dissolving
PT   nucleoside in aprotic solvent, cooling, treating with base, warming,
PT   cooling and reacting with ester.
XX
PS   Example 46; Col 31; 24pp; English.
XX
CC   The present invention relates to a novel method of selective alkylation
CC   of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
CC   The method involves dissolving the nucleoside in at least one aprotic
CC   solvent, cooling, treating with base, warming, cooling and reacting with
CC   a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC   nucleotides, nucleosides and nucleoside surrogates used for preparation
CC   of oligomeric compounds having improved hybridisation affinity and
CC   nuclear resistance, which are useful as therapeutics, diagnostics and
CC   research reagents. The present sequence is a modified oligonucleotide
CC   used to illustrate the method of the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 912
AAD41998/c
ID   AAD41998 standard; DNA; 19 BP.
XX
AC   AAD41998;
XX
DT   04-NOV-2002  (first entry)
XX
DE   Oligonucleotide #1 used to illustrate the method of the invention.
XX
KW   Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW   nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   15. .18
FT                   /*tag=  a
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FT                   /mod_base= OTHER
FT                   /note= "5-methyl, 2'-aminooxyethoxy (2'-AOE) residues"
XX
PN   US6403779-B1.
XX
PD   11-JUN-2002.
XX
PF   08-JAN-1999;   99US-00227782.
XX
PR   08-JAN-1999;   99US-00227782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Kawasaki AM,  Fraser AS,  Manoharan M,  Cook PD,  Prakash TP;
XX
DR   WPI; 2002-546338/58.
XX
PT   Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
PT   for preparation of 2'-O-alkylated compounds comprises dissolving
PT   nucleoside in aprotic solvent, cooling, treating with base, warming,
PT   cooling and reacting with ester.
XX
PS   Example 46; Col 31; 24pp; English.
XX
CC   The present invention relates to a novel method of selective alkylation
CC   of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
CC   The method involves dissolving the nucleoside in at least one aprotic
CC   solvent, cooling, treating with base, warming, cooling and reacting with
CC   a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC   nucleotides, nucleosides and nucleoside surrogates used for preparation
CC   of oligomeric compounds having improved hybridisation affinity and
CC   nuclear resistance, which are useful as therapeutics, diagnostics and
CC   research reagents. The present sequence is a modified oligonucleotide
CC   used to illustrate the method of the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 913
AAD41999
ID   AAD41999 standard; DNA; 19 BP.
XX
AC   AAD41999;
XX
DT   04-NOV-2002  (first entry)
XX
DE   Oligonucleotide #2 used to illustrate the method of the invention.
XX
KW   Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW   nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   15. .18
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "5-methyl, 2'-dimethylaminooxyethoxy (2'-DMAOE)
FT                   residues"
XX
PN   US6403779-B1.
XX
PD   11-JUN-2002.
XX
PF   08-JAN-1999;   99US-00227782.
XX
PR   08-JAN-1999;   99US-00227782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Kawasaki AM,  Fraser AS,  Manoharan M,  Cook PD,  Prakash TP;
XX
DR   WPI; 2002-546338/58.
XX
PT   Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
PT   for preparation of 2'-O-alkylated compounds comprises dissolving
PT   nucleoside in aprotic solvent, cooling, treating with base, warming,
PT   cooling and reacting with ester.
XX
PS   Example 46; Col 31; 24pp; English.
XX
CC   The present invention relates to a novel method of selective alkylation
CC   of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
CC   The method involves dissolving the nucleoside in at least one aprotic
CC   solvent, cooling, treating with base, warming, cooling and reacting with
CC   a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC   nucleotides, nucleosides and nucleoside surrogates used for preparation
CC   of oligomeric compounds having improved hybridisation affinity and
CC   nuclear resistance, which are useful as therapeutics, diagnostics and
CC   research reagents. The present sequence is a modified oligonucleotide
CC   used to illustrate the method of the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 914
AAD41999/c
ID   AAD41999 standard; DNA; 19 BP.
XX
AC   AAD41999;
XX
DT   04-NOV-2002  (first entry)
XX
DE   Oligonucleotide #2 used to illustrate the method of the invention.
XX
KW   Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW   nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   15. .18
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "5-methyl, 2'-dimethylaminooxyethoxy (2'-DMAOE)
FT                   residues"
XX
PN   US6403779-B1.
XX
PD   11-JUN-2002.
XX
PF   08-JAN-1999;   99US-00227782.
XX
PR   08-JAN-1999;   99US-00227782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Kawasaki AM,  Fraser AS,  Manoharan M,  Cook PD,  Prakash TP;
XX
DR   WPI; 2002-546338/58.
```

```
XX
PT   Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
PT   for preparation of 2'-O-alkylated compounds comprises dissolving
PT   nucleoside in aprotic solvent, cooling, treating with base, warming,
PT   cooling and reacting with ester.
XX
PS   Example 46; Col 31; 24pp; English.
XX
CC   The present invention relates to a novel method of selective alkylation
CC   of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
CC   The method involves dissolving the nucleoside in at least one aprotic
CC   solvent, cooling, treating with base, warming, cooling and reacting with
CC   a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC   nucleotides, nucleosides and nucleoside surrogates used for preparation
CC   of oligomeric compounds having improved hybridisation affinity and
CC   nuclear resistance, which are useful as therapeutics, diagnostics and
CC   research reagents. The present sequence is a modified oligonucleotide
CC   used to illustrate the method of the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 915
AAD42009
ID   AAD42009 standard; DNA; 19 BP.
XX
AC   AAD42009;
XX
DT   04-NOV-2002  (first entry)
XX
DE   Oligonucleotide #12 used to illustrate the method of the invention.
XX
KW   Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW   nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   15. .18
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-dimethylaminooxyethyl thymidine (T-2'DMAOE)"
XX
PN   US6403779-B1.
XX
PD   11-JUN-2002.
XX
PF   08-JAN-1999;   99US-00227782.
XX
PR   08-JAN-1999;   99US-00227782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Kawasaki AM,  Fraser AS,  Manoharan M,  Cook PD,  Prakash TP;
XX
DR   WPI; 2002-546338/58.
XX
PT   Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
PT   for preparation of 2'-O-alkylated compounds comprises dissolving
PT   nucleoside in aprotic solvent, cooling, treating with base, warming,
PT   cooling and reacting with ester.
XX
PS   Example 46; Col 35; 24pp; English.
XX
CC   The present invention relates to a novel method of selective alkylation
CC   of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
CC   The method involves dissolving the nucleoside in at least one aprotic
CC   solvent, cooling, treating with base, warming, cooling and reacting with
CC   a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC   nucleotides, nucleosides and nucleoside surrogates used for preparation
CC   of oligomeric compounds having improved hybridisation affinity and
CC   nuclear resistance, which are useful as therapeutics, diagnostics and
CC   research reagents. The present sequence is a modified oligonucleotide
CC   used to illustrate the method of the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 916
AAD42009/c
ID   AAD42009 standard; DNA; 19 BP.
XX
AC   AAD42009;
XX
DT   04-NOV-2002  (first entry)
XX
DE   Oligonucleotide #12 used to illustrate the method of the invention.
XX
KW   Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW   nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   15. .18
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-dimethylaminooxyethyl thymidine (T-2'DMAOE)"
XX
PN   US6403779-B1.
XX
PD   11-JUN-2002.
XX
PF   08-JAN-1999;   99US-00227782.
XX
PR   08-JAN-1999;   99US-00227782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Kawasaki AM,  Fraser AS,  Manoharan M,  Cook PD,  Prakash TP;
XX
DR   WPI; 2002-546338/58.
XX
PT   Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
PT   for preparation of 2'-O-alkylated compounds comprises dissolving
PT   nucleoside in aprotic solvent, cooling, treating with base, warming,
PT   cooling and reacting with ester.
XX
PS   Example 46; Col 35; 24pp; English.
XX
CC   The present invention relates to a novel method of selective alkylation
CC   of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
CC   The method involves dissolving the nucleoside in at least one aprotic
CC   solvent, cooling, treating with base, warming, cooling and reacting with
CC   a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC   nucleotides, nucleosides and nucleoside surrogates used for preparation
CC   of oligomeric compounds having improved hybridisation affinity and
CC   nuclear resistance, which are useful as therapeutics, diagnostics and
CC   research reagents. The present sequence is a modified oligonucleotide
CC   used to illustrate the method of the invention
```

```
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 917
ABZ58336
ID   ABZ58336 standard; DNA; 19 BP.
XX
AC   ABZ58336;
XX
DT   28-APR-2003  (first entry)
XX
DE   Oligonucleotide with 2'-O-(2-(methylthio)ethyl)-5-methyluridine.
XX
KW   Oligonucleotide; 2'-O-(2-(methylthio)ethyl)-5-methyluridine; antisense;
KW   DNA-RNA hybrid; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   16
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-O-(2-methylthio)ethyl)-5-methyluridine"
FT   modified_base   17
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-O-(2-methylthio)ethyl)-5-methyluridine"
FT   modified_base   18
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-(2-methylthio)ethyl)-5-methyluridine"
FT   modified_base   19
FT                   /*tag=  d
FT                   /mod_base= OTHER
FT                   /note= "2'-O-(2-methylthio)ethyl)-5-methyluridine"
XX
PN   WO2003004603-A2.
XX
PD   16-JAN-2003.
XX
PF   01-JUL-2002; 2002WO-US020940.
XX
PR   03-JUL-2001; 2001US-0302683P.
PR   28-JAN-2002; 2002US-00058740.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Prakash TP,  Manoharan M;
XX
DR   WPI; 2003-239204/23.
XX
PT   Increasing binding of oligomeric compound to proteins useful in
PT   preparation of antisense therapeutics, involves use of modified
PT   oligomeric compound having oligonucleotide group.
XX
PS   Example 27; Page 72; 122pp; English.
XX
CC   The present sequence is an example of an oligonucleotide of the invention
CC   containing 2'-O-(2-(methylthio)ethyl)-5-methyluridine (2'-O-(MTE)-5-
CC   methyluridine) modifications. In examples of the invention, 2'-O-MTE was
CC   incorporated into oligonucleotides and evaluated for antisense properties
CC   in comparison with the known 2'-O-(2-methoxyethyl) (2'-O-MOE)
CC   modification. The 2'-O-MTE modified oligonucleotides exhibited similar
CC   binding affinity to target RNA as their 2'-O-MOE equivalent while binding
CC   to human serum albumin was improved. The modification can be used to
CC   modulate the pharmacokinetics of oligonucleotides, e.g. in antisense
CC   therapy
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 15 T; 4 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 5.5e+02;
  Matches   15;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||::::
Db          1 TTTTTTTTTTTTTTTUUUU 19


RESULT 918
ABZ58336/c
ID   ABZ58336 standard; DNA; 19 BP.
XX
AC   ABZ58336;
XX
DT   28-APR-2003  (first entry)
XX
DE   Oligonucleotide with 2'-O-(2-(methylthio)ethyl)-5-methyluridine.
XX
KW   Oligonucleotide; 2'-O-(2-(methylthio)ethyl)-5-methyluridine; antisense;
KW   DNA-RNA hybrid; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   16
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-O-(2-methylthio)ethyl)-5-methyluridine"
FT   modified_base   17
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-O-(2-methylthio)ethyl)-5-methyluridine"
FT   modified_base   18
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-(2-methylthio)ethyl)-5-methyluridine"
FT   modified_base   19
FT                   /*tag=  d
FT                   /mod_base= OTHER
FT                   /note= "2'-O-(2-methylthio)ethyl)-5-methyluridine"
XX
PN   WO2003004603-A2.
XX
PD   16-JAN-2003.
XX
PF   01-JUL-2002; 2002WO-US020940.
XX
PR   03-JUL-2001; 2001US-0302683P.
PR   28-JAN-2002; 2002US-00058740.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Prakash TP,  Manoharan M;
XX
DR   WPI; 2003-239204/23.
XX
PT   Increasing binding of oligomeric compound to proteins useful in
PT   preparation of antisense therapeutics, involves use of modified
PT   oligomeric compound having oligonucleotide group.
XX
PS   Example 27; Page 72; 122pp; English.
XX
CC   The present sequence is an example of an oligonucleotide of the invention
CC   containing 2'-O-(2-(methylthio)ethyl)-5-methyluridine (2'-O-(MTE)-5-
CC   methyluridine) modifications. In examples of the invention, 2'-O-MTE was
CC   incorporated into oligonucleotides and evaluated for antisense properties
```

```
CC   in comparison with the known 2'-O-(2-methoxyethyl) (2'-O-MOE)
CC   modification. The 2'-O-MTE modified oligonucleotides exhibited similar
CC   binding affinity to target RNA as their 2'-O-MOE equivalent while binding
CC   to human serum albumin was improved. The modification can be used to
CC   modulate the pharmacokinetics of oligonucleotides, e.g. in antisense
CC   therapy
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 15 T; 4 U; 0 Other;

  Query Match              0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 919
AAQ25565/c
ID   AAQ25565 standard; DNA; 20 BP.
XX
AC   AAQ25565;
XX
DT   25-MAR-2003  (revised)
DT   02-DEC-1992  (first entry)
XX
DE   Dye-coupled 3'-amino modified oligonucleotide.
XX
KW   DNA synthesis; RNA; antisense strands; detection; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   20
FT                   /*tag=  a
FT                   /note= "3-amino modified"
XX
PN   EP490281-A1.
XX
PD   17-JUN-1992.
XX
PF   06-DEC-1991;   91EP-00120935.
XX
PR   11-DEC-1990;   90DE-04039488.
XX
PA   (FARH ) HOECHST AG.
XX
PI   Engels J,  Herrlein M,  Konrad R,  Mag M;
XX
DR   WPI; 1992-201578/25.
XX
PT   New dye-coupled modified nucleosides, nucleotides and oligo:nucleotides -
PT   useful for synthesis of antisense DNA and RNA strands in presence of
PT   template, also for in=vivo and in=vitro detection of genetic material.
XX
PS   Example; Page 9; 17pp; German.
XX
CC   The sequence is an example of a dye coupled 3'-amino modified oligo-
CC   nucleotide, it can be used in the synthesis of DNA and RNA nucleosides,
CC   nucleotides and oligonucleotides and for the synthesis of opposite
CC   strands in the presence of a template strand and in fluorescence
CC   microscopic and macroscopic detection in vivo and in vitro of genetic
CC   material. It is labelled with a fluorescent dye. See also AAQ25566 and
CC   AAQ25567. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match              0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         20 AAAAAAAAAAAAAAAAAAA 2


RESULT 920
AAQ33554/c
ID   AAQ33554 standard; DNA; 20 BP.
XX
AC   AAQ33554;
XX
DT   25-MAR-2003  (revised)
DT   02-FEB-1993  (first entry)
XX
DE   Microsatellite sequence from clone AGLA247.
XX
KW   PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW   genetic mapping; traits; amplification; ss.
XX
OS   Bos taurus.
XX
PN   WO9213102-A1.
XX
PD   06-AUG-1992.
XX
PF   15-JAN-1992;   92WO-US000340.
XX
PR   15-JAN-1991;   91US-00642342.
XX
PA   (GENM-) GENMARK.
XX
PI   Georges M,  Massey JM;
XX
DR   WPI; 1992-284684/34.
XX
PT   Polymorphic bovine DNA markers - used in genetic identification, gene
PT   mapping, and selective breeding.
XX
PS   Table 7; Page 150; 517pp; English.
XX
CC   The sequence is that of a bovine microsatellite sequence obtd. by
CC   screening a library of bovine MboI DNA fragments of between 250 and 500
CC   bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
CC   clones cross-hybridised. Assuming independent distribution of
CC   microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
CC   in the bovine genome is estimated at >100, 000. The sequence information
CC   for ca. 230 such bovine microsatellites is summarised in the
CC   specification and indexed herein (see below). The sequences upstream and
CC   downstream of the microsatellite sequence were used to generate the
CC   required PCR primers for in vitro amplification of the corresp.
CC   microsatellite (using the program OPTIPRIM). The microsatellites may be
CC   used to identify individuals, for parentage testing, and in the genetic
CC   mapping of economic trait loci, or genes involved the determinism of
CC   economically important traits esp. in cattle, to allow selective
CC   breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
CC   field.)
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match              0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         20 AAAAAAAAAAAAAAAAAAA 2


RESULT 921
AAQ58578
ID   AAQ58578 standard; RNA; 20 BP.
XX
AC   AAQ58578;
XX
```

```
DT   25-MAR-2003  (revised)
DT   21-AUG-1994  (first entry)
XX
DE   Sequence of synthetic RNA oligo which is a target nucleotide for a novel
DE   receptor.
XX
KW   Novel receptor; nucleic acid; transport; oligo; ss.
XX
OS   Synthetic.
XX
PN   WO9404194-A1.
XX
PD   03-MAR-1994.
XX
PF   13-AUG-1993;   93WO-US007603.
XX
PR   14-AUG-1992;   92US-00930087.
XX
PA   (MASI ) MASSACHUSETTS INST TECHNOLOGY.
XX
PI   Usman N,  Rebek J,  De Mendoza J;
XX
DR   WPI; 1994-082846/10.
XX
PT   Transport of nucleic acid derivs. across membranes - using new receptors
PT   which use salt bridging, aromatic stacking, hydrogen bonding and
PT   chelation.
XX
PS   Example; Table 1, page 38; 103pp; English.
XX
CC   The inventors claim a method of transporting a nucleic acid deriv. accros
CC   a membrane which comprises using a receptor that uses salt bridgin,
CC   aromatic stacking, H bonding and chelation to recognise the nucleic acid
CC   deriv. AAQ56305, AAQ58577-86 are nucleic acid derivs used in the
CC   examples. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 922
AAQ94205/c
ID   AAQ94205 standard; DNA; 20 BP.
XX
AC   AAQ94205;
XX
DT   25-MAR-2003  (revised)
DT   24-AUG-1995  (first entry)
XX
DE   Alpha-anomeric oligonucleotide ligand 1803 for oestradiol hapten.
XX
KW   Oligonucleotide ligand; steroid hormone; hapten; immobilisation;
KW   immunodetection; estradiol; alpha-anomer; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .21
FT                   /*tag=  b
FT                   /note= "the glycosidic bonds between nucleotides are all
FT                   in the alpha-anomer form"
FT   modified_base   20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "carries a group derived ffrom aminopropanediol"
XX
PN   WO9429723-A1.
XX
PD   22-DEC-1994.
XX
PF   10-JUN-1994;   94WO-FR000689.
XX
PR   11-JUN-1993;   93FR-00007093.
XX
PA   (CROS/) CROS P.
PA   (KURF/) KURFURST R.
PA   (BATT/) BATTAIL N.
PA   (PIGA/) PIGA N.
XX
PI   Cros P,  Kurfurst R,  Battail N,  Piga N;
XX
DR   WPI; 1995-036665/05.
XX
PT   Assay device for hapten or its specific antibodies - comprises support
PT   having competitive reagent immobilised via nucleic acid ligand to improve
PT   orientation and accessibility.
XX
PS   Example 1; Page 10; 39pp; French.
XX
CC   Oligonucleotides (AAQ94201-Q94205) were synthesised for use as ligands.
CC   The ligands are covalently linked to a hapten (esp. a steroid hormone) to
CC   form a conjugate which is then immobilised on a solid support for
CC   interaction with antibodies against the hapten. Nucleic acid ligands are
CC   less likely to be recognised by the antibodies than are peptide ligands
CC   and nucleic acids are also less likely to undergo intramolecular
CC   organisation which interferes with accessibility of the hapten to the
CC   antibodies. For immunodiagnosis of oestradiol, the active hapten
CC   oestradiol-6-carboxymethoxime-N- hydroxysuccinimide ester was used.
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         20 AAAAAAAAAAAAAAAAAAA 2


RESULT 923
AAQ90405/c
ID   AAQ90405 standard; DNA; 20 BP.
XX
AC   AAQ90405;
XX
DT   08-JAN-1996  (first entry)
XX
DE   T2 (synthetic DNA probe with 5' amino terminal #4).
XX
KW   T2; HLA; dQa; self-addressable electronic device; SAED; hybridisation;
KW   ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1
FT                   /*tag=  a
FT                   /note= "3' aminolink2 Thymine; allows binding to any
FT                   amine"
XX
PN   WO9512808-A1.
XX
PD   11-MAY-1995.
XX
PF   26-OCT-1994;   94WO-US012270.
XX
PR   01-NOV-1993;   93US-00146504.
```

```
XX
PA   (NANO-) NANOGEN INC.
XX
PI   Heller MJ,  Tu E;
XX
DR   WPI; 1995-185870/24.
XX
PT   New self-addressable electronic devices - used for multi-step and
PT   multiplex reactions such as DNA hybridisation(s), clinical diagnostics
PT   and bio:polymer synthesis.
XX
PS   Example 1; Page 41; 86pp; English.
XX
CC   The sequences represented by, AAQ90402-15 are synthetic DNA probes
CC   containing 5' amino termini. The sequences shown in AAQ90390-401 are
CC   synthetic DNA probes with 3' ribonucleoside termini. These sequences were
CC   specific for the polymorphisms of HLA gene dQa. The sequences were used
CC   in the device of the invention. This is a self-addressable electronic
CC   device (SAED) that can be used to carry out multi-step and multiplex
CC   reactions, such as nucleic acid hybridisations. The advantages of this
CC   method are that these reactions can be carried out with complete and
CC   precise electronic control, and that the rate, specificity and
CC   sensitivity of these reactions are greatly improved at micro-locations
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         20 AAAAAAAAAAAAAAAAAAA 2

RESULT 924
AAV07752/c
ID   AAV07752 standard; DNA; 20 BP.
XX
AC   AAV07752;
XX
DT   07-DEC-1998  (first entry)
XX
DE   Phosphorothioate oligonucleotide.
XX
KW   phosphorothioate; sulphurisation; heterocycle; automated synthesis;
KW   antisense; EDITH; Beaucage reagent; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .20
FT                   /*tag=  a
FT                   /note= "phosphorothioate internucleotide linkages"
XX
PN   WO9741130-A2.
XX
PD   06-NOV-1997.
XX
PF   29-APR-1997;   97WO-US007118.
XX
PR   30-APR-1996;   96US-00641920.
XX
PA   (MINU ) UNIV MINNESOTA.
PA   (LOUU ) UNIV LOUISIANA STATE & AGRIC.
XX
PI   Barany G,  Musier-Forsyth K,  Xu Q,  Chen L,  Hammer RP;
XX
DR   WPI; 1997-549671/50.
XX
PT   Sulphurisation of phosphorus-containing compounds, e.g.
PT   oligo:nucleotide(s) - by contacting the compound with a di:sulphide-
PT   containing five-membered heterocycle.
XX
PS   Example 7; Page 30; 51pp; English.
XX
CC   The present invention provides a method for sulphurising phosphorus-
CC   containing compounds. It comprises contacting the phosphorus-containing
CC   compound which a 1,2,4-dithiazolidine-2,5-dione compound or a 3-
CC   substituted-1,2,4-dithiazolin-5-one compound. The method is especially
CC   useful for incorporation of phosphorothioate linkages into biologically
CC   important molecules such as DNA, RNA and phosphopeptides. Molecules
CC   containing such linkages are useful e.g. as antisense compounds for
CC   inhibiting gene expression, as reagents for studying DNA-protein or RNA-
CC   protein interactions, or as catalytic RNA. The present sequence
CC   represents an oligonucleotide with phosphorothioate linkages prepared by
CC   the method of the invention
XX
SQ   Sequence 20 BP; 1 A; 0 C; 0 G; 0 T; 19 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1

RESULT 925
AAT63649/c
ID   AAT63649 standard; DNA; 20 BP.
XX
AC   AAT63649;
XX
DT   06-JUN-1997  (first entry)
XX
DE   Anti-HTLV antisense reference oligonucleotide HT.
XX
KW   antisense; complementary; tax gene; inhibit; HTLV-1;
KW   human T-cell lymphotropic virus type 1; viral antigen expression; ss.
XX
OS   Synthetic.
XX
PN   JP09052898-A.
XX
PD   25-FEB-1997.
XX
PF   09-AUG-1995;   95JP-00224606.
XX
PR   09-AUG-1995;   95JP-00224606.
XX
PA   (SOYA-) SOYAKU GIJUTSU KENKYUSHO KK.
XX
DR   WPI; 1997-197252/18.
XX
PT   Anti-HTLV-1 anti-sense oligo:nucleotide - is complementary to region of
PT   tax gene from human T-cell lymphotropic virus type 1 and inhibits viral
PT   antigen expression.
XX
PS   Example 1; Page 8; 10pp; Japanese.
XX
CC   Oligonucleotides having a partial sequence consisting of at least 15
CC   bases of AAT63641 (an antisense oligo complementary to a region of the
CC   tax gene which can inhibit human T-cell lymphotropic virus type 1 (HTLV-
CC   1) viral antigen expression) are claimed. In an example, six antisense
CC   oligos were designed, T1-T6 (AAT63650-55) and were compared to six oligos
CC   derived from other regions of HTLV-1, i.e. SJ1 (splice junction), P1
CC   (p21), R1 (rex), RR1 (rex response element), E1 (env) and G1 (gag), four
CC   reference oligonucleotides TIS (tax-sense), HC (dC20), HT (dT20)
CC   (AAT63647-49) and a random 20mer (RAN) in a HTLV-1 virus antigen
CC   expression inhibiting test. Oligonucleotide T1 gave the best results
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
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```
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         20 AAAAAAAAAAAAAAAAAAA 2

RESULT 926
AAV34591
ID   AAV34591 standard; DNA; 20 BP.
XX
AC   AAV34591;
XX
DT   25-AUG-1998  (first entry)
XX
DE   M. vaccae antigenic sequence hybridising oligo AD12.
XX
KW   Mycobacterium vaccae; antigen; therapy; prevention; cytokine production;
KW   M. avium; M. tuberculosis; immune response enhancer; cell proliferation;
KW   mycobacteria infection; vaccine; cancer; ss.
XX
OS   Synthetic.
OS   Mycobacterium vaccae.
XX
PN   WO9808542-A2.
XX
PD   05-MAR-1998.
XX
PF   28-AUG-1997;   97WO-NZ000105.
XX
PR   29-AUG-1996;   96US-00705347.
PR   12-JUN-1997;   97US-00873970.
XX
PA   (GENE-) GENESIS RES & DEV CORP.
XX
PI   Tan P,  Hiyama J,  Visser E,  Skinner MA,  Scott LM,  Prestidge RL;
XX
DR   WPI; 1998-216926/19.
XX
PT   Mycobacterium vaccae polypeptides - used to develop products for use in
PT   detection, therapy and prevention of mycobacteria infections or as immune
PT   response enhancers.
XX
PS   Example 8; Page 99; 153pp; English.
XX
CC   This oligonucleotide is used in the DNA cloning strategies of the
CC   Mycobacterium vaccae antigens. The invention provides M. vaccae
CC   polypeptides that comprise an immunogenic portion of a soluble M. vaccae
CC   antigen, or a variant, where the antigen induces an immune response in
CC   patients previously exposed to a mycobacterium. Such M. vaccae
CC   polypeptides can be used in methods for enhancing non-specific immune
CC   response. The methods and products can be used for the detection,
CC   treatment and prevention of infectious diseases caused by mycobacteria
CC   such as M. vaccae, M. avium or M. tuberculosis. The products also have
CC   the ability to induce cell proliferation and cytokine production (e.g.
CC   interferon-gamma and interleukin-12 production) in T cells, NK cells, B
CC   cells, or macrophages. They can be used for enhancing immune responses
CC   for use in vaccines or immunotherapy of infectious diseases and cancers
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19

RESULT 927
AAT86606/c
ID   AAT86606 standard; DNA; 20 BP.
XX
AC   AAT86606;
XX
DT   04-JUN-1998  (first entry)
XX
DE   Oligonucleotide separated by capillary affinity gel electrophoresis.
XX
KW   Capillary afinity gel electrophoresis; separation; polymer-gel;
KW   polyacrylamide; ss.
XX
OS   Synthetic.
XX
PN   WO9745721-A1.
XX
PD   04-DEC-1997.
XX
PF   23-MAY-1997;   97WO-EP002647.
XX
PR   24-MAY-1996;   96CH-00001320.
XX
PA   (NOVS ) NOVARTIS AG.
XX
PI   Muscate A,  Paulus A,  Natt F;
XX
DR   WPI; 1998-041763/04.
XX
PT   Separation of electrically charged target molecules - by capillary
PT   affinity gel electrophoresis using polymer-gel to which receptors for
PT   target molecules are bound.
XX
PS   Example D3; Page 25; 41pp; English.
XX
CC   A mixture of oligonucleotides (AAT86604-7) were separated by a new
CC   process using capillary affinity gel electrophoresis. The invention
CC   relates to selective separation of electrically charged target molecules
CC   in an analytical mixture. It comprises capillary affinity gel
CC   electrophoresis using a capillary tube which is at least partly filled
CC   with a polymer gel. Receptors for target molecules are covalently bound
CC   to the polymer. An electric field of at least 50 volts/cm is applied. The
CC   capillary tube is charged with the analytical mixture. In a first
CC   separation stage, the target molecules in the mixture are bound to the
CC   receptors and the remaining components are eluted, optionally whilst
CC   splitting open. In a second stage, the elution conditions are changed,
CC   optionally in stages, so that the affinity of the target molecules for
CC   the receptor is eliminated and the target molecules are eluted and
CC   detected, optionally whilst splitting open. The process is useful for
CC   selective separation and/or determination of charged organic compounds,
CC   such as oligonucleotides, peptides or carbohydrates. It may be used, e.g.
CC   for isolation of specific proteins and DNA molecules, purification of
CC   antibodies, analysis of antisense compounds or screening for enzyme
CC   inhibitors. The process achieves higher resolution and selectivity than
CC   prior art processes, especially in the case of complex biological
CC   analytical mixtures. It has high sensitivity, even with small amounts of
CC   samples. The derivatised polymers may be synthesised specifically using
CC   standard methods
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         20 AAAAAAAAAAAAAAAAAAA 2

RESULT 928
AAX27533/c
ID   AAX27533 standard; RNA; 20 BP.
XX
AC   AAX27533;
```

```
XX
DT   27-MAY-1999  (first entry)
XX
DE   Synthetic RNA sequence produced by the method of the invention.
XX
KW   Silyloxymethyl; phosphonate; silyloxymethyl halide; diagnosis; ss;
KW   cyanoethyl phosphoramidate coupling; isomerisation; steric hindrance.
XX
OS   Synthetic.
XX
PN   WO9909044-A1.
XX
PD   25-FEB-1999.
XX
PF   17-AUG-1998;   98WO-EP005215.
XX
PR   18-AUG-1997;   97CH-00001931.
XX
PA   (PITS/) PITSCH S.
PA   (WEIS/) WEISS P A.
PA   (JENN/) JENNY L.
XX
PI   Pitsch S,  Weiss PA,  Jenny L;
XX
DR   WPI; 1999-180963/15.
XX
PT   2-Silyloxymethyl ribonucleosides and their phosphonate derivatives - have
PT   high purity, use in machine synthesis of ribonucleic acids, enable longer
PT   oligonucleotide chain construction, and larger amounts.
XX
PS   Example 6; Page 25; 38pp; English.
XX
CC   The invention relates to silyloxymethyl protected D- or L-ribonucleosides
CC   and their phosphonates (I), and silyloxymethyl halides (II). (I) are
CC   intermediates for synthesis of RNA-oligonucleotides with predetermined
CC   nucleotide sequence, particularly by machine synthesis. The groups
CC   specified above, apart from those on silyl, are those particularly for
CC   the cyanoethyl phosphoramidate coupling. Uses of the oligoribonucleotide
CC   products in diagnosis, therapy, and as research tools, are well known,
CC   and are not dealt with in detail. (II) is an intermediate for (I). The
CC   silyloxymethyl halide reagent is easy to prepare, and yields are high.
CC   Introduction of the silyloxymethyl group into the ribonucleoside is
CC   simple and rapid, and the acetal bond formed does not migrate,
CC   eliminating particularly the prior art problem of 2' to 3' isomerisation.
CC   The methylenedioxy group spacer between the silyl group and nucleoside
CC   ring results in less steric hindrance than bulky direct silyloxy
CC   linkages, enabling first, a range of choices for the silyl substituents,
CC   to provide, e.g., acid or base stability; and second, higher yields in
CC   coupling. Purer products are therefore obtained than in prior art,
CC   enabling larger quantities and longer chains of oligoribonucleotides to
CC   be synthesised successfully, and in shorter times
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 0 T; 20 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         20 AAAAAAAAAAAAAAAAAAA 2

RESULT 929
AAZ11326
ID   AAZ11326 standard; DNA; 20 BP.
XX
AC   AAZ11326;
XX
DT   25-OCT-1999  (first entry)
XX
DE   Mycobacterial 16S rRNA specific oligo AD12.
XX
KW   Mycobacterium vaccae protein; antigen; T cell activation; cytokine;
KW   dendritic cell maturation; infectious disease; immune disorder; cancer;
KW   respiratory system; mycobacterial infection; allergy; tuberculosis;
KW   leprosy; sarcoidosis; lung cancer; asthma; skin disorder; psoriasis;
KW   dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma;
KW   squamous cell carcinoma; melanoma; PCR primer; ss.
XX
OS   Synthetic.
OS   Mycobacterium vaccae.
XX
PN   WO9932634-A2.
XX
PD   01-JUL-1999.
XX
PF   23-DEC-1998;   98WO-NZ000189.
XX
PR   23-DEC-1997;   97US-00996624.
PR   23-DEC-1997;   97US-00997080.
PR   23-DEC-1997;   97US-00997362.
PR   11-JUN-1998;   98US-00095855.
PR   17-SEP-1998;   98US-00156181.
PR   04-DEC-1998;   98US-00205426.
XX
PA   (GENE-) GENESIS RES & DEV CORP LTD.
XX
PI   Tan P,  Watson J,  Visser ES,  Skinner MA,  Prestidge RL;
XX
DR   WPI; 1999-430163/36.
XX
PT   Enhancing immune response to an antigen.
XX
PS   Example 15; Page 177; 243pp; English.
XX
CC   The invention provides heat-killed Mycobacterium vaccae, or recombinant
CC   M. vaccae proteins. The M. vaccae proteins may be employed to activate T
CC   cells and natural killer cells, to stimulate the production of cytokines,
CC   to enhance the expression of co-stimulatory molecules on dendritic cells
CC   and monocytes, and to enhance dendritic cell maturation and function. The
CC   proteins can be expressed by standard recombinant methodology.
CC   Pharmaceutical compositions comprising the proteins or nucleic acid
CC   sequences encoding the proteins can be used for the treatment,
CC   prevention, and detection of disorders including infectious diseases,
CC   immune disorders and cancer. In particular, the compounds and methods are
CC   used for treatment of diseases of the respiratory system, such as
CC   mycobacterial infections, asthma, allergies, tuberculosis, leprosy,
CC   sarcoidosis and lung cancers, and disorders of the skin such as
CC   psoriasis, atopic dermatitis, eczema, allergic contact dermatitis,
CC   alopecia areata, and skin cancers such as basal carcinoma, squamous cell
CC   carcinoma and melanoma
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19

RESULT 930
AAA40449
ID   AAA40449 standard; DNA; 20 BP.
XX
AC   AAA40449;
XX
DT   13-NOV-2000  (first entry)
XX
DE   Electochemical detection method sample DNA target.
XX
KW   Electrochemical detection; glucose; cholesterol; urea nitrogen;
KW   bilirubin; uric acid; haemoglobin; lactic acid; body fluid; blood;
```

KW plasma; serum; urine; lymph diagnosis; ss.
XX
OS Synthetic.
XX
PN EP1018646-A2.
XX
PD 12-JUL-2000.
XX
PF 07-JAN-2000; 2000EP-00100126.
XX
PR 06-JAN-1999; 99JP-00001111.
PR 24-MAY-1999; 99JP-00143599.
XX
PA (FUJF) FUJI PHOTO FILM CO LTD.
XX
PI Ogawa M, Takenaka S, Takagi M;
XX
DR WPI; 2000-444372/39.
XX
PT Quantitative analysis of a biochemical compound such as glucose, in body
PT a body fluid such as blood, comprising detecting enhanced electron
PT transfer between an oxidase and a DNA-immobilized electrode, useful for
PT diagnosis of disease.
XX
PS Example 1; Page 8; 14pp; English.
XX
CC This invention describes a novel method for quantitatively analysing a
CC biochemical compound (I) which comprises contacting (I) with double
CC stranded DNA fixed to the surface of an electrode at their terminals in
CC which electrochemically active threading intercalators are intercalated,
CC in an aqueous medium under application of electric potential to the
CC electrode in the presence of an oxidase which oxidizes the biochemical
CC compound and becomes reduced, and detecting electric current flowing
CC between the electrode and a second electrode in the aqueous medium. The
CC method is useful for detection of biochemical compounds such as glucose,
CC cholesterol, urea nitrogen, bilirubin, uric acid, haemoglobin and lactic
CC acid in body fluids such as whole blood, plasma, serum, urine, and lymph
CC for diagnosis of various diseases. The method allows detection of
CC biochemical compounds quickly and easily with a high sensitivity using a
CC simple apparatus. This sequence represents DNA fragment used as a target
CC sample in the method of the invention
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAAA 19

RESULT 931
AAA40448/c
ID AAA40448 standard; DNA; 20 BP.
XX
AC AAA40448;
XX
DT 13-NOV-2000 (first entry)
XX
DE Electochemical detection method fixed probe DNA.
XX
KW Electrochemical detection; glucose; cholesterol; urea nitrogen;
KW bilirubin; uric acid; haemoglobin; lactic acid; body fluid; blood;
KW plasma; serum; urine; lymph diagnosis; probe; ss.
XX
OS Synthetic.
XX
PN EP1018646-A2.
XX
PD 12-JUL-2000.
XX
PF 07-JAN-2000; 2000EP-00100126.
XX
PR 06-JAN-1999; 99JP-00001111.
PR 24-MAY-1999; 99JP-00143599.
XX
PA (FUJF) FUJI PHOTO FILM CO LTD.
XX
PI Ogawa M, Takenaka S, Takagi M;
XX
DR WPI; 2000-444372/39.
XX
PT Quantitative analysis of a biochemical compound such as glucose, in body
PT a body fluid such as blood, comprising detecting enhanced electron
PT transfer between an oxidase and a DNA-immobilized electrode, useful for
PT diagnosis of disease.
XX
PS Example 1; Page 7; 14pp; English.
XX
CC This invention describes a novel method for quantitatively analysing a
CC biochemical compound (I) which comprises contacting (I) with double
CC stranded DNA fixed to the surface of an electrode at their terminals in
CC which electrochemically active threading intercalators are intercalated,
CC in an aqueous medium under application of electric potential to the
CC electrode in the presence of an oxidase which oxidizes the biochemical
CC compound and becomes reduced, and detecting electric current flowing
CC between the electrode and a second electrode in the aqueous medium. The
CC method is useful for detection of biochemical compounds such as glucose,
CC cholesterol, urea nitrogen, bilirubin, uric acid, haemoglobin and lactic
CC acid in body fluids such as whole blood, plasma, serum, urine, and lymph
CC for diagnosis of various diseases. The method allows detection of
CC biochemical compounds quickly and easily with a high sensitivity using a
CC simple apparatus. This sequence represents DNA fragment used as fixed
CC probe DNA in the method of the invention
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 20 AAAAAAAAAAAAAAAAAAA 2

RESULT 932
AAZ91117/c
ID AAZ91117 standard; DNA; 20 BP.
XX
AC AAZ91117;
XX
DT 06-JUN-2000 (first entry)
XX
DE Oligonucleotide #5 for conjugation to abietane derivative.
XX
KW Abietane derivative; labelling; diagnostic test; biotin substitute; ss.
XX
OS Synthetic.
XX
PN FR2781802-A1.
XX
PD 04-FEB-2000.
XX
PF 31-JUL-1998; 98FR-00010084.
XX
PR 31-JUL-1998; 98FR-00010084.
XX
PA (INMR) BIO MERIEUX.
XX
PI Charles MH, Piga N, Battail PN, Veron L, Delair T, Mandrand B;
XX
DR WPI; 2000-239603/21.
XX

```
PT   Saturated and unsaturated derivatives of abietic acid and their
PT   conjugated derivatives with natural and synthetic polymers, having use in
PT   diagnostics, chemical reactions and analysis.
XX
PS   Example 5; Page 20; 39pp; French.
XX
CC   The invention relates to novel saturated and unsaturated abietane
CC   derivatives. The new compounds may be used directly or indirectly in the
CC   development of new diagnostic tests, to follow infections, especially
CC   viral infections, to follow and/or measure chemical products, especially
CC   potential pollutants. In diagnostic tests they may be used as markers, or
CC   to form a universal solid phase after immobilization on a solid support,
CC   to produce monoclonal antibodies or polyclonal antibodies having
CC   diagnostic uses. The oligonucleotides AAZ91113-Z91117 represent examples
CC   of sequences that can be labeled with the new abietane derivatives. The
CC   new derivatives may be used to substitute for biotin in diagnostic tests,
CC   but because they are not found naturally in humans the risk of potential
CC   interactions with biological molecules is eliminated
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         20 AAAAAAAAAAAAAAAAAAA 2

RESULT 933
AAA50193/c
ID   AAA50193 standard; DNA; 20 BP.
XX
AC   AAA50193;
XX
DT   07-NOV-2000  (first entry)
XX
DE   2'-Methoxyethoxy-modified oligonucleotide.
XX
KW   Phosphodiester oligonucleotide; H-phosphonate chemistry; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .19
FT                    /*tag=  a
FT                    /note= "2'-methoxyethoxy modified thymidine"
XX
PN   WO200047593-A1.
XX
PD   17-AUG-2000.
XX
PF   11-FEB-2000; 2000WO-US003543.
XX
PR   12-FEB-1999;   99US-00250075.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Manoharan M,  Maier MA;
XX
DR   WPI; 2000-558188/51.
XX
PT   Preparation of mixed backbone oligomeric compounds useful as e.g. primers
PT   for diagnostic tests, involves oxidation of H-phosphonate internucleoside
PT   linkages to phosphodiester internucleoside linkages.
XX
PS   Example 12; Page 34; 49pp; English.
XX
CC   The present sequence is that of a phosphodiester oligonucleotide
CC   containing 20 T nucleobases, 19 having a 2'-methoxyethoxy group on its 5'
CC   ribosyl sugar moiety. It is an example of an oligomeric compound produced
CC   according to the methods of the invention. The invention provides
CC   compounds and methods for the preparation of mixed backbone oligomeric,
CC   or chimeric, compounds having phosphodiester internucleoside linkages in
CC   addition to phosphorothioate and/or phosphoramidate internucleoside
CC   linkages. The methods also include incorporation of boranophosphate
CC   internucleoside linkages. The methods utilise H-phosphonate intermediates
CC   that are coupled together forming contiguous regions of 1 or more H-
CC   phosphonate internucleoside linkages. Each contiguous region is
CC   subsequently oxidized to phosphodiester, phosphorothioate,
CC   phosphoroamidate or boranophosphate internucleoside linkages prior to
CC   further elongation. Mixed backbone oligomeric compounds are prepared in
CC   this manner by oxidizing adjacent regions with different reagents.
CC   Oligomeric compounds of the invention are prepared using novel oxidation
CC   steps that oxidize a region of 1 or more H-phosphonate internucleoside
CC   linkages without degrading existing linkages that have been previously
CC   oxidized. The oligonucleotides obtained are useful as primers in PCR,
CC   probes, linkers, gene fragments and for other diagnostic tests on e.g.
CC   biological tissue, fluid, cells etc., as research reagents, and as
CC   antiviral agents
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         20 AAAAAAAAAAAAAAAAAAA 2

RESULT 934
AAC87238/c
ID   AAC87238 standard; DNA; 20 BP.
XX
AC   AAC87238;
XX
DT   09-MAR-2001  (first entry)
XX
DE   Phosphorothioate poly T oligonucleotide, SEQ ID NO:17.
XX
KW   Immunostimulatory oligodeoxynucleotide; immunostimulatory ODN;
KW   immunostimulatory DNA-binding protein; nucleolin; hnRNP D; AUF1;
KW   hnRNP A1; lupus La protein; functional modifier identification; agonist;
KW   antagonist; mimic; inhibitor; drug screening;
KW   cellular target identification; oligonucleotide optimisation;
KW   immunotherapy; ss.
XX
OS   Synthetic.
XX
PN   WO200067023-A1.
XX
PD   09-NOV-2000.
XX
PF   28-APR-2000; 2000WO-US011697.
XX
PR   29-APR-1999;   99US-0131830P.
PR   03-MAR-2000; 2000US-0186845P.
XX
PA   (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.
PA   (IOWA ) UNIV IOWA RES FOUND.
XX
PI   Noll BO,  Schetter C,  Krieg AM;
XX
DR   WPI; 2001-016002/02.
XX
PT   Immunostimulatory DNA binding proteins to identify immunostimulatory DNA
PT   functional modifiers, immunostimulatory DNA binding competitors and to
PT   optimize immunostimulatory oligodeoxynucleotides for stimulation.
XX
PS   Example 1; Page 45; 95pp; English.
XX
CC   The invention relates to the use of an immunostimulatory single-stranded
CC   DNA-binding protein in screening assays to identify compounds which bind
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CC   to it and thereby act as functional modifiers of immunostimulatory
CC   oligodeoxynucleotide (ODN) activity. Such modifiers of ODN activity
CC   consist of immunostimulatory DNA binding inhibitors, immunostimulatory
CC   DNA mimics, and immunostimulatory DNA agonists and antagonists.
CC   Immunostimulatory DNA-binding proteins can also be used in screening
CC   methods to identify immunostimulatory DNA binding competitors, and to
CC   optimize an immunostimulatory ODN for immune stimulation. Isolated
CC   complexes of an immunostimulatory DNA-binding protein bound to an
CC   immunostimulatory ODN can additionally be used to screen a panel of
CC   candidate target molecules to identify the cellular target molecules of
CC   the immunostimulatory ODN. The immunostimulatory DNA-binding proteins
CC   used in the methods of the invention are the RNA-binding proteins
CC   nucleolin, hnRNP D, AUF1, hnRNP A1 and lupus La protein. The screening
CC   methods are useful for identifying a compound that inhibits interaction
CC   between immunostimulatory DNA and an immunostimulatory DNA-binding
CC   protein and for identifying agonists useful in immunotherapy. The complex
CC   is useful in screening for immunostimulatory DNA cellular target
CC   molecules. The candidate immunostimulatory ODN competitors allow the
CC   investigation of structure/activity relationships of immunostimulatory
CC   DNA-binding proteins and immunostimulatory ODNs. The present sequence
CC   represents an oligonucleotide used in an exemplification of the invention
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         20 AAAAAAAAAAAAAAAAAAA 2

RESULT 935
AAC87230/c
ID   AAC87230 standard; DNA; 20 BP.
XX
AC   AAC87230;
XX
DT   09-MAR-2001  (first entry)
XX
DE   Digoxigenin-labelled poly T oligonucleotide, SEQ ID NO:9.
XX
KW   Immunostimulatory oligodeoxynucleotide; immunostimulatory ODN;
KW   immunostimulatory DNA-binding protein; nucleolin; hnRNP D; AUF1;
KW   hnRNP A1; lupus La protein; functional modifier identification; agonist;
KW   antagonist; mimic; inhibitor; drug screening;
KW   cellular target identification; oligonucleotide optimisation;
KW   immunotherapy; ss.
XX
OS   Synthetic.
XX
PN   WO200067023-A1.
XX
PD   09-NOV-2000.
XX
PF   28-APR-2000; 2000WO-US011697.
XX
PR   29-APR-1999;   99US-0131830P.
PR   03-MAR-2000; 2000US-0186845P.
XX
PA   (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.
PA   (IOWA ) UNIV IOWA RES FOUND.
XX
PI   Noll BO,  Schetter C,  Krieg AM;
XX
DR   WPI; 2001-016002/02.
XX
PT   Immunostimulatory DNA binding proteins to identify immunostimulatory DNA
PT   functional modifiers, immunostimulatory DNA binding competitors and to
PT   optimize immunostimulatory oligodeoxynucleotides for stimulation.
XX
PS   Example 1; Page 45; 95pp; English.
XX
CC   The invention relates to the use of an immunostimulatory single-stranded
CC   DNA-binding protein in screening assays to identify compounds which bind
CC   to it and thereby act as functional modifiers of immunostimulatory
CC   oligodeoxynucleotide (ODN) activity. Such modifiers of ODN activity
CC   consist of immunostimulatory DNA binding inhibitors, immunostimulatory
CC   DNA mimics, and immunostimulatory DNA agonists and antagonists.
CC   Immunostimulatory DNA-binding proteins can also be used in screening
CC   methods to identify immunostimulatory DNA binding competitors, and to
CC   optimize an immunostimulatory ODN for immune stimulation. Isolated
CC   complexes of an immunostimulatory DNA-binding protein bound to an
CC   immunostimulatory ODN can additionally be used to screen a panel of
CC   candidate target molecules to identify the cellular target molecules of
CC   the immunostimulatory ODN. The immunostimulatory DNA-binding proteins
CC   used in the methods of the invention are the RNA-binding proteins
CC   nucleolin, hnRNP D, AUF1, hnRNP A1 and lupus La protein. The screening
CC   methods are useful for identifying a compound that inhibits interaction
CC   between immunostimulatory DNA and an immunostimulatory DNA-binding
CC   protein and for identifying agonists useful in immunotherapy. The complex
CC   is useful in screening for immunostimulatory DNA cellular target
CC   molecules. The candidate immunostimulatory ODN competitors allow the
CC   investigation of structure/activity relationships of immunostimulatory
CC   DNA-binding proteins and immunostimulatory ODNs. The present sequence
CC   represents an oligonucleotide used in an exemplification of the invention
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         20 AAAAAAAAAAAAAAAAAAA 2

RESULT 936
AAC87241/c
ID   AAC87241 standard; DNA; 20 BP.
XX
AC   AAC87241;
XX
DT   09-MAR-2001  (first entry)
XX
DE   Poly T oligonucleotide, SEQ ID NO:20.
XX
KW   Immunostimulatory oligodeoxynucleotide; immunostimulatory ODN;
KW   immunostimulatory DNA-binding protein; nucleolin; hnRNP D; AUF1;
KW   hnRNP A1; lupus La protein; functional modifier identification; agonist;
KW   antagonist; mimic; inhibitor; drug screening;
KW   cellular target identification; oligonucleotide optimisation;
KW   immunotherapy; ss.
XX
OS   Synthetic.
XX
PN   WO200067023-A1.
XX
PD   09-NOV-2000.
XX
PF   28-APR-2000; 2000WO-US011697.
XX
PR   29-APR-1999;   99US-0131830P.
PR   03-MAR-2000; 2000US-0186845P.
XX
PA   (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.
PA   (IOWA ) UNIV IOWA RES FOUND.
XX
PI   Noll BO,  Schetter C,  Krieg AM;
XX
DR   WPI; 2001-016002/02.
XX
PT   Immunostimulatory DNA binding proteins to identify immunostimulatory DNA
PT   functional modifiers, immunostimulatory DNA binding competitors and to
```

PT optimize immunostimulatory oligodeoxynucleotides for stimulation.
XX
PS Example 1; Page 45; 95pp; English.
XX
CC The invention relates to the use of an immunostimulatory single-stranded
CC DNA-binding protein in screening assays to identify compounds which bind
CC to it and thereby act as functional modifiers of immunostimulatory
CC oligodeoxynucleotide (ODN) activity. Such modifiers of ODN activity
CC consist of immunostimulatory DNA binding inhibitors, immunostimulatory
CC DNA mimics, and immunostimulatory DNA agonists and antagonists.
CC Immunostimulatory DNA-binding proteins can also be used in screening
CC methods to identify immunostimulatory DNA binding competitors, and to
CC optimize an immunostimulatory ODN for immune stimulation. Isolated
CC complexes of an immunostimulatory DNA-binding protein bound to an
CC immunostimulatory ODN can additionally be used to screen a panel of
CC candidate target molecules to identify the cellular target molecules of
CC the immunostimulatory ODN. The immunostimulatory DNA-binding proteins
CC used in the methods of the invention are the RNA-binding proteins
CC nucleolin, hnRNP D, AUF1, hnRNP A1 and lupus La protein. The screening
CC methods are useful for identifying a compound that inhibits interaction
CC between immunostimulatory DNA and an immunostimulatory DNA-binding
CC protein and for identifying agonists useful in immunotherapy. The complex
CC is useful in screening for immunostimulatory DNA cellular target
CC molecules. The candidate immunostimulatory ODN competitors allow the
CC investigation of structure/activity relationships of immunostimulatory
CC DNA-binding proteins and immunostimulatory ODNs. The present sequence
CC represents an oligonucleotide used in an exemplification of the invention
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 20 AAAAAAAAAAAAAAAAAAA 2

RESULT 937
AAS10402/c
ID AAS10402 standard; DNA; 20 BP.
XX
AC AAS10402;
XX
DT 24-OCT-2001 (first entry)
XX
DE DNA template for 3' end labeling of an RNA molecule, #14.
XX
KW 3' RNA end labeling; DNA template; Okazaki fragment; 5' overhang; ss.
XX
OS Synthetic.
XX
PN US6238865-B1.
XX
PD 29-MAY-2001.
XX
PF 16-OCT-1998; 98US-00173936.
XX
PR 17-OCT-1997; 97US-0063757P.
XX
PA (CHEN/) CHEN G.
PA (HUAN/) HUANG Z.
PA (SZOS/) SZOSTAK J W.
XX
PI Huang Z, Szostak JW;
XX
DR WPI; 2001-366470/38.
XX
PT Modifying a 3' terminus of a pre-selected DNA sequence, useful for
PT labeling and modifying 3'-termini of other nucleic acids, comprises using
PT a synthetic nucleotide template with a defined overhang nucleotide.
XX
PS Example 5; Col 13; 22pp; English.
XX
CC The sequence represents a synthetic DNA template molecule used to
CC demonstrate the method of the invention. The invention relates to a
CC method of modifying (e.g. 3' end labelling with 32P dATP) the 3' terminus
CC of an RNA molecule by providing a DNA oligonucleotide, complimentary to
CC the 3' end of the RNA molecule, with an overhang at the 5' end which
CC allows incorporation of the labeling nucleotide into the RNA molecule.
CC The method, based on the synthesis of Okazaki fragments, is useful for
CC labeling and modifying the 3'-termini of other nucleic acids such as DNA
CC fragments. The method is a simple and efficient way of labeling or
CC modifying RNA 3'-termini using DNA polymerase and a synthetic template
CC with defined overhang nucleotides
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 20 AAAAAAAAAAAAAAAAAAA 2

RESULT 938
AAD16997/c
ID AAD16997 standard; DNA; 20 BP.
XX
AC AAD16997;
XX
DT 29-NOV-2001 (first entry)
XX
DE Capture probe CP5'.
XX
KW Scaffold protein; antibody mimic; fibronectin type III domain;
KW randomised loop; randomised beta-sheet; diagnostic purpose;
KW protein designing; probe; tenth module of human Fn3; 10Fn3;
KW fibronectin module of type III; Fn3; ss.
XX
OS Unidentified.
XX
PN WO200164942-A1.
XX
PD 07-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US006414.
XX
PR 29-FEB-2000; 2000US-00515260.
XX
PA (PHYL-) PHYLOS INC.
XX
PI Lipovsek D, Wagner RW, Kuimelis RG;
XX
DR WPI; 2001-557782/62.
XX
PT Fibronectin scaffold protein array for obtaining a protein/compound which
PT binds to a compound/protein, comprises a fibronectin type III domain
PT having a randomized loop, a randomized beta-sheet or their combination.
XX
PS Disclosure; Page 41; 67pp; English.
XX
CC The present invention relates to an array of proteins (antibody mimics)
CC comprising a fibronectin type III domain having a randomised loop, a
CC randomised beta-sheet, or their combination, and has the capacity to bind
CC to a compound that is not bound by a corresponding naturally- occurring
CC fibronectin, immobilised onto a solid support. The antibody mimics is
CC useful for detecting a compound preferably a protein, in a biological
CC sample. It is also useful to detect one or more different analytes
CC simultaneously in a sample. Hence is useful for diagnostic purposes. It
CC is also useful for the purpose of designing proteins capable of binding
CC to virtually any compound of interest. The present sequence is a capture
CC probe used to self-assemble and anchor the tenth module of human

CC fibronectin module of type III (Fn3) (10Fn3) which is used in an
CC exemplification of the invention
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 20 AAAAAAAAAAAAAAAAAAA 2

RESULT 939
AAF60896
ID AAF60896 standard; DNA; 20 BP.
XX
AC AAF60896;
XX
DT 15-MAY-2001 (first entry)
XX
DE Conjugate forming oligonucleotide ON5 SEQ ID 5.
XX
KW Transport; membrane; cytostatic; virucide; vasotropic; dermatological;
KW antipsoriatic; antiasthmatic; gene therapy; tumor cell; antisense;
KW tumor therapy; drug; phosphodiester linkage; ss.
XX
OS Unidentified.
XX
PN DE19935302-A1.
XX
PD 08-FEB-2001.
XX
PF 28-JUL-1999; 99DE-01035302.
XX
PR 28-JUL-1999; 99DE-01035302.
XX
PA (AVET) AVENTIS PHARMA DEUT GMBH.
XX
PI Uhlmann E, Greiner B, Unger E, Gothe G, Schwerdel M;
XX
DR WPI; 2001-203679/21.
XX
PT New substituted aryl conjugates of parent molecules, especially
PT oligonucleotides, having improved transmembrane and intracellular
PT transport properties, useful as medicaments or diagnostic agents.
XX
PS Disclosure; Page 9; 28pp; German.
XX
CC This invention describes a novel conjugate (I) which consists of (A) a
CC molecule to be transported and (B) at least one aryl residue of formula -
CC Ar-(X-C(Y)-R_1)_n (II). Ar = group containing at least one aromatic ring;
CC X = O or N (sic); Y = O, S or NH-R_2 (sic); R_1 = optionally substituted
CC 1-23C alkyl (optionally containing double and/or triple bonds); R_2 =
CC optionally substituted 1-18C alkyl (optionally containing double and/or
CC triple bonds); n = integer of 1 or more. (A) is bonded to (B) directly or
CC via a chemical group, provided that the chemical group is other than CH_2
CC -S if the bond is via a phosphodiester linkage of (A). The invention also
CC describes (i) the preparation of a conjugate (I') of (A') a molecule to
CC be transported and (B') at least one aryl residue (not restricted to
CC (II)), by preparing (A') containing a reactive function at the position
CC at which (B') is to be bonded, preparing (B') and reacting (A') and (B');
CC and (ii) the use of aryl groups (II) (optionally bonded via a chemical
CC group) for transporting (A) across biological membranes. The products of
CC the invention have cytostatic, virucide, vasotropic, dermatological,
CC antipsoriatic and antiasthmatic activity and can be used for gene
CC therapy. Conjugation of (A) with (B) is useful for transporting (A)
CC across biological membranes or into eukaryotic or prokaryotic cells
CC (specifically bacterial, yeast or mammalian cells, including human cells,
CC particularly tumor cells). Medicaments, diagnostic agents and test kits
CC containing (I) are also claimed. Typically (I) are antisense
CC oligonucleotide derivatives for tumor therapy; oligonucleotide drugs for
CC treating viral infections or diseases associated with integrins or cell-
CC cell interactions (e.g. restenosis, vitiligo, psoriasis or asthma); or
CC labeled oligonucleotides for in vivo diagnostic use, e.g. by in situ
CC hybridization. Conjugation with (B) markedly improves the cellular uptake
CC of (A), e.g. in tumor cells. (B) include fluorescein derivative residues,
CC in which case the conjugates (I) are fluorescently labeled, allowing
CC microscopic monitoring of cellular uptake etc. The cellular uptake of (I)
CC is superior to that obtained using other conjugated groups related to
CC (II); e.g. oligonucleotides conjugated with fluorescein diacetate (within
CC the scope of (B)) have superior uptake to corresponding fluorescein
CC conjugates
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAAA 19

RESULT 940
AAS63428
ID AAS63428 standard; DNA; 20 BP.
XX
AC AAS63428;
XX
DT 29-JAN-2002 (first entry)
XX
DE Oligonucleotide-nanoparticle probe #52.
XX
KW Oligonucleotide-nanoparticle probe; diagnostic; forensic analysis;
KW nucleic acid detection; nanostructure; biochip; biofilter; drug delivery;
KW ss.
XX
OS Synthetic.
XX
PN WO200173123-A2.
XX
PD 04-OCT-2001.
XX
PF 28-MAR-2001; 2001WO-US010071.
XX
PR 28-MAR-2000; 2000US-0192699P.
PR 26-APR-2000; 2000US-0200161P.
PR 26-JUN-2000; 2000US-00603830.
PR 26-JUN-2000; 2000US-0213906P.
PR 08-DEC-2000; 2000US-0254392P.
PR 11-DEC-2000; 2000US-0255235P.
PR 12-JAN-2001; 2001US-00760500.
PR 28-MAR-2001; 2001US-00820279.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA, Park S, Li Z;
XX
DR WPI; 2001-656926/75.
XX
PT Detecting and separating nucleic acid, useful e.g. for diagnosis,
PT comprises reaction with nanoparticles that carry oligonucleotides
PT complementary to parts of the target.
XX
PS Example 18; Page 158; 404pp; English.
XX
CC The invention relates to a method for detection of nucleic acid (I)
CC having at least 2 portions, comprising treatment with nanoparticles that
CC carry oligonucleotides complementary to at least 2 parts of (I), where
CC detectable change caused by hybridisation of the oligonucleotide to (I)
CC is observed. The method is used to detect (or to separate) specific (I),
CC e.g. for diagnosing a wide variety of diseases, sequencing, in forensic

CC analysis etc., and generally to detect analytes other than (I). The
CC oligonucleotide-derivatised nanoparticles are also useful for preparing
CC nanostructures useful, for example, as biochips, biofilters, mechanical
CC devices, separation membranes, chemical sensors, in computers, and for
CC drug delivery. Very stable nanoparticle-oligonucleotide conjugates can be
CC produced, allowing their direct use (as probes) in polymerase chain
CC reaction, i.e. they survive multiple heating/cooling cycles so do not
CC need to be added after amplification. (I) are detected by simple colour
CC change, without the need for special equipment, making possible rapid
CC field testing for e.g. pathogens. AAS63374-AAS63448 represent
CC oligonucleotide-nanoparticle probes, and related sequences, used in the
CC method of the invention
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAAA 19

RESULT 941
AAF28481
ID AAF28481 standard; DNA; 20 BP.
XX
AC AAF28481;
XX
DT 03-APR-2001 (first entry)
XX
DE Random oligonucleotide, SEQ ID NO: 53.
XX
KW Nucleic acid detection; nanoparticle-oligonucleotide conjugate;
KW disease diagnosis; forensic analysis; DNA sequencing; paternity testing;
KW cell line authentication; gene therapy; ss.
XX
OS Synthetic.
XX
PN WO200100876-A1.
XX
PD 04-JAN-2001.
XX
PF 26-JUN-2000; 2000WO-US017507.
XX
PR 25-JUN-1999; 99US-00344667.
PR 26-APR-2000; 2000US-0200161P.
XX
PA (MIRK/) MIRKIN C A.
PA (LETS/) LETSINGER R L.
PA (MUCI/) MUCIC R C.
PA (STOR/) STORHOFF J J.
PA (ELGH/) ELGHANIAN R.
PA (TATO/) TATON T A.
XX
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA;
XX
DR WPI; 2001-061976/07.
XX
PT Detecting nucleic acid, useful for e.g. diagnosis of diseases, forensics
PT and DNA sequencing, comprises observing detectable change brought about
PT by hybridization of nucleic acid with substrate or particle bound
PT oligonucleotides.
XX
PS Disclosure; Page 199; 205pp; English.
XX
CC The present sequence is an oligonucleotide used in a method for detecting
CC a nucleic acid having at least 2 portions. The method comprises
CC hybridising the nucleic acid with oligonucleotides, such as the present
CC sequence, attached to a substrate and/or particle and detecting a change
CC in colour, conductivity or optical density. The method is useful for the
CC diagnosis and/or monitoring of diseases, in forensics, in DNA sequencing,
CC for paternity testing, for cell line authentication and for monitoring
CC gene therapy. Detecting nucleic acids based upon observing a colour
CC change is cheap, fast, simple, and does not require specialised or
CC expensive equipment. The nanoparticle oligonucleotide conjugates remain
CC stable for at least 6 months. A single base mismatch and as little as 20
CC femtomoles (fM) of target can be detected using the conjugates
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAAA 19

RESULT 942
AAS10371
ID AAS10371 standard; DNA; 20 BP.
XX
AC AAS10371;
XX
DT 24-OCT-2001 (first entry)
XX
DE Oligonucleotide-cyclic disulphide linker, d.
XX
KW Nanoparticle; cyclic disulphide-oligonucleotide; DNA detection;
KW DNA isolation; genetic disease; bacterial disease; viral disease;
KW forensic science; paternity testing; gene therapy; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1
FT /*tag= a
FT /note= "A is covalently linked to a cyclic-disulphide
FT moiety"
XX
PN WO200151665-A2.
XX
PD 19-JUL-2001.
XX
PF 12-JAN-2001; 2001WO-US001190.
XX
PR 13-JAN-2000; 2000US-0176409P.
PR 26-APR-2000; 2000US-0200161P.
PR 26-JUN-2000; 2000US-00603830.
PR 12-JAN-2001; 2001US-00760500.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA, Li Z;
XX
DR WPI; 2001-451868/48.
XX
PT Detecting a nucleic acid useful in e.g. diagnosing genetic, bacterial or
PT viral diseases, by contacting the nucleic acid with oligonucleotides
PT attached to nanoparticles and having sequences complementary a portion of
PT the nucleic acid.
XX
PS Example 24; Fig 44; 323pp; English.
XX
CC The sequence represents a cyclic disulphide linked oligonucleotide which
CC may be coupled with colloidal gold particles (nanoparticles) and used to
CC demonstrate the method of the invention. The invention relates to
CC isolating or detecting a nucleic acid of interest, in a mixture of
CC nucleic acids, by binding it to 2 or more complimentary nucleotides which
CC have a nanoparticle attached to their 5' ends. The nanoparticles (e.g.
CC colloidal gold) are used to both isolate and detect (e.g. by linking the

CC particle to a fluorescent probe) the resultant complex. The methods are
CC useful for detecting nucleic acids, natural or synthetic, and modified or
CC unmodified. The methods may also be applied in the diagnosis of genetic,
CC bacterial and viral diseases, in forensics, in DNA sequencing, for
CC paternity testing, for cell line authentication, and for monitoring gene
CC therapy. The methods are further useful in research and analytical
CC laboratories in DNA sequencing, in the field to detect the presence of
CC specific pathogens, for quick identification of an infection to assist in
CC drug prescription, and in homes and health centres for inexpensive first-
CC line screening. The methods, which are based on observing colour change
CC with the naked eye, are cheap, fast, simple, robust (reagents are
CC stable), do not require specialised or expensive equipment, and little or
CC no instrumentation is required
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAAA 19

RESULT 943
AAF99427/c
ID AAF99427 standard; DNA; 20 BP.
XX
AC AAF99427;
XX
DT 12-JUN-2001 (first entry)
XX
DE Immunostimulatory nucleic acid #543.
XX
KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200122972-A2.
XX
PD 05-APR-2001.
XX
PF 25-SEP-2000; 2000WO-US026383.
XX
PR 25-SEP-1999; 99US-0156113P.
PR 27-SEP-1999; 99US-0156135P.
PR 23-AUG-2000; 2000US-0227436P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
XX
PI Krieg AM, Schetter C, Vollmer J;
XX
DR WPI; 2001-273485/28.
XX
PT Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids.
XX
PS Claim 101; Page 49; 338pp; English.
XX
CC The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells. Note: the
CC present sequence may have a phosphorothioate backbone
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 20 AAAAAAAAAAAAAAAAAAA 2

RESULT 944
AAF99099/c
ID AAF99099 standard; DNA; 20 BP.
XX
AC AAF99099;
XX
DT 12-JUN-2001 (first entry)
XX
DE Immunostimulatory nucleic acid #215.
XX
KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200122972-A2.
XX
PD 05-APR-2001.
XX
PF 25-SEP-2000; 2000WO-US026383.
XX
PR 25-SEP-1999; 99US-0156113P.
PR 27-SEP-1999; 99US-0156135P.
PR 23-AUG-2000; 2000US-0227436P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
XX
PI Krieg AM, Schetter C, Vollmer J;
XX
DR WPI; 2001-273485/28.
XX
PT Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids.
XX
PS Claim 101; Page 42; 338pp; English.
XX
CC The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells. Note: the
CC present sequence may have a phosphorothioate backbone
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

```
  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         20 AAAAAAAAAAAAAAAAAAA 2
```

RESULT 945
AAF99431
ID AAF99431 standard; DNA; 20 BP.
XX
AC AAF99431;
XX
DT 12-JUN-2001 (first entry)
XX
DE Immunostimulatory nucleic acid #547.
XX
KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200122972-A2.
XX
PD 05-APR-2001.
XX
PF 25-SEP-2000; 2000WO-US026383.
XX
PR 25-SEP-1999; 99US-0156113P.
PR 27-SEP-1999; 99US-0156135P.
PR 23-AUG-2000; 2000US-0227436P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
XX
PI Krieg AM, Schetter C, Vollmer J;
XX
DR WPI; 2001-273485/28.
XX
PT Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids.
XX
PS Claim 101; Page 49; 338pp; English.
XX
CC The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells. Note: the
CC present sequence may have a phosphorothioate backbone
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

```
  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19
```

RESULT 946
AAH46465/c
ID AAH46465 standard; DNA; 20 BP.
XX
AC AAH46465;
XX
DT 14-SEP-2001 (first entry)
XX
DE Oligonucleotide #13.
XX
KW Phosphorothioate; anti-viral therapy; stereochemical pathway; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1. .20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "All bases are phosphorothioate"
FT modified_base 1
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Modified with 2'-O-methyl"
XX
PN US6242591-B1.
XX
PD 05-JUN-2001.
XX
PF 11-JAN-2000; 2000US-00481486.
XX
PR 15-OCT-1997; 97US-00950779.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Cole DL, Ravikumar VT, Cheruvallath ZS;
XX
DR WPI; 2001-407218/43.
XX
PT Preparing sulfurized 2' substituted phosphorothioate oligonucleotides
PT useful in biological research, comprises phosphitylating the 5'-hydroxyl
PT of a nucleic acid having a nucleoside with a 2' modification.
XX
PS Example 23; Col 11; 7pp; English.
XX
CC The present invention relates to a method for preparing phosphorothioate
CC oligonucleotides having at least one nucleoside with a 2' modification.
CC The method comprises phosphitylating the 5'-hydroxyl of a nucleic acid
CC group having at least one nucleoside with a 2' modification in an
CC acetonitrile. The present sequence was used to illustrate the method of
CC the present invention. The method is useful for synthesising sulphurised
CC 2' substituted phosphorothioate oligonucleotides, which may be used in
CC molecular biological research, in applications such as anti-viral
CC therapy, and for determining the stereochemical pathways of certain
CC enzymes which recognise nucleic acids
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

```
  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         20 AAAAAAAAAAAAAAAAAAA 2
```

RESULT 947
AAH78547
ID AAH78547 standard; cDNA; 20 BP.
XX
AC AAH78547;
XX

DT 10-DEC-2001 (first entry)
XX
DE Nucleotide sequence of a cDNA sequence.
XX
KW Nucleic acid identification; DNA library screening; ss.
XX
OS Synthetic.
XX
PN US6274321-B1.
XX
PD 14-AUG-2001.
XX
PF 03-DEC-1999; 99US-00454704.
XX
PR 03-DEC-1999; 99US-00454704.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Blumberg B;
XX
DR WPI; 2001-588900/66.
XX
PT Screening nucleic acids (NA) in pool of interest comprises pooling,
PT expressing NA to form expression product pool and identifying NA in NA
PT pool corresponding to expression product pool having interaction with
PT target moiety.
XX
PS Disclosure; Col 22; 19pp; English.
XX
CC The specification describes a method for identifying a nucleic acid in a
CC pool of interest. The method comprises pooling individually identifiable
CC nucleic acids into at least two pools of one nucleic acid each;
CC expressing nucleic acid pools to obtain protein expression product pools;
CC assaying protein expression product pools for products having interaction
CC with target molecule; selecting nucleic acid pools corresponding to
CC identified protein expression product pools; and identifying individual
CC nucleic acids in identified nucleic acid pools. The method is useful for
CC identifying a nucleic acid (e.g. cDNA) in a pool of interest and for
CC functionally screening several nucleic acids. The method is also useful
CC for screening genomic DNA libraries or other source of individual cDNAs,
CC mRNAs, synthetic libraries of nucleic acids e.g. combinatorial libraries.
CC The present sequence was used in the course of the invention
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAAA 19

RESULT 948
AAF28351
ID AAF28351 standard; DNA; 20 BP.
XX
AC AAF28351;
XX
DT 02-APR-2001 (first entry)
XX
DE DNA oligomer #1.
XX
KW Deoxynucleic S-Methythiourea; DNmt; antisense therapy;
KW cardiovascular disease; inflammatory disease; neurocellular disease;
KW antiviral therapy; human immunodeficiency virus; human-cytomegalovirus;
KW influenza; herpes; infection; ss.
XX
OS Unidentified.
XX
PN US6169176-B1.
XX
PD 02-JAN-2001.
XX
PF 28-SEP-1999; 99US-00407675.
XX
PR 02-JUL-1998; 98US-0091481P.
PR 11-DEC-1998; 98US-0111800P.
PR 02-JUL-1999; 99US-00347443.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Dev AP, Bruice TC;
XX
DR WPI; 2001-122276/13.
XX
PT Preparing novel deoxynucleic alkyl thiourea oligonucleotide for use in
PT antisense therapy, by synthesizing oligonucleotides comprising backbone
PT of alkyl or alkoxy thiourea linkages in solution or on solid phase.
XX
PS Example 7; Fig 16; 48pp; English.
XX
CC The present sequence was used to demonstrate the ability of deoxynucleic
CC S-Methythiourea (DNmt) compounds to form triplexes with DNA oligomers. An
CC increase in the C content of the oligos resulted in a large decrease in
CC binding. This experiment was performed as an example of a method for
CC preparing oligonucleotides comprising a backbone of alkyl or alkoxy
CC thiourea linkages. The method is useful for preparing oligonucleotides
CC for use in antisense or antigene therapy, to inhibit production of
CC proteins associated with genetic diseases, cardiovascular, inflammatory
CC and neurocellular diseases, and for antiviral therapy, e.g. to treat
CC human immunodeficiency virus, human-cytomegalovirus, influenza and herpes
CC infections. The compounds are also useful as diagnostic reagents to
CC detect the presence or absence of the target DNA or RNA sequences to
CC which they specifically bind and by antagonising the normal biological
CC activity of a target protein, they can be used in the manipulation of
CC tissue e.g. tissue differentiation, both in vivo and in ex vivo tissue
CC cultures. The method provides an efficient and rapid solid-phase method
CC for the synthesis of thiourea and S-methylthiourea
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAAA 19

RESULT 949
ABS77742/c
ID ABS77742 standard; DNA; 20 BP.
XX
AC ABS77742;
XX
DT 13-DEC-2002 (first entry)
XX
DE Angiogenesis inhibitory oligonucleotide #226.
XX
KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW plaque neovascularisation; telangiectasia; haemophiliac joint;
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW scleroderma; hypertrophic scar.
XX
OS Synthetic.
XX
PN WO200253141-A2.
XX
PD 11-JUL-2002.

XX
PF 14-DEC-2001; 2001WO-US048458.
XX
PR 14-DEC-2000; 2000US-0255534P.
XX
PA (COLE-) COLEY PHARM GROUP INC.
XX
PI Bratzler RL;
XX
DR WPI; 2002-566690/60.
XX
PT Inhibiting angiogenesis in a subject, involves administering at least one
PT antiangiogenic nucleic acid molecule to the subject.
XX
PS Claim 2; Page 23; 276pp; English.
XX
CC The invention relates to inhibiting angiogenesis in a subject, comprising
CC administering at least one antiangiogenic nucleic acid molecule. Also
CC included is a kit comprising a first container housing the antiangiogenic
CC nucleic acids, and instructions for administering them to a subject
CC having a condition characterised by unwanted angiogenesis. The method is
CC useful for inhibiting angiogenesis associated with solid tumour growth,
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC acid of the invention
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 20 AAAAAAAAAAAAAAAAAAA 2

RESULT 950
ABS78072/c
ID ABS78072 standard; DNA; 20 BP.
XX
AC ABS78072;
XX
DT 13-DEC-2002 (first entry)
XX
DE Angiogenesis inhibitory oligonucleotide #556.
XX
KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW plaque neovascularisation; telangiectasia; haemophiliac joint;
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW scleroderma; hypertrophic scar.
XX
OS Synthetic.
XX
PN WO200253141-A2.
XX
PD 11-JUL-2002.
XX
PF 14-DEC-2001; 2001WO-US048458.
XX
PR 14-DEC-2000; 2000US-0255534P.
XX
PA (COLE-) COLEY PHARM GROUP INC.
XX
PI Bratzler RL;
XX
DR WPI; 2002-566690/60.
XX
PT Inhibiting angiogenesis in a subject, involves administering at least one
PT antiangiogenic nucleic acid molecule to the subject.
XX
PS Claim 2; Page 29; 276pp; English.
XX
CC The invention relates to inhibiting angiogenesis in a subject, comprising
CC administering at least one antiangiogenic nucleic acid molecule. Also
CC included is a kit comprising a first container housing the antiangiogenic
CC nucleic acids, and instructions for administering them to a subject
CC having a condition characterised by unwanted angiogenesis. The method is
CC useful for inhibiting angiogenesis associated with solid tumour growth,
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC acid of the invention
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 20 AAAAAAAAAAAAAAAAAAA 2

RESULT 951
ABS78076
ID ABS78076 standard; DNA; 20 BP.
XX
AC ABS78076;
XX
DT 13-DEC-2002 (first entry)
XX
DE Angiogenesis inhibitory oligonucleotide #560.
XX
KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW plaque neovascularisation; telangiectasia; haemophiliac joint;
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW scleroderma; hypertrophic scar.
XX
OS Synthetic.
XX
PN WO200253141-A2.
XX
PD 11-JUL-2002.
XX
PF 14-DEC-2001; 2001WO-US048458.
XX
PR 14-DEC-2000; 2000US-0255534P.
XX
PA (COLE-) COLEY PHARM GROUP INC.
XX
PI Bratzler RL;
XX
DR WPI; 2002-566690/60.
XX
PT Inhibiting angiogenesis in a subject, involves administering at least one
PT antiangiogenic nucleic acid molecule to the subject.
XX

PS Claim 2; Page 29; 276pp; English.
XX
CC The invention relates to inhibiting angiogenesis in a subject, comprising
CC administering at least one antiangiogenic nucleic acid molecule. Also
CC included is a kit comprising a first container housing the antiangiogenic
CC nucleic acids, and instructions for administering them to a subject
CC having a condition characterised by unwanted angiogenesis. The method is
CC useful for inhibiting angiogenesis associated with solid tumour growth,
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC acid of the invention
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAAA 19

RESULT 952
ABL39402/c
ID ABL39402 standard; DNA; 20 BP.
XX
AC ABL39402;
XX
DT 16-APR-2002 (first entry)
XX
DE Immunostimulatory nucleic acid SEQ ID NO: 838.
XX
KW Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
KW angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1. .20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "phosphorothioate backbone"
XX
PN WO200197843-A2.
XX
PD 27-DEC-2001.
XX
PF 22-JUN-2001; 2001WO-US020154.
XX
PR 22-JUN-2000; 2000US-0213346P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PI Weiner G, Hartmann G;
XX
DR WPI; 2002-154611/20.
XX
PT Treating or preventing cancer, such as basal cell carcinoma, comprises
PT administering immunostimulatory nucleic acids that induce expression of
PT cell surface antigens and antibodies to a subject having or at risk of
PT developing cancer.
XX
PS Disclosure; Page 309; 312pp; English.
XX
CC The present invention relates to methods for treating or preventing
CC cancer, involving administering to a subject having or at risk of
CC developing cancer immunostimulatory nucleic acids that induce expression
CC of cell surface antigens and antibodies. The methods are useful for
CC treating or preventing cancer such as basal cell carcinoma, bladder
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC breast cancer, cervical cancer, colon and rectum cancer, connective
CC tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx
CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC present sequence is an immunostimulatory oligonucleotide described in the
CC exemplification of the invention
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 20 AAAAAAAAAAAAAAAAAAA 2

RESULT 953
ABL38648
ID ABL38648 standard; DNA; 20 BP.
XX
AC ABL38648;
XX
DT 16-APR-2002 (first entry)
XX
DE Immunostimulatory nucleic acid SEQ ID NO: 2.
XX
KW Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
KW angiogenesis; metastasis; cytostatic; ss.
XX
OS Synthetic.
XX
PN WO200197843-A2.
XX
PD 27-DEC-2001.
XX
PF 22-JUN-2001; 2001WO-US020154.
XX
PR 22-JUN-2000; 2000US-0213346P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PI Weiner G, Hartmann G;
XX
DR WPI; 2002-154611/20.
XX
PT Treating or preventing cancer, such as basal cell carcinoma, comprises
PT administering immunostimulatory nucleic acids that induce expression of
PT cell surface antigens and antibodies to a subject having or at risk of
PT developing cancer.
XX
PS Disclosure; Page 95; 312pp; English.
XX
CC The present invention relates to methods for treating or preventing
CC cancer, involving administering to a subject having or at risk of
CC developing cancer immunostimulatory nucleic acids that induce expression
CC of cell surface antigens and antibodies. The methods are useful for
CC treating or preventing cancer such as basal cell carcinoma, bladder
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC breast cancer, cervical cancer, colon and rectum cancer, connective
CC tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx
CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC present sequence is an immunostimulatory oligonucleotide described in the
CC exemplification of the invention

```
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 954
ABL39403/c
ID   ABL39403 standard; DNA; 20 BP.
XX
AC   ABL39403;
XX
DT   16-APR-2002  (first entry)
XX
DE   Immunostimulatory nucleic acid SEQ ID NO: 839.
XX
KW   Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
KW   angiogenesis; metastasis; cytostatic; ss.
XX
OS   Synthetic.
XX
PN   WO200197843-A2.
XX
PD   27-DEC-2001.
XX
PF   22-JUN-2001; 2001WO-US020154.
XX
PR   22-JUN-2000; 2000US-0213346P.
XX
PA   (IOWA ) UNIV IOWA RES FOUND.
XX
PI   Weiner G,  Hartmann G;
XX
DR   WPI; 2002-154611/20.
XX
PT   Treating or preventing cancer, such as basal cell carcinoma, comprises
PT   administering immunostimulatory nucleic acids that induce expression of
PT   cell surface antigens and antibodies to a subject having or at risk of
PT   developing cancer.
XX
PS   Disclosure; Page 309; 312pp; English.
XX
CC   The present invention relates to methods for treating or preventing
CC   cancer, involving administering to a subject having or at risk of
CC   developing cancer immunostimulatory nucleic acids that induce expression
CC   of cell surface antigens and antibodies. The methods are useful for
CC   treating or preventing cancer such as basal cell carcinoma, bladder
CC   cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC   breast cancer, cervical cancer, colon and rectum cancer, connective
CC   tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx
CC   cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
CC   Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC   cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC   cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC   present sequence is an immunostimulatory oligonucleotide described in the
CC   exemplification of the invention
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         20 AAAAAAAAAAAAAAAAAAA 2


RESULT 955
ABL54775/c
ID   ABL54775 standard; DNA; 20 BP.
XX
AC   ABL54775;
XX
DT   10-JUN-2002  (first entry)
XX
DE   CD14 receptor PCR primer SEQ ID NO 9.
XX
KW   Angiotensin-I converting enzyme; ACE; CD14; receptor; SNP;
KW   single-nucleotide polymorphism; PCR; primer; ss.
XX
OS   Synthetic.
XX
PN   JP2002034599-A.
XX
PD   05-FEB-2002.
XX
PF   26-JUL-2000; 2000JP-00225354.
XX
PR   26-JUL-2000; 2000JP-00225354.
XX
PA   (TOYM ) TOYOBO KK.
XX
DR   WPI; 2002-275727/32.
XX
PT   Detecting 1 base polymorphism on a sequence of a chromosome or it's
PT   fragment.
XX
PS   Example 2; Page 10; 10pp; Japanese.
XX
CC   The invention relates to a method for detecting 1 base polymorphism on
CC   the sequence of a chromosome or its fragment in which a sample nucleic
CC   acid is reacted with a reaction liquor containing a nucleic acid primer
CC   having a base adjacent to the polymorphic base at its 3'-end, one
CC   dideoxynucleotide corresponding to a polymorphic base having a
CC   distinguishable feature or its mixture, DNA polymerase and a composition
CC   required for its activity expression to detect the presence of taking
CC   dideoxynucleotide in the nucleic acid primer and to detect the type of
CC   the base to be specified. The method is used for detecting 1 base
CC   polymorphism on the sequence of a chromosome or its fragment. The present
CC   sequence is that of a PCR primer, useful in examples of the invention
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         20 AAAAAAAAAAAAAAAAAAA 2


RESULT 956
ABK65035
ID   ABK65035 standard; DNA; 20 BP.
XX
AC   ABK65035;
XX
DT   02-JUL-2002  (first entry)
XX
DE   Nanoparticle-oligonucleotide #55.
XX
KW   Nanoparticle-oligonucleotide; nanofabrication; nucleic acid detection;
KW   ss.
XX
OS   Synthetic.
XX
PN   WO200218643-A2.
XX
```

```
PD   07-MAR-2002.
XX
PF   10-AUG-2001; 2001WO-US025237.
XX
PR   11-AUG-2000; 2000US-0224631P.
PR   08-DEC-2000; 2000US-0254392P.
PR   11-DEC-2000; 2000US-0255235P.
PR   12-JAN-2001; 2001US-00760500.
PR   28-MAR-2001; 2001US-00820279.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA,  Garimella V,  Li Z,  Park S;
XX
DR   WPI; 2002-258024/30.
XX
PT   Detecting nucleic acid, useful for diagnosis of genetic, viral or
PT   bacterial disease, comprises hybridizing nanoparticles with attached
PT   oligonucleotides to nucleic acid and detecting change brought about by
PT   hybridization.
XX
PS   Example 18; Page 410; 412pp; English.
XX
CC   The invention relates to a method of detecting a nucleic acid (NA) having
CC   at least 2 portions comprising: (a) providing nanoparticles (NP) with
CC   attached oligonucleotides (OGN), where OGN has a sequence complementary
CC   to the sequence of NA; (b) contacting NA and NP under conditions
CC   effective to allow hybridisation of OGN with NA; and (c) observing a
CC   detectable change brought about by hybridisation of OGN with NA. The
CC   method is useful for detecting a nucleic acid, separating a selected
CC   nucleic acid from others and methods of nanofabrication. Detecting
CC   analytes such as nucleic acids and proteins are useful for the diagnosis
CC   of genetic, bacterial and viral diseases. The OGN-NP conjugates that use
CC   cyclic disulphide linkers improve the sensitivity of diagnostic assays.
CC   In particular assays using OGN-NP conjugates prepared using linkers
CC   comprising a steroid residue attached to a cyclic disulphide have been
CC   found to be approximately 10 times more sensitive than assays employing
CC   conjugates prepared using alkanethiols or acyclic disulphides as the
CC   linker. The OGN-NP conjugates are stable allowing them to be used
CC   directly in PCR solutions. Therefore conjugates added as probes to a DNA
CC   target to be PCR amplified can be carried through the 30 or 40 heating
CC   cooling cycles of the PCR and are still able to detect the amplicons
CC   without opening the tubes and causing contamination. ABK64981-ABK65055
CC   represent nanoparticle-oligonucleotides of the invention
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 957
ABK65050
ID   ABK65050 standard; DNA; 20 BP.
XX
AC   ABK65050;
XX
DT   02-JUL-2002  (first entry)
XX
DE   Nanoparticle-oligonucleotide #70.
XX
KW   Nanoparticle-oligonucleotide; nanofabrication; nucleic acid detection;
KW   ss.
XX
OS   Synthetic.
XX
PN   WO200218643-A2.
XX
PD   07-MAR-2002.
XX
PF   10-AUG-2001; 2001WO-US025237.
XX
PR   11-AUG-2000; 2000US-0224631P.
PR   08-DEC-2000; 2000US-0254392P.
PR   11-DEC-2000; 2000US-0255235P.
PR   12-JAN-2001; 2001US-00760500.
PR   28-MAR-2001; 2001US-00820279.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA,  Garimella V,  Li Z,  Park S;
XX
DR   WPI; 2002-258024/30.
XX
PT   Detecting nucleic acid, useful for diagnosis of genetic, viral or
PT   bacterial disease, comprises hybridizing nanoparticles with attached
PT   oligonucleotides to nucleic acid and detecting change brought about by
PT   hybridization.
XX
PS   Example 24; Fig 44; 412pp; English.
XX
CC   The invention relates to a method of detecting a nucleic acid (NA) having
CC   at least 2 portions comprising: (a) providing nanoparticles (NP) with
CC   attached oligonucleotides (OGN), where OGN has a sequence complementary
CC   to the sequence of NA; (b) contacting NA and NP under conditions
CC   effective to allow hybridisation of OGN with NA; and (c) observing a
CC   detectable change brought about by hybridisation of OGN with NA. The
CC   method is useful for detecting a nucleic acid, separating a selected
CC   nucleic acid from others and methods of nanofabrication. Detecting
CC   analytes such as nucleic acids and proteins are useful for the diagnosis
CC   of genetic, bacterial and viral diseases. The OGN-NP conjugates that use
CC   cyclic disulphide linkers improve the sensitivity of diagnostic assays.
CC   In particular assays using OGN-NP conjugates prepared using linkers
CC   comprising a steroid residue attached to a cyclic disulphide have been
CC   found to be approximately 10 times more sensitive than assays employing
CC   conjugates prepared using alkanethiols or acyclic disulphides as the
CC   linker. The OGN-NP conjugates are stable allowing them to be used
CC   directly in PCR solutions. Therefore conjugates added as probes to a DNA
CC   target to be PCR amplified can be carried through the 30 or 40 heating
CC   cooling cycles of the PCR and are still able to detect the amplicons
CC   without opening the tubes and causing contamination. ABK64981-ABK65055
CC   represent nanoparticle-oligonucleotides of the invention
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 958
AAL45122/c
ID   AAL45122 standard; DNA; 20 BP.
XX
AC   AAL45122;
XX
DT   24-MAY-2002  (first entry)
XX
DE   Oligonucleotide synthesis method related DNA #1.
XX
KW   Oligonucleotide synthesis; polynucleotide array; protecting group;
KW   oxidation; ss.
XX
OS   Synthetic.
XX
```

PN EP1176151-A1.
XX
PD 30-JAN-2002.
XX
PF 27-JUL-2001; 2001EP-00118360.
XX
PR 28-JUL-2000; 2000US-00627249.
XX
PA (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI Dellinger DJ, Perbost MGM, Betley JR, Caruthers M;
XX
DR WPI; 2002-156732/21.
XX
PT Synthesis of polynucleotide useful during fabrication of an array
PT involves coupling nucleoside phosphoramidite and a solid-supported
PT nucleoside and treating the product with an oxidation/deprotection
PT composition.
XX
PS Example 1; Page 15; 36pp; English.
XX
CC The present invention relates to a method for the synthesis of a
CC polynucleotide which involves coupling a second nucleoside to a first
CC nucleoside through a phosphite linkage, where the second nucleoside has a
CC non-carbonate protecting group protecting a hydroxyl, and exposing the
CC product to a composition which concurrently oxidizes the phosphite formed
CC to a phosphate and deprotects the protected hydroxyl of the second
CC nucleoside. The method is useful for synthesizing the polynucleotides,
CC for carrying out either 3' to 5' or 5' to 3' synthesis and for
CC fabricating an addressable array of polynucleotides on a substrate. The
CC present sequence is an oligonucleotide produced to demonstrate the method
CC of the invention
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 20 AAAAAAAAAAAAAAAAAAA 2

RESULT 959
ABL36232
ID ABL36232 standard; DNA; 20 BP.
XX
AC ABL36232;
XX
DT 08-APR-2002 (first entry)
XX
DE M tuberculosis rRNA probe SEQ ID NO: 83.
XX
KW Skin disorder; psoriasis; atopic dermatitis; allergic contact dermatitis;
KW alopecia areata; skin cancer; Mycobacterium vaccae; melanoma; cytostatic;
KW antipsoriatic; dermatological; antiinflammatory; antiallergic;
KW Th2 immune response; immunomodulatory; probe; ss.
XX
OS Mycobacterium tuberculosis.
XX
PN US6328978-B1.
XX
PD 11-DEC-2001.
XX
PF 02-JUN-1999; 99US-00324542.
XX
PR 23-DEC-1997; 97US-00997080.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
XX
PI Watson JD, Tan PLJ, Prestidge R;
XX
DR WPI; 2002-138361/18.
XX
PT Inhibiting skin inflammation associated with skin disorder e.g.
PT psoriasis, by administering composition comprising delipidated and
PT deglycolipidated Mycobacterium vaccae cells or Mycobacterium vaccae
PT culture filtrate.
XX
PS Example 5; Col 99-100; 116pp; English.
XX
CC The present invention relates to a method of inhibiting skin inflammation
CC associated with a skin disorder selected from psoriasis, atopic
CC dermatitis and allergic contact dermatitis, which involves administering
CC a composition containing delipidated and deglycolipidated Mycobacterium
CC vaccae cells or M. vaccae culture filtrate. The skin disorder to be
CC treated may also include alopecia areata, and skin cancers such as basal
CC cell carcinoma, squamous cell carcinoma and melanoma. The composition
CC acts by inhibiting the Th2 immune response. The present sequence is a
CC probe described in the exemplification of the invention
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAAA 19

RESULT 960
ABS64673
ID ABS64673 standard; DNA; 20 BP.
XX
AC ABS64673;
XX
DT 15-NOV-2002 (first entry)
XX
DE Nucleic acid detection method associated polynucleotide #55.
XX
KW Nucleic acid detection method; nanoparticle-oligonucleotide conjugate;
KW nanoparticle; viral RNA detection; bacterial DNA detection;
KW fungal DNA detection; nanoprobe conjugate; ss.
XX
OS Synthetic.
XX
PN WO200246472-A2.
XX
PD 13-JUN-2002.
XX
PF 07-DEC-2001; 2001WO-US046418.
XX
PR 08-DEC-2000; 2000US-0254392P.
PR 08-DEC-2000; 2000US-0254418P.
PR 11-DEC-2000; 2000US-0255235P.
PR 11-DEC-2000; 2000US-0255236P.
PR 12-JAN-2001; 2001US-00760500.
PR 28-MAR-2001; 2001US-00820279.
PR 09-APR-2001; 2001US-0282640P.
PR 10-AUG-2001; 2001US-00927777.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA, Garimella V, Li Z, Park S;
XX
DR WPI; 2002-608256/65.
XX
PT Detecting nucleic acid having two portions, by providing nanoparticles
PT having oligonucleotides attached to it, contacting nucleic acid and
PT nanoparticles to allow hybridization, and observing detectable change.
XX
PS Example 18; Page 437; 442pp; English.

XX
CC The invention describes a method of detecting (M1) a nucleic acid having
CC two portions, involving providing nanoparticles having oligonucleotides
CC attached to it, which has a sequence complementary to sequence of two
CC portions of nucleic acid, contacting nucleic acid and nanoparticles, to
CC allow hybridisation of oligonucleotides with two or more portions of
CC nucleic acid, and observing a detectable change brought about by
CC hybridisation. (M1), nanoparticles (I), nanoparticle-oligonucleotide
CC conjugates (II) and the aggregate probe are useful for detecting two or
CC more nucleic acids (from a biological source) having at least two
CC portions, such as viral RNA, bacterial or fungal DNA, a gene associated
CC with a disease, synthetic, or structurally-modified natural or synthetic
CC RNA or DNA, or a product of a polymerase chain reaction amplification.
CC (II) is useful for preparing a nanoprobe conjugate for detecting an
CC analyte, and for detecting a nucleic acid bound to an electrode surface.
CC (I) and (II) are useful for fabrication, and for separating a selected
CC nucleic acid having two portions from other nucleic acids. (I), (II) and
CC the aggregate probe are useful for detecting an analyte (especially
CC polyvalent analyte) in a sample. This sequence represents a
CC polynucleotide used to demonstrate the method of the invention
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAAA 19

RESULT 961
ABS64688
ID ABS64688 standard; DNA; 20 BP.
XX
AC ABS64688;
XX
DT 15-NOV-2002 (first entry)
XX
DE Nucleic acid detection method associated polynucleotide #70.
XX
KW Nucleic acid detection method; nanoparticle-oligonucleotide conjugate;
KW nanoparticle; viral RNA detection; bacterial DNA detection;
KW fungal DNA detection; nanoprobe conjugate; ss.
XX
OS Synthetic.
XX
PN WO200246472-A2.
XX
PD 13-JUN-2002.
XX
PF 07-DEC-2001; 2001WO-US046418.
XX
PR 08-DEC-2000; 2000US-0254392P.
PR 08-DEC-2000; 2000US-0254418P.
PR 11-DEC-2000; 2000US-0255235P.
PR 11-DEC-2000; 2000US-0255236P.
PR 12-JAN-2001; 2001US-00760500.
PR 28-MAR-2001; 2001US-00820279.
PR 09-APR-2001; 2001US-0282640P.
PR 10-AUG-2001; 2001US-00927777.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA, Garimella V, Li Z, Park S;
XX
DR WPI; 2002-608256/65.
XX
PT Detecting nucleic acid having two portions, by providing nanoparticles
PT having oligonucleotides attached to it, contacting nucleic acid and
PT nanoparticles to allow hybridization, and observing detectable change.
XX
PS Example 24; Fig 44; 442pp; English.
XX
CC The invention describes a method of detecting (M1) a nucleic acid having
CC two portions, involving providing nanoparticles having oligonucleotides
CC attached to it, which has a sequence complementary to sequence of two
CC portions of nucleic acid, contacting nucleic acid and nanoparticles, to
CC allow hybridisation of oligonucleotides with two or more portions of
CC nucleic acid, and observing a detectable change brought about by
CC hybridisation. (M1), nanoparticles (I), nanoparticle-oligonucleotide
CC conjugates (II) and the aggregate probe are useful for detecting two or
CC more nucleic acids (from a biological source) having at least two
CC portions, such as viral RNA, bacterial or fungal DNA, a gene associated
CC with a disease, synthetic, or structurally-modified natural or synthetic
CC RNA or DNA, or a product of a polymerase chain reaction amplification.
CC (II) is useful for preparing a nanoprobe conjugate for detecting an
CC analyte, and for detecting a nucleic acid bound to an electrode surface.
CC (I) and (II) are useful for fabrication, and for separating a selected
CC nucleic acid having two portions from other nucleic acids. (I), (II) and
CC the aggregate probe are useful for detecting an analyte (especially
CC polyvalent analyte) in a sample. This sequence represents a
CC polynucleotide used to demonstrate the method of the invention
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAAA 19

RESULT 962
ABN87103/c
ID ABN87103 standard; DNA; 20 BP.
XX
AC ABN87103;
XX
DT 30-JUL-2002 (first entry)
XX
DE Capture probe CP5' SEQ ID NO:23.
XX
KW Protein scaffold; antibody; binding protein; immunoglobulin;
KW tumour necrosis factor alpha; TNF-alpha; protein framework; probe; ss.
XX
OS Synthetic.
XX
PN WO200232925-A2.
XX
PD 25-APR-2002.
XX
PF 16-OCT-2001; 2001WO-US032233.
XX
PR 16-OCT-2000; 2000US-00688566.
XX
PA (PHYL-) PHYLOS INC.
XX
PI Lipovsek D, Wagner RW, Kuimelis RG;
XX
DR WPI; 2002-444238/47.
XX
PT New non-antibody proteins having an immunoglobulin fold, useful in
PT research, therapeutic or diagnostic fields, particularly as scaffolds for
PT designing proteins with specific properties, e.g. for binding any antigen
PT of interest.
XX
PS Disclosure; Page 58; 94pp; English.
XX
CC The present invention describes a non-antibody protein, comprising a
CC domain having an immunoglobulin-like fold, derived from a reference
CC protein having a mutated amino acid sequence, where the non-antibody

CC protein binds with a Kd at least as tight as 10 nM to a compound that is
CC not bound as tightly by the reference protein. The non-antibody protein
CC is useful as scaffolds for selecting or designing a protein framework
CC with specific and favourable properties, e.g. for binding any antigen of
CC interest, or for destroying or inactivating antibody molecules. The non-
CC antibody protein is also useful in all areas where antibodies are used,
CC e.g. research, therapeutic or diagnostic fields, and for screening novel
CC binding proteins useful in the above-mentioned fields. The present
CC proteins have thermodynamic properties superior to those of natural
CC antibodies, and can be evolved rapidly in vitro. The present proteins or
CC antibody mimics exhibit improved biophysical properties, such as
CC stability under reducing conditions and solubility at high
CC concentrations. In addition, these molecules are readily expressed and
CC folded in prokaryotic systems (e.g. Escherichia coli), in eukaryotic
CC systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit
CC reticulocyte lysate system). Furthermore, these proteins are extremely
CC amenable to affinity maturation techniques involving multiple cycles of
CC selection, e.g. in vitro selection using RNA-protein fusion technology,
CC phage display or yeast display systems. The present sequence is used in
CC the exemplification of the present invention
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 20 AAAAAAAAAAAAAAAAAAA 2

RESULT 963
ABZ88267
ID ABZ88267 standard; DNA; 20 BP.
XX
AC ABZ88267;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 3509; 872pp; English.
XX

CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAAA 19

RESULT 964
ABZ88565
ID ABZ88565 standard; DNA; 20 BP.
XX
AC ABZ88565;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 3807; 872pp; English.
XX

CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAAA 19

RESULT 965
ABZ88619
ID ABZ88619 standard; DNA; 20 BP.
XX
AC ABZ88619;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 3861; 872pp; English.
XX

CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAAA 19

RESULT 966
ABZ89705
ID ABZ89705 standard; DNA; 20 BP.
XX
AC ABZ89705;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4947; 872pp; English.
XX

CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAAA 19

RESULT 967
ABZ88816
ID ABZ88816 standard; DNA; 20 BP.
XX
AC ABZ88816;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4058; 872pp; English.
XX

CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAAA 19

RESULT 968
ABZ88881
ID ABZ88881 standard; DNA; 20 BP.
XX
AC ABZ88881;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4123; 872pp; English.
XX

CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAAA 19

RESULT 969
ABZ89706
ID ABZ89706 standard; DNA; 20 BP.
XX
AC ABZ89706;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4948; 872pp; English.
XX

CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAAA 19

RESULT 970
ABZ88620
ID ABZ88620 standard; DNA; 20 BP.
XX
AC ABZ88620;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 3862; 872pp; English.
XX

```
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 971
ABZ88880
ID   ABZ88880 standard; DNA; 20 BP.
XX
AC   ABZ88880;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 4122; 872pp; English.
XX
```

```
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 19 A; 0 C; 0 G; 1 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          2 AAAAAAAAAAAAAAAAAAA 20


RESULT 972
ABZ89179
ID   ABZ89179 standard; DNA; 20 BP.
XX
AC   ABZ89179;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 4421; 872pp; English.
XX
```

```
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 19 A; 0 C; 0 G; 1 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          2 AAAAAAAAAAAAAAAAAAA 20


RESULT 973
ABZ88814
ID   ABZ88814 standard; DNA; 20 BP.
XX
AC   ABZ88814;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 4056; 872pp; English.
XX
```

```
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 974
ABZ89241
ID   ABZ89241 standard; DNA; 20 BP.
XX
AC   ABZ89241;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 4483; 872pp; English.
XX
```

```
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 975
ABZ90650
ID   ABZ90650 standard; DNA; 20 BP.
XX
AC   ABZ90650;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 5892; 872pp; English.
XX
```

```
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 976
ABZ99050
ID   ABZ99050 standard; DNA; 20 BP.
XX
AC   ABZ99050;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human PDE4C oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 14292; 872pp; English.
XX
```

```
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 0 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 977
ABZ88815
ID   ABZ88815 standard; DNA; 20 BP.
XX
AC   ABZ88815;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 4057; 872pp; English.
XX
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```
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 978
ABZ85311/c
ID   ABZ85311 standard; DNA; 20 BP.
XX
AC   ABZ85311;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
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PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
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DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Claim 15; SEQ ID NO 553; 872pp; English.
XX
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```
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
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CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
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Db         20 AAAAAAAAAAAAAAAAAAA 2


RESULT 979
ABZ85435/c
ID   ABZ85435 standard; DNA; 20 BP.
XX
AC   ABZ85435;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
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PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Claim 15; SEQ ID NO 677; 872pp; English.
XX
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```
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         20 AAAAAAAAAAAAAAAAAAA 2


RESULT 980
ABZ88817
ID   ABZ88817 standard; DNA; 20 BP.
XX
AC   ABZ88817;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
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PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 4059; 872pp; English.
XX
```

CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAAA 19

RESULT 981
ABZ88939
ID ABZ88939 standard; DNA; 20 BP.
XX
AC ABZ88939;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4181; 872pp; English.
XX

CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAAA 19

RESULT 982
ABZ89302
ID ABZ89302 standard; DNA; 20 BP.
XX
AC ABZ89302;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4544; 872pp; English.
XX

CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAAA 19

RESULT 983
ABZ87681
ID ABZ87681 standard; DNA; 20 BP.
XX
AC ABZ87681;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
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PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 2923; 872pp; English.
XX

CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 0 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTT 2184
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Db 1 TTTTTTTTTTTTTTTTTTT 19

RESULT 984
ABZ88566
ID ABZ88566 standard; DNA; 20 BP.
XX
AC ABZ88566;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
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PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
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DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
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PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 3808; 872pp; English.
XX

```
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CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
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CC   use in antisense gene therapy. The composition is useful for treating or
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CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 985
ABZ89086
ID   ABZ89086 standard; DNA; 20 BP.
XX
AC   ABZ89086;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
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DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 4328; 872pp; English.
XX
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```
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
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CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 986
ABZ85533
ID   ABZ85533 standard; DNA; 20 BP.
XX
AC   ABZ85533;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Claim 15; SEQ ID NO 775; 872pp; English.
XX
```

```
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 987
ABZ89015
ID   ABZ89015 standard; DNA; 20 BP.
XX
AC   ABZ89015;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 4257; 872pp; English.
XX
```

```
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 988
ABZ89441
ID   ABZ89441 standard; DNA; 20 BP.
XX
AC   ABZ89441;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 4683; 872pp; English.
XX
```

CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAAA 19

RESULT 989
ABZ89016
ID ABZ89016 standard; DNA; 20 BP.
XX
AC ABZ89016;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4258; 872pp; English.
XX

CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAAA 19

RESULT 990
ABZ89120
ID ABZ89120 standard; DNA; 20 BP.
XX
AC ABZ89120;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4362; 872pp; English.
XX

```
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
                ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 991
ABZ89704
ID   ABZ89704 standard; DNA; 20 BP.
XX
AC   ABZ89704;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 4946; 872pp; English.
XX
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```
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
                ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 992
ACD27320
ID   ACD27320 standard; DNA; 20 BP.
XX
AC   ACD27320;
XX
DT   15-OCT-2003  (first entry)
XX
DE   Nanotechnology nucleic acid detection method associated #54.
XX
KW   Nanotechnology; ss; nucleic acid detection; nanoparticle;
KW   virus detection; human immunodeficiency virus; HIV; hepatitis; herpes;
KW   cytomegalovirus; Epstein-Barr virus; bacterial disease; DNA sequencing;
KW   sexually transmitted disease; inherited disorder; forensic;
KW   paternity testing; cell line authentication.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER= Thiol modified" "
XX
PN   US2002155461-A1.
XX
PD   24-OCT-2002.
XX
PF   12-OCT-2001; 2001US-00976378.
XX
PR   29-JUL-1996;   96US-0031809P.
PR   21-JUL-1997;   97WO-US012783.
PR   29-JAN-1999;   99US-00240755.
PR   25-JUN-1999;   99US-00344667.
PR   26-APR-2000; 2000US-0200161P.
PR   26-JUN-2000; 2000US-00603830.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA;
```

XX
DR WPI; 2003-228115/22.
XX
PT Detecting nucleic acids having 2 portions e.g. for detecting disease,
PT comprises use of nanoparticles which have oligonucleotides attached to
PT them that are complementary to portions of the nucleic acid sequence.
XX
PS Example 18; Page 44; 130pp; English.
XX
CC This invention relates to a novel method for detecting a nucleic acid
CC having 2 portions. The method comprises providing nanoparticles having
CC oligonucleotides attached, where the oligonucleotide on each nanoparticle
CC has a sequence complementary to a sequence of 2 portions of nucleic acid.
CC The nucleic acid and nanoparticle are contacted to allow hybridisation of
CC the oligonucleotide on the nanoparticle with two or more portions of
CC nucleic acid and observing a detectable change brought about by the
CC hybridisation. The method of the invention is useful for separating a
CC selected nucleic acid having 2 portions, from other nucleic acids, and
CC for detecting nucleic acids having 2 portions. The method of the
CC invention is useful for detecting any type of nucleic acids which may be
CC used for diagnosis of disease and in sequencing of nucleic acids.
CC Preferably, the method is useful for detecting nucleic acids for
CC diagnosis and/or monitoring of viral diseases (human immunodeficiency
CC virus, hepatitis virus, herpes virus, cytomegalovirus and Epstein-Barr
CC virus), bacterial diseases, sexually transmitted diseases, inherited
CC disorders, in forensics, in DNA sequencing, for paternity testing, for
CC cell line authentication, for monitoring gene therapy, etc. This method
CC involves detecting nucleic acids based on observing a colour change with
CC the naked eye so is cheap, fast, simple and robust, and does not require
CC specialised expensive equipment. The present sequence represents a thiol
CC modified oligonucleotide sequence used to demonstrate the method of the
CC invention
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAAA 19

RESULT 993
ACC58867/c
ID ACC58867 standard; DNA; 20 BP.
XX
AC ACC58867;
XX
DT 08-SEP-2003 (first entry)
XX
DE Doubly labelled DNA probe.
XX
KW Probe; nucleic acid detection; ss.
XX
OS Synthetic.
XX
PN WO2003043402-A2.
XX
PD 30-MAY-2003.
XX
PF 21-OCT-2002; 2002WO-US033699.
XX
PR 19-OCT-2001; 2001US-0336432P.
XX
PA (PROL-) PROLIGO LLC.
XX
PI Bruce I, Davies M, Wolter A;
XX
DR WPI; 2003-505122/47.
XX
PT Detection or quantification of nucleic acid analyte, by hybridizing a
PT nucleic acid probe having non-identical covalently attached dyes, with
PT nucleic acid analyte, and measuring change in fluorescence of the probes.
XX
PS Example 9; Page 32; 110pp; English.
XX
CC The present sequence is an example of nucleic acid probes of the
CC invention. The probe may be doubly labelled with non-identical covalently
CC attached dyes, e.g. the fluorescent intercalator ethidium, which serves
CC as the detector dye and the fluorescent dye fluorescein, which serves as
CC the donor dye of a fluorescent resonance energy transfer (FRET) system. A
CC bifunctional linker was used to attach the dyes to the oligonucleotide.
CC The probe generates a fluorescent signal upon hybridisation to a
CC complementary nucleic acid based on the interaction of the intercalator
CC with the formed double-stranded DNA. Nucleic acid probes of the invention
CC can be used in homogeneous assays, real-time PCR monitoring,
CC transcription assays, expression analysis on nucleic acid microarrays and
CC other microarray applications such as genotyping
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 20 AAAAAAAAAAAAAAAAAAA 2

RESULT 994
ABZ22916/c
ID ABZ22916 standard; DNA; 20 BP.
XX
AC ABZ22916;
XX
DT 08-APR-2003 (first entry)
XX
DE Phosphorothioate 20-mer oligonucleotide #1.
XX
KW Chiral; phosphorothioate; oligonucleotide synthesis; enantiomer; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1. .20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages"
XX
PN WO2002102815-A2.
XX
PD 27-DEC-2002.
XX
PF 13-JUN-2002; 2002WO-US018581.
XX
PR 14-JUN-2001; 2001US-00881535.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Ravikumar VT;
XX
DR WPI; 2003-157021/15.
XX
PT Preparing internucleotide phosphorothioate linkage enhanced in Sp/Rp
PT enantiomer, by coupling a synthon with 2'-substituted nucleoside in
PT presence of coupling agent having a pKa that enhances linkage in Sp/Rp
PT enantiomer.
XX
PS Example 1; Page 31; 65pp; English.
XX
CC The present invention describes a method (M1) for preparing an
CC internucleotide phosphorothioate linkage enriched in the Sp or Rp
CC enantiomer between a synthon having a hydroxyl moiety at the 5' position

CC and a 2'-substituted nucleoside having an activated phosphate moiety at
CC the 3'-position, comprising coupling a synthon with a 2'-substituted
CC nucleoside in the presence of coupling agent that is selected to enhance
CC either the Rp or Sp enantiomer according to its pKa. This method is
CC useful for preparing an oligonucleotide having at least one region of
CC internucleotide linkages that is enhanced in the Sp or Rp enantiomer,
CC which involves providing a nucleotide having a hydroxyl moiety at the 5'-
CC position or a growing oligonucleotide chain having a hydroxyl moiety at
CC the 5'-position, coupling the nucleotide or growing oligonucleotide chain
CC to a 2'-substituted nucleoside having an activated phosphate moiety at
CC the 3' position in the presence of the coupling agent, and repeating the
CC coupling step until the desired number of linkages is established. The
CC oligonucleotide having a region of internucleotide linkages that is
CC enhanced in the Sp enantiomer is further processed to include another
CC region of internucleotide linkages that is enhanced in the Sp and/or Rp
CC enantiomer. Oligonucleotides prepared by the method lead to improved
CC drugs, diagnostics and research reagents. The present sequence represents
CC an oligonucleotide used in the exemplification of the present invention
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 20 AAAAAAAAAAAAAAAAAAA 2

RESULT 995
AAL61645
ID AAL61645 standard; DNA; 20 BP.
XX
AC AAL61645;
XX
DT 22-SEP-2003 (first entry)
XX
DE Thiol-modified oligo #4 used in the nucleic acid detection method.
XX
KW Nucleic acid detection; fabrication; ss.
XX
OS Unidentified.
XX
PN WO2003035829-A2.
XX
PD 01-MAY-2003.
XX
PF 08-OCT-2002; 2002WO-US032088.
XX
PR 09-OCT-2001; 2001US-0327864P.
PR 07-DEC-2001; 2001US-00008978.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Park S, Taton TA, Mirkin CA;
XX
DR WPI; 2003-430409/40.
XX
PT Detecting nucleic acid having two portions, by providing nanoparticles
PT having oligonucleotides attached to it, contacting nucleic acid and
PT nanoparticles to allow hybridization, and observing detectable change.
XX
PS Example 18; Page 179; 467pp; English.
XX
CC The invention relates to a method of detecting a nucleic acid having two
CC portions. The method involves providing nanoparticles having
CC oligonucleotides attached to it which has a sequence complementary to
CC sequence of two portions of nucleic acid, contacting nucleic acid and
CC nanoparticles to allow hybridisation of oligonucleotides with two or more
CC portions of nucleic acid and observing a detectable change brought about
CC by hybridisation. The method and aggregate probes are useful for
CC detecting two or more nucleic acids (from a biological source) having at
CC least two portions such as viral RNA, bacterial or fungal DNA, a gene
CC associated with a disease, synthetic or structurally modified natural or
CC synthetic RNA or DNA, or a product of a polymerase chain reaction
CC amplification. The invention is useful for preparing a nanoprobe
CC conjugate for detecting an analyte and for detecting a nucleic acid bound
CC to an electrode surface. It is also useful for fabrication and for
CC separating a selected nucleic acid having two portions from other nucleic
CC acids. The present sequence is an oligo used to illustrate the method of
CC the invention
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAAA 19

RESULT 996
ABZ59815/c
ID ABZ59815 standard; RNA; 20 BP.
XX
AC ABZ59815;
XX
DT 01-APR-2003 (first entry)
XX
DE Potato gene PCR primer dT20.
XX
KW Potato; plant; mitochondrial carrier protein; elongation factor EF-2;
KW transferrin binding protein; receptor-like protein kinase; helicase;
KW non-long terminal repeat retroelement reverse transcriptase;
KW overwatering; transgenic; reverse transcriptase; PCR; primer; ss.
XX
OS Synthetic.
XX
PN DE10114063-A1.
XX
PD 10-OCT-2002.
XX
PF 22-MAR-2001; 2001DE-01014063.
XX
PR 22-MAR-2001; 2001DE-01014063.
XX
PA (MPBC-) MPB COLOGNE GMBH MOLECULAR PLANT & PROTE.
XX
PI Buelow L, Tscharntke M, Haussuehl K;
XX
DR WPI; 2003-041808/04.
XX
PT New DNA sequences from potato, useful for producing plants with altered
PT properties, e.g. tolerance of flooding, also related proteins, antibodies
PT and inhibitory sequences.
XX
PS Example 1; Page 8; 26pp; German.
XX
CC The invention relates to DNA sequences (I) that encode six specific plant
CC proteins: (i) a protein (ABP60425) with mitochondrial carrier protein
CC activity (IIa); (ii) a protein (ABP60426) with transferrin binding
CC protein activity (IIb); (iii) a protein (ABP60427) with receptor-like
CC protein kinase activity (IIc); (iv) a protein (ABP60428) with elongation
CC factor EF-2 activity (IId); (v) a protein (ABP60429) with non-long
CC terminal repeat retroelement reverse transcriptase activity (IIe); or
CC (vi) a protein (ABP60430) with helicase activity (IIf). (I), also related
CC sequences, derived ribozymes and antisense sequences, expression vectors,
CC encoded proteins and antibodies against the proteins, are used to produce
CC plants with altered properties, including tolerance of overwatering. The
CC antibodies are also used for isolation of the proteins and in
CC immunoassays. Also (I) or their primer or probe fragments are used to
CC screen for terminators and constitutively, aerobically or anaerobically
CC inducible plant promoters, specifically for use in potatoes and the

```
CC   sequence that encodes (IId) is used to alter the translation profile in
CC   plants. Since (I) are derived from potato, their promoters and
CC   terminators provide high level transgene expression in potato, with
CC   improved tissue specificity and inducibility, and can also be used to
CC   control endogenous genes. The present sequence is that of a PCR primer
CC   used in the first strand synthesis of cDNAs derived from Potato
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         20 AAAAAAAAAAAAAAAAAAA 2

RESULT 997
ABX79181
ID   ABX79181 standard; DNA; 20 BP.
XX
AC   ABX79181;
XX
DT   15-APR-2003  (first entry)
XX
DE   Thio-modified 20dA oligonucleotide.
XX
KW   Nanoparticle; ss; nucleic acid detection; viral disease; probe;
KW   human immunodeficiency virus infection; hepatitis virus infection;
KW   herpes virus infection; cytomegalovirus infection; forensic science;
KW   Epstein-Barr virus infection; bacterial disease; gene therapy;
KW   sexually transmitted disease; inherited disorder; DNA sequencing;
KW   paternity testing; cell line authentication.
XX
OS   Synthetic.
XX
PN   US2002155462-A1.
XX
PD   24-OCT-2002.
XX
PF   12-OCT-2001; 2001US-00976577.
XX
PR   29-JUL-1996;   96US-0031809P.
PR   21-JUL-1997;   97WO-US012783.
PR   29-JAN-1999;   99US-00240755.
PR   25-JUN-1999;   99US-00344667.
PR   26-APR-2000; 2000US-0200161P.
PR   26-JUN-2000; 2000US-00603830.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA;
XX
DR   WPI; 2003-198491/19.
XX
PT   Detecting nucleic acids having at least 2 portions comprises use of
PT   nanoparticles which have oligonucleotides attached to them that are
PT   complementary to portions of the nucleic acid sequence.
XX
PS   Example 18; Page 44; 130pp; English.
XX
CC   The invention relates to detecting a nucleic acid (NA) having at least 2
CC   portions, comprises providing a type of nanoparticles (NP) having
CC   attached to oligonucleotides (O) ((O) on each NP has a sequence
CC   complementary to sequence of at least 2 portions of NA), contacting NA
CC   and NP to allow hybridisation of (O) on NP with 2 or more portions of NA,
CC   and observing a detectable change brought about by hybridisation of (O)
CC   on NP with NA. The nanoparticle is useful for separating a selected
CC   nucleic acid having at least 2 portions, from other nucleic acids, and
CC   for detecting nucleic acids having at least 2 portions. The method of
CC   using NP is useful for detecting any type of nucleic acids which may be
CC   used for diagnosis of disease and in sequencing of nucleic acids.
CC   Preferably, the method is useful for detecting nucleic acids for
CC   diagnosis and/or monitoring of viral diseases (human immunodeficiency
CC   virus, hepatitis virus, herpes virus, cytomegalovirus and Epstein-Barr
CC   virus), bacterial diseases, sexually transmitted diseases, inherited
CC   disorders, in forensics, in DNA sequencing, for paternity testing, for
CC   cell line authentication and for monitoring gene therapy. The method is
CC   useful in research and analytical laboratories in DNA sequencing and in
CC   the field to detect the presence of specific pathogens. Detecting nucleic
CC   acids based on observing a colour change with the naked eye is cheap,
CC   fast, simple and robust, and do not require specialised expensive
CC   equipment. The present sequence is a nanoparticle (e.g. gold particles)
CC   labelled probe used to demonstrate the method of the invention
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19

RESULT 998
ABX92177
ID   ABX92177 standard; DNA; 20 BP.
XX
AC   ABX92177;
XX
DT   12-MAY-2003  (first entry)
XX
DE   Nanoparticle-associated oligonucleotide SEQ ID 55.
XX
KW   Nonoparticle; nucleic acid detection; hybridisation; diagnosis;
KW   sequencing; viral infection; human immunodeficiency virus; HIV;
KW   hepatitis virus; herpes virus; cytomegalovirus; Epstein-Barr virus;
KW   bacterial infection; sexually transmitted disease; inherited disorder;
KW   forensic; paternity testing; cell line authentication; gene therapy; ss.
XX
OS   Synthetic.
XX
PN   US2002155458-A1.
XX
PD   24-OCT-2002.
XX
PF   28-SEP-2001; 2001US-00967409.
XX
PR   29-JUL-1996;   96US-0031809P.
PR   21-JUL-1997;   97WO-US012783.
PR   29-JAN-1999;   99US-00240755.
PR   25-JUN-1999;   99US-00344667.
PR   26-APR-2000; 2000US-0200161P.
PR   26-JUN-2000; 2000US-00603830.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA;
XX
DR   WPI; 2003-182627/18.
XX
PT   Detecting nucleic acids having at least two portions involves use of
PT   nanoparticles which have oligonucleotides attached to them that are
PT   complementary to portions of the nucleic acid sequence.
XX
PS   Disclosure; Page 59; 130pp; English.
XX
CC   This invention describes a novel method of detecting nucleic acid having
CC   at least two portions. The method involves providing nanoparticles
CC   attached to oligonucleotides, where the oligonucleotide on each
CC   nanoparticle have a sequence complementary to a sequence of at least two
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```
CC   portions of nucleic acid, contacting nucleic acid and nanoparticle to
CC   allow hybridisation of the oligonucleotide on the nanoparticle with two
CC   or more portions of nucleic acid and observing a detectable change
CC   brought about by hybridisation of the oligonucleotide nanoparticle with
CC   nucleic acid. The method is useful for separating a selected nucleic acid
CC   having at least two portions, from other nucleic acids and for detecting
CC   nucleic acids having at least two portions. The method is useful for
CC   detecting any type of nucleic acids which may be used for diagnosis of
CC   disease and in sequencing of nucleic acids. Preferably, the method is
CC   useful for detecting nucleic acids for diagnosis and/or monitoring of
CC   viral infections (human immunodeficiency virus (HIV), hepatitis virus,
CC   herpes virus, cytomegalovirus and Epstein-Barr virus), bacterial
CC   diseases, sexually transmitted diseases, inherited disorders, in
CC   forensics, in DNA sequencing, for paternity testing, for cell line
CC   authentication, and for monitoring gene therapy. The method is useful in
CC   research and analytical laboratories in DNA sequencing, in the field to
CC   detect the presence of specific pathogens. Detecting nucleic acids based
CC   on observing a colour change with the naked eye is cheap, fast, simple
CC   and robust and does not require specialised expensive equipment. ABX92123
CC   -ABX92186 and ABQ77356 represent oligonucleotides used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 999
ACD27255
ID   ACD27255 standard; DNA; 20 BP.
XX
AC   ACD27255;
XX
DT   15-OCT-2003  (first entry)
XX
DE   Nanotechnology nucleic acid detection method associated #54.
XX
KW   Nanotechnology; ss; nucleic acid detection; nanoparticle;
KW   virus detection; human immunodeficiency virus; HIV; hepatitis; herpes;
KW   cytomegalovirus; Epstein-Barr virus; bacterial disease; DNA sequencing;
KW   sexually transmitted disease; inherited disorder; forensic;
KW   paternity testing; cell line authentication.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER= Thiol modified" "
XX
PN   US2002155459-A1.
XX
PD   24-OCT-2002.
XX
PF   11-OCT-2001; 2001US-00975062.
XX
PR   29-JUL-1996;   96US-0031809P.
PR   21-JUL-1997;   97WO-US012783.
PR   29-JAN-1999;   99US-00240755.
PR   25-JUN-1999;   99US-00344667.
PR   26-APR-2000; 2000US-0200161P.
PR   26-JUN-2000; 2000US-00603830.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA;
XX
DR   WPI; 2003-228114/22.
XX
PT   Detecting nucleic acids having 2 portions e.g. for detecting disease,
PT   comprises use of nanoparticles which have oligonucleotides attached to
PT   them that are complementary to portions of the nucleic acid sequence.
XX
PS   Example 18; Page 43; 129pp; English.
XX
CC   This invention relates to a novel method for detecting a nucleic acid
CC   having 2 portions. The method comprises providing nanoparticles having
CC   oligonucleotides attached, where the oligonucleotide on each nanoparticle
CC   has a sequence complementary to a sequence of 2 portions of nucleic acid.
CC   The nucleic acid and nanoparticle are contacted to allow hybridisation of
CC   the oligonucleotide on the nanoparticle with two or more portions of
CC   nucleic acid and observing a detectable change brought about by the
CC   hybridisation. The method of the invention is useful for separating a
CC   selected nucleic acid having 2 portions, from other nucleic acids, and
CC   for detecting nucleic acids having 2 portions. The method of the
CC   invention is useful for detecting any type of nucleic acids which may be
CC   used for diagnosis of disease and in sequencing of nucleic acids.
CC   Preferably, the method is useful for detecting nucleic acids for
CC   diagnosis and/or monitoring of viral diseases (human immunodeficiency
CC   virus, hepatitis virus, herpes virus, cytomegalovirus and Epstein-Barr
CC   virus), bacterial diseases, sexually transmitted diseases, inherited
CC   disorders, in forensics, in DNA sequencing, for paternity testing, for
CC   cell line authentication, for monitoring gene therapy, etc. This method
CC   involves detecting nucleic acids based on observing a colour change with
CC   the naked eye so is cheap, fast, simple and robust, and does not require
CC   specialised expensive equipment. The present sequence represents a thiol
CC   modified oligonucleotide sequence used to demonstrate the method of the
CC   invention
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 1000
ACD27125
ID   ACD27125 standard; DNA; 20 BP.
XX
AC   ACD27125;
XX
DT   15-OCT-2003  (first entry)
XX
DE   Nanotechnology nucleic acid detection method oligonucleotide #54.
XX
KW   Nanotechnology; nucleic acid detection; nanoparticle; ss; forensic;
KW   DNA sequencing; paternity testing; cell line authentication.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER= Thiol modified" "
XX
PN   US2002164605-A1.
XX
PD   07-NOV-2002.
XX
PF   28-SEP-2001; 2001US-00966312.
XX
PR   29-JUL-1996;   96US-0031809P.
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```
PR   21-JUL-1997;   97WO-US012783.
PR   29-JAN-1999;   99US-00240755.
PR   25-JUN-1999;   99US-00344667.
PR   26-APR-2000; 2000US-0200161P.
PR   26-JUN-2000; 2000US-00603830.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA;
XX
DR   WPI; 2003-247253/24.
XX
PT   Detecting nucleic acid having two portions, by providing nanoparticles
PT   having oligonucleotides attached to it, contacting nucleic acid and
PT   nanoparticles to allow hybridization, and observing detectable change,
PT   useful in forensics.
XX
PS   Example 18; Page 44; 130pp; English.
XX
CC   This invention relates to a novel method for detecting nucleic acid
CC   sequences having two portions. The method involves providing
CC   nanoparticles having oligonucleotides attached to them, which has a
CC   sequence complementary to sequence of two portions of nucleic acid,
CC   contacting nucleic acid and nanoparticles, to allow hybridisation of
CC   oligonucleotides with two or more portions of nucleic acid, and observing
CC   a detectable change brought about by hybridisation. The method of the
CC   invention and the aggregate probes are useful for detecting two or more
CC   nucleic acids (from a biological source) having at least two portions,
CC   such as viral RNA or DNA, bacterial or fungal DNA, a gene associated with
CC   a disease, synthetic, or structurally- modified natural or synthetic RNA
CC   or DNA, or a product of a polymerase chain reaction amplification.
CC   Nanoparticles and nanoparticle- oligonucleotide conjugates of the
CC   invention are useful for nanofabrication, and for separating a selected
CC   nucleic acid having two portions from other nucleic acids. The method of
CC   the invention is useful in forensics, DNA sequencing, for paternity
CC   testing, cell line authentication, and monitoring gene therapy.
CC   Diagnostic assays employing the nanoparticle-oligonucleotide conjugates
CC   of the invention improve the sensitivity of the nucleic acid detection
CC   assay. The present sequence represents a thiol modified oligonucleotide
CC   sequence used to demonstrate the method of the invention
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 1001
ACD27385
ID   ACD27385 standard; DNA; 20 BP.
XX
AC   ACD27385;
XX
DT   15-OCT-2003  (first entry)
XX
DE   Nanotechnology nucleic acid detection method associated #54.
XX
KW   Nanoparticle; ss; nucleic acid detection; DNA sequencing;
KW   pathogen detection.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "OTHER= Thiol modified" "
XX
PN   US2002182611-A1.
XX
PD   05-DEC-2002.
XX
PF   28-SEP-2001; 2001US-00966491.
XX
PR   29-JUL-1996;   96US-0031809P.
PR   21-JUL-1997;   97WO-US012783.
PR   29-JAN-1999;   99US-00240755.
PR   25-JUN-1999;   99US-00344667.
PR   26-APR-2000; 2000US-0200161P.
PR   26-JUN-2000; 2000US-00603830.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA;
XX
DR   WPI; 2003-596264/56.
XX
PT   Detection of nucleic acid for, e.g. research and analytical laboratories
PT   in deoxyribonucleic acid sequencing, involves contacting nucleic acid
PT   with nanoparticles having oligonucleotides.
XX
PS   Example 18; Page 43; 109pp; English.
XX
CC   This invention relates to a novel method for detecting a nucleic acid by
CC   contacting a nucleic acid with at least two types of nanoparticles having
CC   oligonucleotides attached, allowing hybridisation of the oligonucleotides
CC   on the nanoparticles, and observing a detectable change. The
CC   oligonucleotides on each nanoparticle have a sequence complementary to
CC   its respective portion of the sequence of the nucleic acid to be
CC   detected. The method of the invention may be used for the detection of a
CC   nucleic acid used in, e.g. research and analytical laboratories in DNA
CC   sequencing, in the field to detect the presence of specific pathogens, in
CC   the doctor's office for quick identification of an infection to assist in
CC   prescribing a drug for treatment, and in homes and health centres for
CC   inexpensive first-line screening. The method of the invention detects
CC   nucleic acids based on observing a colour change with the naked eye. This
CC   method is cheap, fast, simple, robust and does not require specialised or
CC   expensive equipment. The present sequence represents a thiol modified
CC   oligonucleotide sequence used to demonstrate the method of the invention
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 1002
ACD27190
ID   ACD27190 standard; DNA; 20 BP.
XX
AC   ACD27190;
XX
DT   15-OCT-2003  (first entry)
XX
DE   Nanotechnology nucleic acid detection method associated #54.
XX
KW   Nanoparticle; ss; nucleic acid detection; DNA sequencing.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1
FT                    /*tag=  a
FT                    /mod_base= OTHER
```

```
FT                   /note= "OTHER= Thiol modified" "
XX
PN   US2002182613-A1.
XX
PD   05-DEC-2002.
XX
PF   12-OCT-2001; 2001US-00976971.
XX
PR   29-JUL-1996;   96US-0031809P.
PR   21-JUL-1997;   97WO-US012783.
PR   29-JAN-1999;   99US-00240755.
PR   25-JUN-1999;   99US-00344667.
PR   26-APR-2000; 2000US-0200161P.
PR   26-JUN-2000; 2000US-00603830.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA;
XX
DR   WPI; 2003-596265/56.
XX
PT   Detection of nucleic acid for, e.g. research and analytical laboratories
PT   in deoxyribonucleic acid sequencing, involves contacting nucleic acid
PT   with nanoparticles having oligonucleotides.
XX
PS   Example 18; Page 43; 107pp; English.
XX
CC   This invention relates to a novel method for detecting a nucleic acid by
CC   contacting nucleic acid with at least two types of nanoparticles having
CC   oligonucleotides, allowing hybridisation of the oligonucleotides on the
CC   nanoparticles, and observing a detectable change. The oligonucleotides on
CC   each nanoparticle have a sequence complementary to its respective portion
CC   of the sequence of the nucleic acid. The method of the invention may be
CC   used for the detection of a nucleic acid used in, e.g. research and
CC   analytical laboratories in DNA sequencing, in the field to detect the
CC   presence of specific pathogens, in the doctor's office for quick
CC   identification of an infection to assist in prescribing a drug for
CC   treatment, and in homes and health centres for inexpensive first-line
CC   screening. The inventive method of detecting nucleic acids based on
CC   observing a colour change with the naked eye are cheap, fast, simple,
CC   robust (the reagents are stable), do not require specialised or expensive
CC   equipment, and little or no instrumentation is required. The present
CC   sequence represents a thiol modified oligonucleotide sequence used to
CC   demonstrate the method of the invention
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 1003
ACD27060
ID   ACD27060 standard; DNA; 20 BP.
XX
AC   ACD27060;
XX
DT   15-OCT-2003  (first entry)
XX
DE   Nanotechnology nucleic acid detection method oligonucleotide #54.
XX
KW   Nanotechnology; nucleic acid detection; nanofabrication; nanoprobe; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER= Thiol modified" "
XX
PN   US2003044805-A1.
XX
PD   06-MAR-2003.
XX
PF   15-OCT-2001; 2001US-00981344.
XX
PR   29-JUL-1996;   96US-0031809P.
PR   21-JUL-1997;   97WO-US012783.
PR   29-JAN-1999;   99US-00240755.
PR   25-JUN-1999;   99US-00344667.
PR   26-APR-2000; 2000US-0200161P.
PR   26-JUN-2000; 2000US-00603830.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA;
XX
DR   WPI; 2003-521746/49.
XX
PT   Detection of nucleic acid having -2 portions used to prepare biomaterials
PT   and in nanofabrication methods, comprises providing nanoparticles,
PT   contacting nucleic acid and nanoparticles, and observing change.
XX
PS   Example 18; Page 44; 130pp; English.
XX
CC   This invention relates to a novel method for detecting nucleic acids. The
CC   method comprises providing nanoparticles with oligonucleotides attached
CC   to them, which have a sequence complementary to a sequence of two
CC   portions of nucleic acid, contacting the nucleic acid and nanoparticles
CC   to allow hybridisation of the oligonucleotides with two or more portions
CC   of the nucleic acid, and observing a detectable change brought about by
CC   the hybridisation. The nucleic acid to be detected must have at least two
CC   portions and the distances between these are chosen so that when the
CC   nanoparticle-oligonucleotide conjugate binds the target sequence a
CC   detectable change occurs. The method of the invention is useful for
CC   detecting two or more nucleic acids (from a biological source) having at
CC   least two portions, such as viral RNA, bacterial or fungal DNA, a gene
CC   associated with a disease, synthetic, or structurally- modified natural
CC   or synthetic RNA or DNA, or a product of a polymerase chain reaction
CC   amplification. Nanoparticle-oligonucleotide conjugates of the invention
CC   are useful for preparing a nanoprobe conjugate for detecting an analyte,
CC   and for detecting a nucleic acid bound to an electrode surface.
CC   Nanoparticles and nanoparticle conjugates of the invention are useful for
CC   nanofabrication and for separating a selected nucleic acid having two
CC   portions from other nucleic acids. Diagnostic assays employing
CC   nanoparticle-oligonucleotide conjugates improve the sensitivity of
CC   nucleic acid detection methods and can be used to detect nucleic acids
CC   that are present in only small amounts in a sample. The invention also
CC   provides highly desirable nanoparticle-oligonucleotide conjugates. These
CC   conjugates are stable with tailored hybridisation abilities. The present
CC   sequence represents a thiol modified oligonucleotide sequence used to
CC   demonstrate the method of the invention
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 1004
ACH00064
ID   ACH00064 standard; DNA; 20 BP.
XX
```

```
AC   ACH00064;
XX
DT   15-OCT-2003  (first entry)
XX
DE   Nanotechnology nucleic acid detection method oligonucleotide #54.
XX
KW   Nanotechnology; nucleic acid detection; nanofabrication; nanoprobe; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER= Thiol modified" "
XX
PN   US2003049631-A1.
XX
PD   13-MAR-2003.
XX
PF   10-OCT-2001; 2001US-00974500.
XX
PR   29-JUL-1996;   96US-0031809P.
PR   21-JUL-1997;   97WO-US012783.
PR   29-JAN-1999;   99US-00240755.
PR   25-JUN-1999;   99US-00344667.
PR   26-APR-2000; 2000US-0200161P.
PR   26-JUN-2000; 2000US-00603830.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA;
XX
DR   WPI; 2003-634854/60.
XX
PT   Detection of nucleic acid having at least two portions, by contacting
PT   nucleic acid and nanoparticles under conditions, which allows
PT   hybridization of oligonucleotides on nanoparticles with at least two
PT   portions of nucleic acid.
XX
PS   Example 18; Page 44; 108pp; English.
XX
CC   This invention relates to a novel method for detecting nucleic acids. The
CC   method comprises providing nanoparticles with oligonucleotides attached
CC   to them, which have a sequence complementary to a sequence of two
CC   portions of nucleic acid, contacting the nucleic acid and nanoparticles
CC   to allow hybridisation of the oligonucleotides with two or more portions
CC   of the nucleic acid, and observing a detectable change brought about by
CC   the hybridisation. The nucleic acid to be detected must have at least two
CC   portions and the distances between these are chosen so that when the
CC   nanoparticle-oligonucleotide conjugate binds the target sequence a
CC   detectable change occurs. The method of the invention is useful for
CC   detecting two or more nucleic acids (from a biological source) having at
CC   least two portions, such as viral RNA, bacterial or fungal DNA, a gene
CC   associated with a disease, synthetic, or structurally- modified natural
CC   or synthetic RNA or DNA, or a product of a polymerase chain reaction
CC   amplification. Nanoparticle-oligonucleotide conjugates of the invention
CC   are useful for preparing a nanoprobe conjugate for detecting an analyte,
CC   and for detecting a nucleic acid bound to an electrode surface.
CC   Nanoparticles and nanoparticle conjugates of the invention are useful for
CC   nanofabrication and for separating a selected nucleic acid having two
CC   portions from other nucleic acids. Diagnostic assays employing
CC   nanoparticle-oligonucleotide conjugates improve the sensitivity of
CC   nucleic acid detection methods and can be used to detect nucleic acids
CC   that are present in only small amounts in a sample. The invention also
CC   provides highly desirable nanoparticle-oligonucleotide conjugates. These
CC   conjugates are stable with tailored hybridisation abilities. The present
CC   sequence represents a thiol modified oligonucleotide sequence used to
CC   demonstrate the method of the invention
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 1005
ACD99851
ID   ACD99851 standard; DNA; 20 BP.
XX
AC   ACD99851;
XX
DT   25-SEP-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #537.
XX
KW   Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW   antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW   psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW   inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS   Synthetic.
XX
PN   US2003050268-A1.
XX
PD   13-MAR-2003.
XX
PF   29-MAR-2002; 2002US-00112653.
XX
PR   29-MAR-2001; 2001US-0279642P.
XX
PA   (KRIE/) KRIEG A M.
PA   (BERG/) BERG D J.
XX
PI   Krieg AM,  Berg DJ;
XX
DR   WPI; 2003-521815/49.
XX
PT   Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT   allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT   disease by administering an immunostimulatory nucleic acid.
XX
PS   Disclosure; Page 23; 229pp; English.
XX
CC   The invention describes a method of treating non-allergic inflammatory
CC   disease comprising administering to a subject having or at risk of
CC   developing a non-allergic inflammatory disease an immunostimulatory
CC   nucleic acid for prevention or treatment of the disease. The method is
CC   useful for treating non-allergic inflammatory diseases, such as
CC   psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC   inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC   This sequence represents an immunostimulatory nucleic acid
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 1006
ACD99847/c
ID   ACD99847 standard; DNA; 20 BP.
XX
AC   ACD99847;
XX
```

```
DT   25-SEP-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #533.
XX
KW   Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW   antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW   psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW   inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS   Synthetic.
XX
PN   US2003050268-A1.
XX
PD   13-MAR-2003.
XX
PF   29-MAR-2002; 2002US-00112653.
XX
PR   29-MAR-2001; 2001US-0279642P.
XX
PA   (KRIE/) KRIEG A M.
PA   (BERG/) BERG D J.
XX
PI   Krieg AM,  Berg DJ;
XX
DR   WPI; 2003-521815/49.
XX
PT   Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT   allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT   disease by administering an immunostimulatory nucleic acid.
XX
PS   Disclosure; Page 23; 229pp; English.
XX
CC   The invention describes a method of treating non-allergic inflammatory
CC   disease comprising administering to a subject having or at risk of
CC   developing a non-allergic inflammatory disease an immunostimulatory
CC   nucleic acid for prevention or treatment of the disease. The method is
CC   useful for treating non-allergic inflammatory diseases, such as
CC   psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC   inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC   This sequence represents an immunostimulatory nucleic acid
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         20 AAAAAAAAAAAAAAAAAAA 2


RESULT 1007
ACD99532/c
ID   ACD99532 standard; DNA; 20 BP.
XX
AC   ACD99532;
XX
DT   25-SEP-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #218.
XX
KW   Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW   antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW   psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW   inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS   Synthetic.
XX
PN   US2003050268-A1.
XX
PD   13-MAR-2003.
XX
PF   29-MAR-2002; 2002US-00112653.
XX
PR   29-MAR-2001; 2001US-0279642P.
XX
PA   (KRIE/) KRIEG A M.
PA   (BERG/) BERG D J.
XX
PI   Krieg AM,  Berg DJ;
XX
DR   WPI; 2003-521815/49.
XX
PT   Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT   allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT   disease by administering an immunostimulatory nucleic acid.
XX
PS   Disclosure; Page 14; 229pp; English.
XX
CC   The invention describes a method of treating non-allergic inflammatory
CC   disease comprising administering to a subject having or at risk of
CC   developing a non-allergic inflammatory disease an immunostimulatory
CC   nucleic acid for prevention or treatment of the disease. The method is
CC   useful for treating non-allergic inflammatory diseases, such as
CC   psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC   inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC   This sequence represents an immunostimulatory nucleic acid
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         20 AAAAAAAAAAAAAAAAAAA 2


RESULT 1008
ADA14838
ID   ADA14838 standard; DNA; 20 BP.
XX
AC   ADA14838;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Hairpin target sequence, #2, used in an example of the invention.
XX
KW   Hairpin sensor; hairpin loop; complementary probe; inverse repeat arm;
KW   quenchable fluorescing agent; microarray; semiconductor; nanocrystal;
KW   rhodamine B-labelled dye; detection; gold support; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_binding    1. .20
FT                   /*tag=  a
FT                   /bound_moiety= "Hairpin oligonucleotide #2"
FT                   /note= "Forms a doube-stranded region with the hairpin
FT                   oligonucleotide shown in examples 3, 4 and 5"
XX
PN   US2003013109-A1.
XX
PD   16-JAN-2003.
XX
PF   21-JUN-2002; 2002US-00176055.
XX
PR   21-JUN-2001; 2001US-0299460P.
XX
PA   (BALL/) BALLINGER C T.
PA   (LOCA/) LOCASCIO M.
PA   (LAND/) LANDRY D P.
XX
PI   Ballinger CT,  Locascio M,  Landry DP;
```

```
XX
DR   WPI; 2003-596312/56.
XX
PT   Hairpin sensor useful for detecting a target nucleotide sequence in a
PT   sample, comprises a hairpin loop assembly including a complementary probe
PT   and a quenchable fluorescing agent.
XX
PS   Example 3; Page 11; 16pp; English.
XX
CC   The invention discloses a hairpin sensor comprising a hairpin loop
CC   assembly including a complementary probe positioned between a first
CC   inverse repeat arm and a second inverse repeat arm, and a quenchable
CC   fluorescing agent joined, directly or indirectly, to the end of the
CC   second inverse repeat arm of the hairpin loop assembly opposite the
CC   complementary probe. Also claimed is a microarray comprising the hairpin
CC   sensor, where the end of the first inverse repeat arm opposite the
CC   complementary probe is bound, directly or indirectly, to a support, a kit
CC   for detecting a target nucleotide sequence in a sample comprising the
CC   hairpin sensor, and a support, and a hairpin sensor system, in which the
CC   particle is conductive or semi-conductive, including at least one of the
CC   above hairpin sensor assemblies. The hairpin sensor further comprises a
CC   functional group joined to the end of the first inverse repeat arm
CC   opposite the complementary probe, or first spacer opposite the first
CC   inverse repeat arm, the functional group selected from amino, carboxyl,
CC   thiol and hydroxyl. Further, the sensor comprises a ligand positioned
CC   between the second inverse repeat arm and the quenchable fluorescing
CC   agent, where the ligand is selected from mercapto, hydroxyl, amino,
CC   nitrile and carboxyl, carboxylic acid, organic acid and amino acid. The
CC   second spacer is positioned between the second inverse repeat arm and the
CC   quenchable fluorescing agent which comprises a semiconductor nanocrystal
CC   or rhodamine B-labelled dye. Within the microarray the support is capable
CC   of accepting a charge. At least one hairpin sensor comprises two or more
CC   hairpin sensors. The two or more hairpin sensors include complementary
CC   probes that are the same or different and respective quenchable
CC   fluorescing agents that are the same or different. The two or more
CC   hairpin sensors are arranged in a spatially-defined pattern. The sensor
CC   and system are useful for detecting a target nucleotide sequence in a
CC   sample. Further, the method involves identifying the target nucleotide
CC   sequence by the location of the complementary probe to which the target
CC   nucleotide sequence binds. The two or more hairpin sensors include
CC   complementary probes or quenchable fluorescing agents, that are
CC   different. The sequence presented is the hairpin oligonucleotide target
CC   sequence, #2, used in an example of the invention.
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 1009
ADA06159
ID   ADA06159 standard; DNA; 20 BP.
XX
AC   ADA06159;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Nanoparticle labelled oligonucleotides, spacer DNA #2.
XX
KW   ss; nanoparticle; colloidal gold; semiconductor; nanomaterial;
KW   nanostructure; viral disease; human immunodeficiency virus infection;
KW   hepatitis virus infection; herpes virus infection;
KW   cytomegalovirus virus infection; Epstein-Barr virus; bacterial disease;
KW   sexually transmitted disease; inherited disorders; paternity testing;
KW   cell line authentication; gene therapy.
XX
OS   Synthetic.
XX
PN   US2003068622-A1.
XX
PD   10-APR-2003.
XX
PF   12-OCT-2001; 2001US-00976863.
XX
PR   29-JUL-1996;   96US-0031809P.
PR   21-JUL-1997;   97WO-US012783.
PR   29-JAN-1999;   99US-00240755.
PR   25-JUN-1999;   99US-00344667.
PR   26-APR-2000; 2000US-0200161P.
PR   26-JUN-2000; 2000US-00603830.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA;
XX
DR   WPI; 2003-576420/54.
XX
PT   Detecting nucleic acids having at least 2 portions comprises use of
PT   nanoparticles which have oligonucleotides attached to them that are
PT   complementary to portions of the target nucleic acid sequence.
XX
PS   Example 18; Page 44; 130pp; English.
XX
CC   The invention relates to detecting a nucleic acid (NA) having at least 2
CC   portions comprises providing a type of nanoparticles (NP. e.g. colloidal
CC   gold) having oligonucleotides (O) attached (where (O) on each NP has a
CC   sequence complementary to sequence of at least two portions of NA),
CC   contacting NA and NP to allow hybridisation of (O) on NP with 2 or more
CC   portions of NA, and observing a detectable change brought about by
CC   hybridization of (O) on NP with NA. Also included are aggregate probes,
CC   core probes, substrate having NP attached to it, a metallic or
CC   semiconductor NP having (O) attached to it, nanomaterials/nanostructures
CC   comprising nanoparticles and methods of nanofabrication utilising
CC   nanoparticles and satellite probes. The methods, probes nucleic acids,
CC   nanoparticles and oligonucleotides are useful for separating a selected
CC   nucleic acid having at least two portions, from other nucleic acids, and
CC   for detecting nucleic acids having at least two portions, for detecting
CC   NA having at least two portions. The method is useful for detecting any
CC   type of nucleic acids which may be used for diagnosis of disease and in
CC   sequencing of nucleic acids. Preferably, the method is useful for
CC   detecting nucleic acids for diagnosis and/or monitoring of viral diseases
CC   (human immunodeficiency virus, hepatitis virus, herpes virus,
CC   cytomegalovirus and Epstein-Barr virus), bacterial diseases, sexually
CC   transmitted diseases, inherited disorders, in forensics, in DNA
CC   sequencing, for paternity testing, for cell line authentication, for
CC   monitoring gene therapy, etc. The method is useful in research and
CC   analytical laboratories in DNA sequencing, in the field to detect the
CC   presence of specific pathogens, etc. Detecting nucleic acids based on
CC   observing a colour change with the naked eye is cheap, fast, simple and
CC   robust, and do not require specialised expensive equipment. The present
CC   sequence is a spacer oligonucleotide used to illustrate the method of the
CC   invention.
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 1010
ACD26995
ID   ACD26995 standard; DNA; 20 BP.
XX
AC   ACD26995;
```

```
XX
DT   15-OCT-2003  (first entry)
XX
DE   Nanotechnology nucleic acid detection method oligonucleotide #54.
XX
KW   Nanotechnology; nucleic acid detection; nanofabrication; nanoprobe; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER= Thiol modified" "
XX
PN   US2003049630-A1.
XX
PD   13-MAR-2003.
XX
PF   20-SEP-2001; 2001US-00957318.
XX
PR   29-JUL-1996;   96US-0031809P.
PR   21-JUL-1997;   97WO-US012783.
PR   29-JAN-1999;   99US-00240755.
PR   25-JUN-1999;   99US-00344667.
PR   26-APR-2000; 2000US-0200161P.
PR   26-JUN-2000; 2000US-00603830.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA;
XX
DR   WPI; 2003-615795/58.
XX
PT   Detecting nucleic acid having two portions, by providing nanoparticles
PT   having oligonucleotides attached to it, contacting nucleic acid and
PT   nanoparticles to allow hybridization, and observing detectable change.
XX
PS   Example 18; Page 43; 129pp; English.
XX
CC   This invention relates to a novel method for detecting nucleic acids. The
CC   method comprises providing nanoparticles with oligonucleotides attached
CC   to them, which have a sequence complementary to a sequence of two
CC   portions of nucleic acid, contacting the nucleic acid and nanoparticles
CC   to allow hybridisation of the oligonucleotides with two or more portions
CC   of the nucleic acid, and observing a detectable change brought about by
CC   the hybridisation. The nucleic acid to be detected must have at least two
CC   portions and the distances between these are chosen so that when the
CC   nanoparticle-oligonucleotide conjugate binds the target sequence a
CC   detectable change occurs. The method of the invention is useful for
CC   detecting two or more nucleic acids (from a biological source) having at
CC   least two portions, such as viral RNA, bacterial or fungal DNA, a gene
CC   associated with a disease, synthetic, or structurally- modified natural
CC   or synthetic RNA or DNA, or a product of a polymerase chain reaction
CC   amplification. Nanoparticle-oligonucleotide conjugates of the invention
CC   are useful for preparing a nanoprobe conjugate for detecting an analyte,
CC   and for detecting a nucleic acid bound to an electrode surface.
CC   Nanoparticles and nanoparticle conjugates of the invention are useful for
CC   nanofabrication and for separating a selected nucleic acid having two
CC   portions from other nucleic acids. Diagnostic assays employing
CC   nanoparticle-oligonucleotide conjugates improve the sensitivity of
CC   nucleic acid detection methods and can be used to detect nucleic acids
CC   that are present in only small amounts in a sample. The present sequence
CC   represents a thiol modified oligonucleotide sequence used to demonstrate
CC   the method of the invention
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 1011
ADB36933
ID   ADB36933 standard; DNA; 20 BP.
XX
AC   ADB36933;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #547.
XX
KW   ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW   hypo-responsive subject; immunostimulatory.
XX
OS   Synthetic.
XX
PN   US2003087848-A1.
XX
PD   08-MAY-2003.
XX
PF   02-FEB-2001; 2001US-00776479.
XX
PR   03-FEB-2000; 2000US-0179991P.
XX
PA   (BRAT/) BRATZLER R L.
PA   (PETE/) PETERSEN D M.
PA   (FOUR/) FOURON Y.
XX
PI   Bratzler RL,  Petersen DM,  Fouron Y;
XX
DR   WPI; 2003-657977/62.
XX
PT   Treating and/or preventing allergy or asthma using an immunostimulatory
PT   nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS   Disclosure; Page 13; 221pp; English.
XX
CC   The invention relates to a method of treating or preventing allergy or
CC   asthma which comprises administering to a subject a poly-G nucleic acid
CC   in an aerosol formulation. The methods and compositions of the present
CC   invention are useful for diagnosing and/or treating asthma and allergy
CC   especially in a hypo-responsive subject. The present sequence represents
CC   an immunostimulatory nucleic acid of the invention.
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 1012
ADB36601/c
ID   ADB36601 standard; DNA; 20 BP.
XX
AC   ADB36601;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #215.
XX
KW   ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW   hypo-responsive subject; immunostimulatory.
XX
OS   Synthetic.
```

```
XX
PN   US2003087848-A1.
XX
PD   08-MAY-2003.
XX
PF   02-FEB-2001; 2001US-00776479.
XX
PR   03-FEB-2000; 2000US-0179991P.
XX
PA   (BRAT/) BRATZLER R L.
PA   (PETE/) PETERSEN D M.
PA   (FOUR/) FOURON Y.
XX
PI   Bratzler RL,  Petersen DM,  Fouron Y;
XX
DR   WPI; 2003-657977/62.
XX
PT   Treating and/or preventing allergy or asthma using an immunostimulatory
PT   nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS   Disclosure; Page 8; 221pp; English.
XX
CC   The invention relates to a method of treating or preventing allergy or
CC   asthma which comprises administering to a subject a poly-G nucleic acid
CC   in an aerosol formulation. The methods and compositions of the present
CC   invention are useful for diagnosing and/or treating asthma and allergy
CC   especially in a hypo-responsive subject. The present sequence represents
CC   an immunostimulatory nucleic acid of the invention.
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         20 AAAAAAAAAAAAAAAAAAA 2


RESULT 1013
ADB36929/c
ID   ADB36929 standard; DNA; 20 BP.
XX
AC   ADB36929;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #543.
XX
KW   ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW   hypo-responsive subject; immunostimulatory.
XX
OS   Synthetic.
XX
PN   US2003087848-A1.
XX
PD   08-MAY-2003.
XX
PF   02-FEB-2001; 2001US-00776479.
XX
PR   03-FEB-2000; 2000US-0179991P.
XX
PA   (BRAT/) BRATZLER R L.
PA   (PETE/) PETERSEN D M.
PA   (FOUR/) FOURON Y.
XX
PI   Bratzler RL,  Petersen DM,  Fouron Y;
XX
DR   WPI; 2003-657977/62.
XX
PT   Treating and/or preventing allergy or asthma using an immunostimulatory
PT   nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS   Disclosure; Page 13; 221pp; English.
XX
CC   The invention relates to a method of treating or preventing allergy or
CC   asthma which comprises administering to a subject a poly-G nucleic acid
CC   in an aerosol formulation. The methods and compositions of the present
CC   invention are useful for diagnosing and/or treating asthma and allergy
CC   especially in a hypo-responsive subject. The present sequence represents
CC   an immunostimulatory nucleic acid of the invention.
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         20 AAAAAAAAAAAAAAAAAAA 2


RESULT 1014
AAQ75598/c
ID   AAQ75598 standard; DNA; 20 BP.
XX
AC   AAQ75598;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 1 A; 2 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||||
Db         19 TGAAAAAAAAAAAAAAAAA 1
```

```
RESULT 1015
AAQ75579
ID   AAQ75579 standard; DNA; 20 BP.
XX
AC   AAQ75579;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 2 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAA 2188
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTAA 19


RESULT 1016
AAQ75597/c
ID   AAQ75597 standard; DNA; 20 BP.
XX
AC   AAQ75597;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||||
Db         19 TGAAAAAAAAAAAAAAAAA 1


RESULT 1017
AAQ75581
ID   AAQ75581 standard; DNA; 20 BP.
XX
AC   AAQ75581;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 2 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
```

```
  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAA 2188
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTAA 19


RESULT 1018
AAQ75595/c
ID   AAQ75595 standard; DNA; 20 BP.
XX
AC   AAQ75595;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||
Db         19 TGAAAAAAAAAAAAAAAAA 1


RESULT 1019
AAQ75580
ID   AAQ75580 standard; DNA; 20 BP.
XX
AC   AAQ75580;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 3 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAA 2188
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTAA 19


RESULT 1020
AAT04916
ID   AAT04916 standard; cDNA; 20 BP.
XX
AC   AAT04916;
XX
DT   25-MAR-2003  (revised)
DT   15-MAY-1996  (first entry)
XX
DE   Mammalian stem cell factor (SCF) cDNA oligonucleotide primer 220-7.
XX
KW   Stem cell factor; progenitor; haematopoiesis; SCF; anaemia;
KW   thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft;
KW   transplant; neoplasia; myelosuppression; bone marrow; ss.
XX
OS   Synthetic.
XX
PN   EP676470-A1.
XX
PD   11-OCT-1995.
XX
PF   04-OCT-1990;   95EP-00105391.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   28-SEP-1990;   90WO-US005548.
PR   01-OCT-1990;   90US-00589701.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Zsebo KM,  Suggs SV,  Bosselman RA,  Martin FH;
```

```
XX
DR   WPI; 1995-346090/45.
XX
PT   New stem cell factor polypeptide(s) - for stimulating the growth of
PT   primitive progenitor cells, esp. for treating disorders involving blood
PT   cells.
XX
PS   Example 3; Fig 12C; 127pp; English.
XX
CC   AAT04915-T04922 are oligonucleotide primers and probes used for the
CC   amplification and sequencing of mammalian stem cell factor (SCF). Non-
CC   naturally occuring SCF and C-terminally truncated polypeptides, having
CC   amino acid sequences sufficiently duplicative of naturally ocurring SCF,
CC   stimulate growth of primitive progenitors such as haematopoietic
CC   progenitor cells, neural stem cells and primordial germ stem cells. The
CC   peptides can be used in a composition for treating leucopenia, anaemia or
CC   thrombocytopenia, for enhancing engraftment of bone marrow during
CC   transplantation or for bone marrow recovery after chemotherapy or
CC   radiation-induced bone marrow aplasia or myelosuppression. They can also
CC   be used for treating neoplasia, nerve damage, infertlilty, intestinal
CC   damage or myeloproliferative disorders. Antibodies may be raised against
CC   the peptides for use in detection or neutralisation of SCF in serum. SCF
CC   may be useful for the treatment of AIDS and severe combined
CC   immunodeficiency (SCID) states alone or in combination with other factors
CC   such as IL-7. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTA 19


RESULT 1021
AAT04918/c
ID   AAT04918 standard; cDNA; 20 BP.
XX
AC   AAT04918;
XX
DT   25-MAR-2003  (revised)
DT   15-MAY-1996  (first entry)
XX
DE   Mammalian stem cell factor (SCF) cDNA oligonucleotide primer 220-11.
XX
KW   Stem cell factor; progenitor; haematopoiesis; SCF; anaemia;
KW   thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft;
KW   transplant; neoplasia; myelosuppression; bone marrow; ss.
XX
OS   Synthetic.
XX
PN   EP676470-A1.
XX
PD   11-OCT-1995.
XX
PF   04-OCT-1990;   95EP-00105391.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   28-SEP-1990;   90WO-US005548.
PR   01-OCT-1990;   90US-00589701.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Zsebo KM,  Suggs SV,  Bosselman RA,  Martin FH;
XX
DR   WPI; 1995-346090/45.
XX
PT   New stem cell factor polypeptide(s) - for stimulating the growth of
PT   primitive progenitor cells, esp. for treating disorders involving blood
PT   cells.
XX
PS   Example 3; Fig 12C; 127pp; English.
XX
CC   AAT04915-T04922 are oligonucleotide primers and probes used for the
CC   amplification and sequencing of mammalian stem cell factor (SCF). Non-
CC   naturally occuring SCF and C-terminally truncated polypeptides, having
CC   amino acid sequences sufficiently duplicative of naturally ocurring SCF,
CC   stimulate growth of primitive progenitors such as haematopoietic
CC   progenitor cells, neural stem cells and primordial germ stem cells. The
CC   peptides can be used in a composition for treating leucopenia, anaemia or
CC   thrombocytopenia, for enhancing engraftment of bone marrow during
CC   transplantation or for bone marrow recovery after chemotherapy or
CC   radiation-induced bone marrow aplasia or myelosuppression. They can also
CC   be used for treating neoplasia, nerve damage, infertlilty, intestinal
CC   damage or myeloproliferative disorders. Antibodies may be raised against
CC   the peptides for use in detection or neutralisation of SCF in serum. SCF
CC   may be useful for the treatment of AIDS and severe combined
CC   immunodeficiency (SCID) states alone or in combination with other factors
CC   such as IL-7. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         19 GAAAAAAAAAAAAAAAAAA 1


RESULT 1022
AAA13753
ID   AAA13753 standard; DNA; 20 BP.
XX
AC   AAA13753;
XX
DT   27-JUL-2000  (first entry)
XX
DE   Stem cell factor universal oligonucleotide 220-7.
XX
KW   Stem cell factor; SCF; haematopoietic progenitor cell; blood forming;
KW   primitive progenitor cell; haematopoietic disorder; syngeneic;
KW   allogeneic; autologous bone marrow transplant; gene therapy;
KW   transfection; haematopoietic stem cell; acute blood loss; neoplasia;
KW   cancer; ss.
XX
OS   Synthetic.
XX
PN   EP992579-A1.
XX
PD   12-APR-2000.
XX
PF   04-OCT-1990;   99EP-00122861.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   28-SEP-1990;   90WO-US005548.
PR   01-OCT-1990;   90US-00589701.
PR   04-OCT-1990;   90EP-00310899.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Zsebo KM,  Suggs SV,  Bosselmann RA,  Martin FH;
XX
DR   WPI; 2000-259135/23.
XX
PT   Production of hematopoietic cells suitable for administration to a
PT   subject using progenitor cells and expanding the cells using stem cell
PT   factor.
```

XX
PS Example 3; Fig 12C; 123pp; English.
XX
CC A method has been developed of making haematopoietic cells suitable for
CC administration to a subject. The method comprises: (a) obtaining
CC haematopoietic progenitor cells from a donor; and (b) expanding the cells
CC by adding to the cells a haematopoietically effective dose of a
CC polypeptide product having at least part of the primary structural
CC confirmation and one or more of the biological properties of naturally
CC occurring stem cell factor (SCF). The method is useful for stimulating
CC primitive progenitor cells including early haematopoietic progenitor
CC cells which are capable of maturing to erythroid, megakaryocyte,
CC granulocyte, lymphocyte and macrophage cells. SCF results in absolute
CC increases in haematopoietic cells of both myeloid and lymphoid lineages.
CC SCF is useful for treating haematopoietic disorders. The method is useful
CC for expanding early haematopoietic progenitors in syngeneic, allogeneic
CC or autologous bone marrow transplant. SCF is useful for enhancing the
CC efficiency of gene therapy based on transfecting haematopoietic stem
CC cells. SCF is also useful for combating the myelosuppressive effects of
CC anti-HIV drugs such as AZT and for enhancing haematopoietic recovery
CC after acute blood loss and as a boost to the immune system for fighting
CC neoplasia (cancer). The present sequence represents a universal
CC oligonucleotide which is used in an example from the present invention
XX
SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2169 TTTTTTTTTTTTTTTTTTA 2187
||||||||||||||||||
Db 1 TTTTTTTTTTTTTTTTTTA 19

RESULT 1023
AAA13754/c
ID AAA13754 standard; DNA; 20 BP.
XX
AC AAA13754;
XX
DT 27-JUL-2000 (first entry)
XX
DE Stem cell factor universal oligonucleotide 220-11.
XX
KW Stem cell factor; SCF; haematopoietic progenitor cell; blood forming;
KW primitive progenitor cell; haematopoietic disorder; syngeneic;
KW allogeneic; autologous bone marrow transplant; gene therapy;
KW transfection; haematopoietic stem cell; acute blood loss; neoplasia;
KW cancer; ss.
XX
OS Synthetic.
XX
PN EP992579-A1.
XX
PD 12-APR-2000.
XX
PF 04-OCT-1990; 99EP-00122861.
XX
PR 16-OCT-1989; 89US-00422383.
PR 11-JUN-1990; 90US-00537198.
PR 24-AUG-1990; 90US-00573616.
PR 28-SEP-1990; 90WO-US005548.
PR 01-OCT-1990; 90US-00589701.
PR 04-OCT-1990; 90EP-00310899.
XX
PA (AMGE-) AMGEN INC.
XX
PI Zsebo KM, Suggs SV, Bosselmann RA, Martin FH;
XX
DR WPI; 2000-259135/23.
XX
PT Production of hematopoietic cells suitable for administration to a
PT subject using progenitor cells and expanding the cells using stem cell
PT factor.
XX
PS Example 3; Fig 12C; 123pp; English.
XX
CC A method has been developed of making haematopoietic cells suitable for
CC administration to a subject. The method comprises: (a) obtaining
CC haematopoietic progenitor cells from a donor; and (b) expanding the cells
CC by adding to the cells a haematopoietically effective dose of a
CC polypeptide product having at least part of the primary structural
CC confirmation and one or more of the biological properties of naturally
CC occurring stem cell factor (SCF). The method is useful for stimulating
CC primitive progenitor cells including early haematopoietic progenitor
CC cells which are capable of maturing to erythroid, megakaryocyte,
CC granulocyte, lymphocyte and macrophage cells. SCF results in absolute
CC increases in haematopoietic cells of both myeloid and lymphoid lineages.
CC SCF is useful for treating haematopoietic disorders. The method is useful
CC for expanding early haematopoietic progenitors in syngeneic, allogeneic
CC or autologous bone marrow transplant. SCF is useful for enhancing the
CC efficiency of gene therapy based on transfecting haematopoietic stem
CC cells. SCF is also useful for combating the myelosuppressive effects of
CC anti-HIV drugs such as AZT and for enhancing haematopoietic recovery
CC after acute blood loss and as a boost to the immune system for fighting
CC neoplasia (cancer). The present sequence represents a universal
CC oligonucleotide which is used in an example from the present invention
XX
SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAAAAAAAAA 2803
||||||||||||||||||
Db 19 GAAAAAAAAAAAAAAAAAA 1

RESULT 1024
AAA91207/c
ID AAA91207 standard; DNA; 20 BP.
XX
AC AAA91207;
XX
DT 08-MAY-2001 (first entry)
XX
DE Antisense IGFBP-5 inhibitor #13.
XX
KW Insulin-like growth factor binding protein-5; IGFBP-5; human;
KW antisense oligonucleotide; hormone-regulated cancer; prostatic cancer;
KW breast cancer; therapy; ss.
XX
OS Homo sapiens.
XX
PN WO200105435-A2.
XX
PD 25-JAN-2001.
XX
PF 19-JUL-2000; 2000WO-CA000853.
XX
PR 19-JUL-1999; 99US-0144495P.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
PA (MIYA/) MIYAKE H.
XX
PI Gleave M;
XX
DR WPI; 2001-168448/17.
XX
PT Composition for treating hormone-regulated cancer, e.g. breast and
PT prostatic tumors, comprising an antisense oligonucleotide that inhibits
PT expression of insulin like growth factor binding protein-5 by hormone-
PT regulated tumor cells.
XX

```
PS   Disclosure; Page 34; 45pp; English.
XX
CC   This sequence represents an antisense oligonucleotide targeted against
CC   human insulin-like growth factor binding protein-5 (IGFBP-5). The
CC   invention relates to a composition for treatment of hormone-regulated
CC   cancer, comprising an antisense oligonucleotide (such as this sequence)
CC   which inhibits expression of IGFBP-5 by hormone-regulated tumour cells.
CC   The compositions is useful for delaying progression of hormone-regulated
CC   tumour cells such as prostatic cancer cells or breast cancer cells, to an
CC   androgen-independent state, by treating hormone sensitive tumour cells
CC   with the antisense sequence which inhibits expression of IGFBP-5 by the
CC   tumour cells. The composition can also be used for treating a hormone-
CC   responsive cancer in an individual, and administering the composition to
CC   the individual after initiation of hormone-withdrawal to induce apoptotic
CC   cell death of hormone-responsive tumour cells, and therefore delaying the
CC   progression of hormone-responsive cancer cells to a hormone-independent
CC   state in the individual. It can also be used for inhibiting or delaying
CC   metastatic boney progression of an IGF-1 sensitive tumour in a mammal, by
CC   administering the composition to inhibit the expression of IGFBP-5 by the
CC   hormone-responsive cancer cells, and therefore inhibiting or delaying
CC   metastatic boney progression of the tumour
XX
SQ   Sequence 20 BP; 3 A; 1 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAA 2801
              ||||||||||||||||||
Db         19 TTGAAAAAAAAAAAAAAAA 1


RESULT 1025
AAH41332
ID   AAH41332 standard; DNA; 20 BP.
XX
AC   AAH41332;
XX
DT   21-AUG-2001  (first entry)
XX
DE   Universal stem cell factor (SCF) related oligonucleotide SEQ ID NO:33.
XX
KW   Stem cell factor; SCF; stem cell factor receptor; blood cell disorder;
KW   gene therapy; PCR primer; mutagenesis; probe; ss.
XX
OS   Synthetic.
XX
PN   US6207454-B1.
XX
PD   27-MAR-2001.
XX
PF   31-DEC-1998;   98US-00224681.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   01-OCT-1990;   90US-00589701.
PR   25-NOV-1992;   92US-00982255.
PR   21-DEC-1993;   93US-00172329.
PR   24-MAY-1995;   95US-00449653.
PR   12-JAN-1998;   98US-00005893.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Zsebo KM,  Bosselman RA,  Suggs SV,  Martin FH;
XX
DR   WPI; 2001-366062/38.
XX
PT   Enhancing efficiency of transfer of polynucleotide into a target
PT   mammalian cell in vitro, involves exposing cell that expresses a stem
PT   cell factor receptor to stem cell factor, and introducing polynucleotide
PT   into cell in vitro.
XX
PS   Example 3; Fig 12C; 210pp; English.
XX
CC   The present invention describes a method for enhancing (E) the efficiency
CC   of transfer of a polynucleotide (I) into a target mammalian cell (II) in
CC   vitro, comprising exposing (II) that expresses a stem cell factor (SCF)
CC   receptor to a biologically active SCF, its analogue or fragment, which
CC   induces cell proliferation, and introducing (I) to (II) in vitro.
CC   Exposure of SCF to (II) results in increased uptake of (I) into the cell.
CC   The method is useful for enhancing the efficiency of the transfer of a
CC   polynucleotide into a target mammalian cell in vitro. The method is
CC   useful in gene therapy techniques. AAH41301 to AAH41364 and AAB98351 to
CC   AAB98390 represent sequences used in the exemplification of the present
CC   invention
XX
SQ   Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTA 19


RESULT 1026
AAH41333/c
ID   AAH41333 standard; DNA; 20 BP.
XX
AC   AAH41333;
XX
DT   21-AUG-2001  (first entry)
XX
DE   Universal stem cell factor (SCF) related oligonucleotide SEQ ID NO:34.
XX
KW   Stem cell factor; SCF; stem cell factor receptor; blood cell disorder;
KW   gene therapy; PCR primer; mutagenesis; probe; ss.
XX
OS   Synthetic.
XX
PN   US6207454-B1.
XX
PD   27-MAR-2001.
XX
PF   31-DEC-1998;   98US-00224681.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   01-OCT-1990;   90US-00589701.
PR   25-NOV-1992;   92US-00982255.
PR   21-DEC-1993;   93US-00172329.
PR   24-MAY-1995;   95US-00449653.
PR   12-JAN-1998;   98US-00005893.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Zsebo KM,  Bosselman RA,  Suggs SV,  Martin FH;
XX
DR   WPI; 2001-366062/38.
XX
PT   Enhancing efficiency of transfer of polynucleotide into a target
PT   mammalian cell in vitro, involves exposing cell that expresses a stem
PT   cell factor receptor to stem cell factor, and introducing polynucleotide
PT   into cell in vitro.
XX
PS   Example 3; Fig 12C; 210pp; English.
XX
CC   The present invention describes a method for enhancing (E) the efficiency
CC   of transfer of a polynucleotide (I) into a target mammalian cell (II) in
CC   vitro, comprising exposing (II) that expresses a stem cell factor (SCF)
CC   receptor to a biologically active SCF, its analogue or fragment, which
```

```
CC   induces cell proliferation, and introducing (I) to (II) in vitro.
CC   Exposure of SCF to (II) results in increased uptake of (I) into the cell.
CC   The method is useful for enhancing the efficiency of the transfer of a
CC   polynucleotide into a target mammalian cell in vitro. The method is
CC   useful in gene therapy techniques. AAH41301 to AAH41364 and AAB98351 to
CC   AAB98390 represent sequences used in the exemplification of the present
CC   invention
XX
SQ   Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
                ||||||||||||||||||
Db         19 GAAAAAAAAAAAAAAAAAA 1


RESULT 1027
AAS04112
ID   AAS04112 standard; DNA; 20 BP.
XX
AC   AAS04112;
XX
DT   29-AUG-2001  (first entry)
XX
DE   Human SCF (stem cell factor) cDNA universal PCR primer 220-7.
XX
KW   Human; stem cell factor; SCF; early haematopoietic progenitor cell;
KW   blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
KW   anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6207417-B1.
XX
PD   27-MAR-2001.
XX
PF   07-JUN-1995;   95US-00482918.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   01-OCT-1990;   90US-00589701.
PR   21-DEC-1993;   93US-00172329.
XX
PA   (ZSEB/) ZSEBO K M.
PA   (BOSS/) BOSSELMAN R A.
PA   (SUGG/) SUGGS S V.
PA   (MART/) MARTIN F H.
XX
PI   Zsebo KM,  Bosselman RA,  Suggs SV,  Martin FH;
XX
DR   WPI; 2001-298941/31.
XX
PT   Novel nucleic acids encoding stem cell factor useful for treating
PT   disorders involving blood cells, e.g. leukemia, splenomegaly, Hodgkin's
PT   disease, Kala azar, anemia and septicemia.
XX
PS   Example 3; Fig 12C; 209pp; English.
XX
CC   The present sequence for universal PCR primer 220-7 is 1 of 8 universal
CC   oligonucleotides (AAS04110-AAS04117) used in the isolation of the human
CC   SCF (stem cell factor) cDNA sequence. The present invention relates to
CC   novel stem cell factors (AAU02453-AAU02458, AAU02460, AAU02461) and the
CC   polynucleotides encoding them. SCF stimulate primitive progenitor cells
CC   including early haematopoietic progenitor cells. The invention also
CC   describes SCF peptides (AAU02462-AAU02481) and the oligonucleotides
CC   (AAS04081-AAS04117) used in the isolation of human and rat SCF sequences.
CC   The polynucleotide encoding SCF is useful for producing SCF and useful in
CC   gene therapy. It is useful for treating disorders involving blood cells
CC   such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
CC   myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
CC   congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
CC   disseminated fungus disease, Fulminating septicemia, malaria, vitamin B12
CC   and folic acid deficiency, pyridoxine deficiency, and hypopigmentation
CC   disorders such as piebaldism and vitiligo
XX
SQ   Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTA 2187
                ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTA 19


RESULT 1028
AAS04113/c
ID   AAS04113 standard; DNA; 20 BP.
XX
AC   AAS04113;
XX
DT   29-AUG-2001  (first entry)
XX
DE   Human SCF (stem cell factor) cDNA universal PCR primer 220-11.
XX
KW   Human; stem cell factor; SCF; early haematopoietic progenitor cell;
KW   blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
KW   anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6207417-B1.
XX
PD   27-MAR-2001.
XX
PF   07-JUN-1995;   95US-00482918.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   01-OCT-1990;   90US-00589701.
PR   21-DEC-1993;   93US-00172329.
XX
PA   (ZSEB/) ZSEBO K M.
PA   (BOSS/) BOSSELMAN R A.
PA   (SUGG/) SUGGS S V.
PA   (MART/) MARTIN F H.
XX
PI   Zsebo KM,  Bosselman RA,  Suggs SV,  Martin FH;
XX
DR   WPI; 2001-298941/31.
XX
PT   Novel nucleic acids encoding stem cell factor useful for treating
PT   disorders involving blood cells, e.g. leukemia, splenomegaly, Hodgkin's
PT   disease, Kala azar, anemia and septicemia.
XX
PS   Example 3; Fig 12C; 209pp; English.
XX
CC   The present sequence for universal PCR primer 220-11 is 1 of 8 universal
CC   oligonucleotides (AAS04110-AAS04117) used in the isolation of the human
CC   SCF (stem cell factor) cDNA sequence. The present invention relates to
CC   novel stem cell factors (AAU02453-AAU02458, AAU02460, AAU02461) and the
CC   polynucleotides encoding them. SCF stimulate primitive progenitor cells
CC   including early haematopoietic progenitor cells. The invention also
CC   describes SCF peptides (AAU02462-AAU02481) and the oligonucleotides
CC   (AAS04081-AAS04117) used in the isolation of human and rat SCF sequences.
CC   The polynucleotide encoding SCF is useful for producing SCF and useful in
CC   gene therapy. It is useful for treating disorders involving blood cells
CC   such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
```

```
CC   myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
CC   congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
CC   disseminated fungus disease, Fulminating septicemia, malaria, vitamin B12
CC   and folic acid deficiency, pyridoxine deficiency, and hypopigmentation
CC   disorders such as piebaldism and vitiligo
XX
SQ   Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              |||||||||||||||||||
Db         19 GAAAAAAAAAAAAAAAAAA 1


RESULT 1029
AAF89092
ID   AAF89092 standard; DNA; 20 BP.
XX
AC   AAF89092;
XX
DT   13-JUL-2001  (first entry)
XX
DE   Mammalian stem cell factor PCR primer SEQ ID NO: 33.
XX
KW   Human; rat; mammal; stem cell factor; SCF; cell growth stimulation;
KW   gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia;
KW   neurological damage; intestinal damage; infertility; AIDS; SCID;
KW   severe combined immunodeficiency; PCR primer; ss.
XX
OS   Mammalia.
XX
PN   US6207802-B1.
XX
PD   27-MAR-2001.
XX
PF   09-NOV-1994;   94US-00336728.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   01-OCT-1990;   90US-00589701.
PR   25-NOV-1992;   92US-00982255.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Zsebo KM,  Bosselman RA,  Suggs SV,  Martin FH;
XX
DR   WPI; 2001-353108/37.
XX
PT   Novel isolated non-human mammalian stem cell factor polypeptide
PT   stimulating growth of early hematopoietic progenitor cells, useful for
PT   treating aplastic anemia, lymphoma, Letterer-Siwe disease, Kala azar,
PT   sarcoidosis.
XX
PS   Example 3; Fig 12C; 209pp; English.
XX
CC   The present invention provides the protein and coding sequences of
CC   mammalian stem cell factors (SCFs). These are capable of stimulating the
CC   growth of early haematopoietic progenitor cells, neural stem cells and
CC   primordial germ stem cells. The sequences are useful in the treatment of
CC   leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal
CC   nocturnal haemoglobinuria, malaria, pigmentation disorders, neurological
CC   and intestinal damage, infertility, AIDS and severe combined
CC   immunodeficiency (SCID). The present sequence is primer used to amplify
CC   an SCF in the exemplification of the invention
XX
SQ   Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTA 19


RESULT 1030
AAF89093/c
ID   AAF89093 standard; DNA; 20 BP.
XX
AC   AAF89093;
XX
DT   13-JUL-2001  (first entry)
XX
DE   Mammalian stem cell factor PCR primer SEQ ID NO: 34.
XX
KW   Human; rat; mammal; stem cell factor; SCF; cell growth stimulation;
KW   gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia;
KW   neurological damage; intestinal damage; infertility; AIDS; SCID;
KW   severe combined immunodeficiency; PCR primer; ss.
XX
OS   Mammalia.
XX
PN   US6207802-B1.
XX
PD   27-MAR-2001.
XX
PF   09-NOV-1994;   94US-00336728.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   01-OCT-1990;   90US-00589701.
PR   25-NOV-1992;   92US-00982255.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Zsebo KM,  Bosselman RA,  Suggs SV,  Martin FH;
XX
DR   WPI; 2001-353108/37.
XX
PT   Novel isolated non-human mammalian stem cell factor polypeptide
PT   stimulating growth of early hematopoietic progenitor cells, useful for
PT   treating aplastic anemia, lymphoma, Letterer-Siwe disease, Kala azar,
PT   sarcoidosis.
XX
PS   Example 3; Fig 12C; 209pp; English.
XX
CC   The present invention provides the protein and coding sequences of
CC   mammalian stem cell factors (SCFs). These are capable of stimulating the
CC   growth of early haematopoietic progenitor cells, neural stem cells and
CC   primordial germ stem cells. The sequences are useful in the treatment of
CC   leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal
CC   nocturnal haemoglobinuria, malaria, pigmentation disorders, neurological
CC   and intestinal damage, infertility, AIDS and severe combined
CC   immunodeficiency (SCID). The present sequence is primer used to amplify
CC   an SCF in the exemplification of the invention
XX
SQ   Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              |||||||||||||||||||
Db         19 GAAAAAAAAAAAAAAAAAA 1


RESULT 1031
AAS05714/c
ID   AAS05714 standard; DNA; 20 BP.
```

```
XX
AC   AAS05714;
XX
DT   07-SEP-2001  (first entry)
XX
DE   Aminopurine substituted region of an RP-TFO.
XX
KW   reverse phase triplex forming oligonucleotide; RP-TFO;
KW   protected nucleic acid sequence; PNAS; single nucleotide polymorphism;
KW   SNP; short tandem repeat; cancer; Factor V Leiden SNP; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /label= OTHER
FT                   /note= "A is aminopurine substituted"
FT   modified_base   3
FT                   /*tag=  b
FT                   /label= OTHER
FT                   /note= "A is aminopurine substituted"
FT   modified_base   5
FT                   /*tag=  c
FT                   /label= OTHER
FT                   /note= "A is aminopurine substituted"
FT   Modified_base   7
FT                   /*tag=  d
FT                   /label= OTHER
FT                   /note= "A is aminopurine substituted"
FT   modified_base   9
FT                   /*tag=  f
FT                   /label= OTHER
FT                   /note= "A is aminopurine substituted"
FT   modified_base   11
FT                   /*tag=  g
FT                   /label= OTHER
FT                   /note= "A is aminopurine substituted"
FT   modified_base   13
FT                   /*tag=  g
FT                   /label= OTHER
FT                   /note= "A is aminopurine substituted"
FT   modified_base   15
FT                   /*tag=  h
FT                   /label= OTHER
FT                   /note= "A is aminopurine sustituted"
FT   modified_base   16
FT                   /*tag=  i
FT                   /label= OTHER
FT                   /note= "A is aminopurine substituted"
FT   modified_base   17
FT                   /*tag=  j
FT                   /label= OTHER
FT                   /note= "Other= Hypoxanthine or Inosine"
FT   modified_base   18
FT                   /*tag=  k
FT                   /label= OTHER
FT                   /note= "A is aminopurine substituted"
FT   modified_base   20
FT                   /*tag=  l
FT                   /label= OTHER
FT                   /note= "A is aminopurine substituted"
XX
PN   WO200132929-A1.
XX
PD   10-MAY-2001.
XX
PF   03-NOV-2000; 2000WO-US030534.
XX
PR   03-NOV-1999;   99US-0163356P.
PR   03-NOV-1999;   99US-0163416P.
PR   21-DEC-1999;   99US-0171348P.
PR   07-JUL-2000; 2000US-0216579P.
XX
PA   (CYGE-) CYGENE INC.
PA   (OSTE/) OSTE C C.
XX
PI   Oste CC,  Ramberg ER;
XX
DR   WPI; 2001-343488/36.
XX
PT   Analyzing target nucleic acid sequences, useful for population genetics,
PT   drug development and diagnosing cancer, comprises hybridizing triple
PT   forming oligonucleotide and probe to target sequence.
XX
PS   Example 2; Page 66; 141pp; English.
XX
CC   The sequence is a second reverse phase triplex forming oligonucleotide,
CC   RP-TFO (3' to the SNP) used to analyse Factor V Leiden SNP using the
CC   method of the invention. The invention relates to analysing target
CC   nucleic acid sequences comprising restricting isolated DNA, hybridising
CC   at least one triplex forming oligonucleotide (TFO), adding a 3' to 5'
CC   exonuclease to form a protected nucleic acid sequence (PNAS) tail
CC   structure, hybridising the captured structure with a single nucleotide
CC   polymorphisms (SNP) identification probe and determining the SNP score.
CC   The methods can be used for analysing target nucleic acid sequences,
CC   especially genomic DNA sequences, to determine if they contain SNPs or
CC   short tandem repeats (STRs). The methods can be used to detect SNPs for
CC   use in population genetics, drug development, forensics, cancer, genetic
CC   disease research, genomic analysis, diagnostics and therapeutics in
CC   humans, plants and animals
XX
SQ   Sequence 20 BP; 19 A; 0 C; 0 G; 0 T; 0 U; 1 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
                ||| |||||||||||||||
Db         20 TTTNTTTTTTTTTTTTTTT 1


RESULT 1032
AAS05715
ID   AAS05715 standard; DNA; 20 BP.
XX
AC   AAS05715;
XX
DT   07-SEP-2001  (first entry)
XX
DE   8-aminopurine substituted region of an RP-TFO.
XX
KW   reverse phase triplex forming oligonucleotide; RP-TFO;
KW   protected nucleic acid sequence; PNAS; single nucleotide polymorphism;
KW   SNP; short tandem repeat; cancer; Factor V Leiden SNP; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   17
FT                   /*tag=  a
FT                   /label= OTHER
FT                   /note= "Other= Hypoxanthine or Inosine"
XX
PN   WO200132929-A1.
XX
PD   10-MAY-2001.
XX
PF   03-NOV-2000; 2000WO-US030534.
XX
PR   03-NOV-1999;   99US-0163356P.
PR   03-NOV-1999;   99US-0163416P.
PR   21-DEC-1999;   99US-0171348P.
PR   07-JUL-2000; 2000US-0216579P.
XX
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```
PA   (CYGE-) CYGENE INC.
PA   (OSTE/) OSTE C C.
XX
PI   Oste CC,  Ramberg ER;
XX
DR   WPI; 2001-343488/36.
XX
PT   Analyzing target nucleic acid sequences, useful for population genetics,
PT   drug development and diagnosing cancer, comprises hybridizing triple
PT   forming oligonucleotide and probe to target sequence.
XX
PS   Example 2; Page 66; 141pp; English.
XX
CC   The sequence is a second reverse phase triplex forming oligonucleotide,
CC   RP-TFO (3' to the SNP) used to analyse Factor V Leiden SNP using the
CC   method of the invention. The invention relates to analysing target
CC   nucleic acid sequences comprising restricting isolated DNA, hybridising
CC   at least one triplex forming oligonucleotide (TFO), adding a 3' to 5'
CC   exonuclease to form a protected nucleic acid sequence (PNAS) tail
CC   structure, hybridising the captured structure with a single nucleotide
CC   polymorphisms (SNP) identification probe and determining the SNP score.
CC   The methods can be used for analysing target nucleic acid sequences,
CC   especially genomic DNA sequences, to determine if they contain SNPs or
CC   short tandem repeats (STRs). The methods can be used to detect SNPs for
CC   use in population genetics, drug development, forensics, cancer, genetic
CC   disease research, genomic analysis, diagnostics and therapeutics in
CC   humans, plants and animals
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 1 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||| |||
Db          1 TTTTTTTTTTTTTTTTNTTT 20


RESULT 1033
AAH23891/c
ID   AAH23891 standard; DNA; 20 BP.
XX
AC   AAH23891;
XX
DT   07-AUG-2001  (first entry)
XX
DE   Human SCF (stem cell factor) cDNA universal PCR primer 220-11.
XX
KW   Human; stem cell factor; SCF; early haematopoietic progenitor cell;
KW   blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
KW   anaemia; Kala azar; septicaemia; malaria; hypopigmentation disorder;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6204363-B1.
XX
PD   20-MAR-2001.
XX
PF   25-NOV-1992;   92US-00982255.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   01-OCT-1990;   90US-00589701.
PR   10-APR-1991;   91US-00684535.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Zsebo KM,  Bosselman RA,  Suggs SV,  Martin FH;
XX
DR   WPI; 2001-256683/26.
XX
PT   New stem cell factor polypeptides and their analogs which stimulate
PT   growth of early hematopoietic progenitors, useful for treating aplastic
PT   anemia, carcinoma, multiple myeloma, vitiligo, kala azar, Hodgkin's
PT   disease.
XX
PS   Example 3; Fig 12C; 166pp; English.
XX
CC   The present sequence for universal PCR primer 220-11 is 1 of 8 universal
CC   oligonucleotides (AAH23888-AAH23895) used in the isolation of the human
CC   SCF (stem cell factor) cDNA sequence. The present invention relates to
CC   novel stem cell factors (AAB73561-AAB73568, AAB73571-AAB73576) and the
CC   polynucleotides encoding them. SCF stimulate primitive progenitor cells
CC   including early haematopoietic progenitor cells. The invention also
CC   describes SCF peptides (AAB73578-AAB73597) and the oligonucleotides
CC   (AAH23859-AAH23887) used in the isolation of human and rat SCF sequences.
CC   The polynucleotide encoding SCF is useful for producing SCF and useful in
CC   gene therapy. It is useful for treating disorders involving blood cells
CC   such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
CC   myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
CC   congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
CC   disseminated fungus disease, Fulminating septicaemia, malaria, vitamin
CC   B12 and folic acid deficiency, pyridoxine deficiency, and
CC   hypopigmentation disorders such as piebaldism and vitiligo
XX
SQ   Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              |||||||||||||||||||
Db         19 GAAAAAAAAAAAAAAAAAA 1


RESULT 1034
AAH23890
ID   AAH23890 standard; DNA; 20 BP.
XX
AC   AAH23890;
XX
DT   07-AUG-2001  (first entry)
XX
DE   Human SCF (stem cell factor) cDNA universal PCR primer 220-7.
XX
KW   Human; stem cell factor; SCF; early haematopoietic progenitor cell;
KW   blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
KW   anaemia; Kala azar; septicaemia; malaria; hypopigmentation disorder;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6204363-B1.
XX
PD   20-MAR-2001.
XX
PF   25-NOV-1992;   92US-00982255.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   01-OCT-1990;   90US-00589701.
PR   10-APR-1991;   91US-00684535.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Zsebo KM,  Bosselman RA,  Suggs SV,  Martin FH;
XX
DR   WPI; 2001-256683/26.
XX
PT   New stem cell factor polypeptides and their analogs which stimulate
PT   growth of early hematopoietic progenitors, useful for treating aplastic
```

```
PT   anemia, carcinoma, multiple myeloma, vitiligo, kala azar, Hodgkin's
PT   disease.
XX
PS   Example 3; Fig 12C; 166pp; English.
XX
CC   The present sequence for universal PCR primer 220-7 is 1 of 8 universal
CC   oligonucleotides (AAH23888-AAH23895) used in the isolation of the human
CC   SCF (stem cell factor) cDNA sequence. The present invention relates to
CC   novel stem cell factors (AAB73561-AAB73568, AAB73571-AAB73576) and the
CC   polynucleotides encoding them. SCF stimulate primitive progenitor cells
CC   including early haematopoietic progenitor cells. The invention also
CC   describes SCF peptides (AAB73578-AAB73597) and the oligonucleotides
CC   (AAH23859-AAH23887) used in the isolation of human and rat SCF sequences.
CC   The polynucleotide encoding SCF is useful for producing SCF and useful in
CC   gene therapy. It is useful for treating disorders involving blood cells
CC   such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
CC   myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
CC   congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
CC   disseminated fungus disease, Fulminating septicaemia, malaria, vitamin
CC   B12 and folic acid deficiency, pyridoxine deficiency, and
CC   hypopigmentation disorders such as piebaldism and vitiligo
XX
SQ   Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTA 19


RESULT 1035
AAS04213
ID   AAS04213 standard; DNA; 20 BP.
XX
AC   AAS04213;
XX
DT   29-AUG-2001  (first entry)
XX
DE   Human SCF (stem cell factor) cDNA universal PCR primer 220-7.
XX
KW   Human; stem cell factor; SCF; early haematopoietic progenitor cell;
KW   blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
KW   anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6218148-B1.
XX
PD   17-APR-2001.
XX
PF   21-DEC-1993;   93US-00172329.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   01-OCT-1990;   90US-00589701.
PR   25-NOV-1992;   92US-00982255.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Zsebo KM,  Bosselman RA,  Suggs SV,  Martin FH;
XX
DR   WPI; 2001-281051/29.
XX
PT   Isolated DNA sequence, encoding polypeptide product useful for
PT   stimulating growth of early hematopoietic progenitor cells.
XX
PS   Example 3; Fig 12C; 167pp; English.
XX
CC   The present sequence for universal PCR primer 220-7 is 1 of 8 universal
CC   oligonucleotides (AAS04211-AAS04218) used in the isolation of the human
CC   SCF (stem cell factor) cDNA sequence. The present invention relates to
CC   novel stem cell factors (AAU02761-AAU02767, AAU02770-AAU02775, AAU02797)
CC   and the polynucleotides encoding them. SCF stimulate primitive progenitor
CC   cells including early haematopoietic progenitor cells. The invention also
CC   describes SCF peptides (AAU02777-AAU02794) and the oligonucleotides
CC   (AAS04182-AAS04210) used in the isolation of human and rat SCF sequences.
CC   The polynucleotide encoding SCF is useful for producing SCF and useful in
CC   gene therapy. It is useful for treating disorders involving blood cells
CC   such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
CC   myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
CC   congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
CC   disseminated fungus disease, Fulminating septicemia, malaria, vitamin B12
CC   and folic acid deficiency, pyridoxine deficiency, and hypopigmentation
CC   disorders such as piebaldism and vitiligo
XX
SQ   Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTA 19


RESULT 1036
AAS04214/c
ID   AAS04214 standard; DNA; 20 BP.
XX
AC   AAS04214;
XX
DT   29-AUG-2001  (first entry)
XX
DE   Human SCF (stem cell factor) cDNA universal PCR primer 220-11.
XX
KW   Human; stem cell factor; SCF; early haematopoietic progenitor cell;
KW   blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
KW   anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6218148-B1.
XX
PD   17-APR-2001.
XX
PF   21-DEC-1993;   93US-00172329.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   01-OCT-1990;   90US-00589701.
PR   25-NOV-1992;   92US-00982255.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Zsebo KM,  Bosselman RA,  Suggs SV,  Martin FH;
XX
DR   WPI; 2001-281051/29.
XX
PT   Isolated DNA sequence, encoding polypeptide product useful for
PT   stimulating growth of early hematopoietic progenitor cells.
XX
PS   Example 3; Fig 12C; 167pp; English.
XX
CC   The present sequence for universal PCR primer 220-11 is 1 of 8 universal
CC   oligonucleotides (AAS04211-AAS04218) used in the isolation of the human
CC   SCF (stem cell factor) cDNA sequence. The present invention relates to
CC   novel stem cell factors (AAU02761-AAU02767, AAU02770-AAU02775, AAU02797)
CC   and the polynucleotides encoding them. SCF stimulate primitive progenitor
```

CC cells including early haematopoietic progenitor cells. The invention also
CC describes SCF peptides (AAU02777-AAU02794) and the oligonucleotides
CC (AAS04182-AAS04210) used in the isolation of human and rat SCF sequences.
CC The polynucleotide encoding SCF is useful for producing SCF and useful in
CC gene therapy. It is useful for treating disorders involving blood cells
CC such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
CC myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
CC congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
CC disseminated fungus disease, Fulminating septicemia, malaria, vitamin B12
CC and folic acid deficiency, pyridoxine deficiency, and hypopigmentation
CC disorders such as piebaldism and vitiligo
XX
SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAAAAAAAAA 2803
||||||||||||||||||||
Db 19 GAAAAAAAAAAAAAAAAAA 1

RESULT 1037
AAS10449/c
ID AAS10449 standard; DNA; 20 BP.
XX
AC AAS10449;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human stem cell factor (SCF) cDNA universal PCR primer 220-11.
XX
KW Human; stem cell factor; SCF; haematopoietic progenitor cell;
KW blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency;
KW hypopigmentation disorder; viral disorder; AIDS; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN US6248319-B1.
XX
PD 19-JUN-2001.
XX
PF 24-MAY-1995; 95US-00449653.
XX
PR 16-OCT-1989; 89US-00422383.
PR 11-JUN-1990; 90US-00537198.
PR 24-AUG-1990; 90US-00573616.
PR 01-OCT-1990; 90US-00589701.
PR 10-APR-1991; 91US-00684535.
PR 25-NOV-1992; 92US-00982255.
PR 21-DEC-1993; 93US-00172329.
XX
PA (ZSEB/) ZSEBO K M.
PA (BOSS/) BOSSELMAN R A.
PA (SUGG/) SUGGS S V.
PA (MART/) MARTIN F H.
XX
PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX
DR WPI; 2001-407312/43.
XX
PT Increasing the number of early hematopoietic progenitor cells in the
PT peripheral blood useful for the treatment of blood disorders including
PT Hodgkin's disease comprises the administration of human stem cell factor.
XX
PS Example 3; Fig 12C; 210pp; English.
XX
CC The present sequence for universal PCR primer 220-11 is 1 of 19 PCR
CC primers (AAS10435-AAS10453) used to amplify various portions of the human
CC SCF cDNA sequence. The sequence is described in an invention relating to
CC novel stem cell factors, the polynucleotides encoding them and methods
CC for producing the stem cell factors. The methods involve increasing the
CC number of early haematopoietic progenitor cells in human peripheral blood
CC by administering a haematopoietically effective human stem cell factor
CC polypeptide. The methods are useful for the treatment of blood disorders,
CC including myelofibrosis, myelosclerosis, osteopetrosis, metastatic
CC carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease,
CC lymphoma, Gaucher's disease, Niemann-Pick disease, refractory anaemia,
CC malaria, vitamin B12 and folic acid deficiency, hypopigmentation
CC disorders i.e. piebaldism and viral induced disorders, including AIDS
XX
SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAAAAAAAAA 2803
||||||||||||||||||||
Db 19 GAAAAAAAAAAAAAAAAAA 1

RESULT 1038
AAS10448
ID AAS10448 standard; DNA; 20 BP.
XX
AC AAS10448;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human stem cell factor (SCF) cDNA universal PCR primer 220-7.
XX
KW Human; stem cell factor; SCF; haematopoietic progenitor cell;
KW blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency;
KW hypopigmentation disorder; viral disorder; AIDS; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN US6248319-B1.
XX
PD 19-JUN-2001.
XX
PF 24-MAY-1995; 95US-00449653.
XX
PR 16-OCT-1989; 89US-00422383.
PR 11-JUN-1990; 90US-00537198.
PR 24-AUG-1990; 90US-00573616.
PR 01-OCT-1990; 90US-00589701.
PR 10-APR-1991; 91US-00684535.
PR 25-NOV-1992; 92US-00982255.
PR 21-DEC-1993; 93US-00172329.
XX
PA (ZSEB/) ZSEBO K M.
PA (BOSS/) BOSSELMAN R A.
PA (SUGG/) SUGGS S V.
PA (MART/) MARTIN F H.
XX
PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX
DR WPI; 2001-407312/43.
XX
PT Increasing the number of early hematopoietic progenitor cells in the
PT peripheral blood useful for the treatment of blood disorders including
PT Hodgkin's disease comprises the administration of human stem cell factor.
XX
PS Example 3; Fig 12C; 210pp; English.
XX
CC The present sequence for universal PCR primer 220-7 is 1 of 19 PCR
CC primers (AAS10435-AAS10453) used to amplify various portions of the human
CC SCF cDNA sequence. The sequence is described in an invention relating to
CC novel stem cell factors, the polynucleotides encoding them and methods
CC for producing the stem cell factors. The methods involve increasing the
CC number of early haematopoietic progenitor cells in human peripheral blood
CC by administering a haematopoietically effective human stem cell factor
CC polypeptide. The methods are useful for the treatment of blood disorders,

CC including myelofibrosis, myelosclerosis, osteopetrosis, metastatic
CC carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease,
CC lymphoma, Gaucher's disease, Niemann-Pick disease, refractory anaemia,
CC malaria, vitamin B12 and folic acid deficiency, hypopigmentation
CC disorders i.e. piebaldism and viral induced disorders, including AIDS
XX
SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2169 TTTTTTTTTTTTTTTTTTA 2187
||||||||||||||||||||
Db 1 TTTTTTTTTTTTTTTTTTA 19

RESULT 1039
AAD35465
ID AAD35465 standard; DNA; 20 BP.
XX
AC AAD35465;
XX
DT 25-JUL-2002 (first entry)
XX
DE Rat SCF 5' cDNA amplifying PCR primer, 220-7.
XX
KW Rat; stem cell factor; SCF protein; leucopaenia; thrombocytopaenia;
KW anaemia; myelosuppression; nerve damage; myeloproliferative disorder;
KW infertility; neoplasia; myelofibrosis; myelosclerosis; osteopetrosis;
KW metastatic carcinoma; acute leukaemia; multiple myeloma; sarcoidosis;
KW Hodgkin's disease; lymphoma; Gaucher's disease; Niemann-Pick disease;
KW Letterer-Siwe disease; refractory erythroblastic anaemia; Kala azar;
KW Di Guglielmo syndrome; congestive splenomegaly; splenic pancytopaenia;
KW disseminated fungus disease; Fulminating septicaemia; piebaldism; AIDS;
KW acquired immune deficiency syndrome; malaria; military tuberculosis;
KW pyridoxine deficiency; vitamin B12 deficiency; folic acid deficiency;
KW Diamond Blackfan anaemia; hypopigmentation disorder; vitiligo; PCR;
KW primer; ss.
XX
OS Rattus sp.
XX
PN US2002018763-A1.
XX
PD 14-FEB-2002.
XX
PF 12-JAN-1998; 98US-00005243.
XX
PR 24-MAY-1995; 95US-00449653.
XX
PA (ZSEB/) ZSEBO K M.
PA (BOSS/) BOSSELMAN R A.
PA (SUGG/) SUGGS S V.
PA (MART/) MARTIN F H.
XX
PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX
DR WPI; 2002-350789/38.
XX
PT Novel non-naturally-occurring stem cell factor polypeptide, useful for
PT treating leucopenia, thrombocytopenia, anemia and for enhancing
PT engraftment of bone marrow during transplantation in a mammal.
XX
PS Example 3; Fig 12C; 217pp; English.
XX
CC The present invention relates to novel non-naturally-occurring stem cell
CC factor (SCF) polypeptides having an amino acid sequence sufficiently
CC duplicative of that of naturally-occurring SCF to allow possession of
CC haematopoietic biological activity of naturally occurring SCF. Sequences
CC of the invention are useful for treating leucopaenia, thrombocytopaenia,
CC anaemia and for enhancing bone marrow recovery in treatment of radiation,
CC engraftment of bone marrow during transplantation in mammals and chemical
CC or chemotherapeutic induced bone marrow aplasia or myelosuppression. They
CC are also useful for treating acquired immune deficiency in a human, nerve
CC damage, neoplasia, infertility, myeloproliferative disorder, intestinal
CC damage in a mammal. SCF sequences are useful for preparing biologically
CC active polymer polypeptide adduct, for enhancing transfection of early
CC haematopoietic progenitor cells with a gene, and transfer of a gene into
CC a mammal. They are useful for treating myelofibrosis, myelosclerosis,
CC osteopetrosis, metastatic carcinoma, acute leukaemia, multiple myeloma,
CC Hodgkin's disease, lymphoma, Gaucher's disease, Niemann-Pick disease,
CC Letterer-Siwe disease, refractory erythroblastic anaemia, Di Guglielmo
CC syndrome, congestive splenomegaly, Kala azar, sarcoidosis, primary
CC splenic pancytopaenia, disseminated fungus disease, malaria, military
CC tuberculosis, Fulminating septicaemia, pyridoxine deficiency, vitamin B12
CC and folic acid deficiency, Diamond Blackfan anaemia, hypopigmentation
CC disorders such as piebaldism, AIDS (acquired immune deficiency syndrome)
CC and vitiligo. The present sequence is a PCR primer which is used for
CC amplifying the 5' end of rat SCF cDNA. This sequence is used in the
CC exemplification of the invention
XX
SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2169 TTTTTTTTTTTTTTTTTTA 2187
||||||||||||||||||||
Db 1 TTTTTTTTTTTTTTTTTTA 19

RESULT 1040
AAD35466/c
ID AAD35466 standard; DNA; 20 BP.
XX
AC AAD35466;
XX
DT 25-JUL-2002 (first entry)
XX
DE Rat SCF 5' cDNA amplifying PCR primer, 220-11.
XX
KW Rat; stem cell factor; SCF protein; leucopaenia; thrombocytopaenia;
KW anaemia; myelosuppression; nerve damage; myeloproliferative disorder;
KW infertility; neoplasia; myelofibrosis; myelosclerosis; osteopetrosis;
KW metastatic carcinoma; acute leukaemia; multiple myeloma; sarcoidosis;
KW Hodgkin's disease; lymphoma; Gaucher's disease; Niemann-Pick disease;
KW Letterer-Siwe disease; refractory erythroblastic anaemia; Kala azar;
KW Di Guglielmo syndrome; congestive splenomegaly; splenic pancytopaenia;
KW disseminated fungus disease; Fulminating septicaemia; piebaldism; AIDS;
KW acquired immune deficiency syndrome; malaria; military tuberculosis;
KW pyridoxine deficiency; vitamin B12 deficiency; folic acid deficiency;
KW Diamond Blackfan anaemia; hypopigmentation disorder; vitiligo; PCR;
KW primer; ss.
XX
OS Rattus sp.
XX
PN US2002018763-A1.
XX
PD 14-FEB-2002.
XX
PF 12-JAN-1998; 98US-00005243.
XX
PR 24-MAY-1995; 95US-00449653.
XX
PA (ZSEB/) ZSEBO K M.
PA (BOSS/) BOSSELMAN R A.
PA (SUGG/) SUGGS S V.
PA (MART/) MARTIN F H.
XX
PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX
DR WPI; 2002-350789/38.
XX
PT Novel non-naturally-occurring stem cell factor polypeptide, useful for
PT treating leucopenia, thrombocytopenia, anemia and for enhancing

```
PT   engraftment of bone marrow during transplantation in a mammal.
XX
PS   Example 3; Fig 12C; 217pp; English.
XX
CC   The present invention relates to novel non-naturally-occurring stem cell
CC   factor (SCF) polypeptides having an amino acid sequence sufficiently
CC   duplicative of that of naturally-occurring SCF to allow possession of
CC   haematopoietic biological activity of naturally occurring SCF. Sequences
CC   of the invention are useful for treating leucopaenia, thrombocytopaenia,
CC   anaemia and for enhancing bone marrow recovery in treatment of radiation,
CC   engraftment of bone marrow during transplantation in mammals and chemical
CC   or chemotherapeutic induced bone marrow aplasia or myelosuppression. They
CC   are also useful for treating acquired immune deficiency in a human, nerve
CC   damage, neoplasia, infertility, myeloproliferative disorder, intestinal
CC   damage in a mammal. SCF sequences are useful for preparing biologically
CC   active polymer polypeptide adduct, for enhancing transfection of early
CC   haematopoietic progenitor cells with a gene, and transfer of a gene into
CC   a mammal. They are useful for treating myelofibrosis, myelosclerosis,
CC   osteopetrosis, metastatic carcinoma, acute leukaemia, multiple myeloma,
CC   Hodgkin's disease, lymphoma, Gaucher's disease, Niemann-Pick disease,
CC   Letterer-Siwe disease, refractory erythroblastic anaemia, Di Guglielmo
CC   syndrome, congestive splenomegaly, Kala azar, sarcoidosis, primary
CC   splenic pancytopaenia, disseminated fungus disease, malaria, military
CC   tuberculosis, Fulminating septicaemia, pyridoxine deficiency, vitamin B12
CC   and folic acid deficiency, Diamond Blackfan anaemia, hypopigmentation
CC   disorders such as piebaldism, AIDS (acquired immune deficiency syndrome)
CC   and vitiligo. The present sequence is a PCR primer which is used for
CC   amplifying the 5' end of rat SCF cDNA. This sequence is used in the
CC   exemplification of the invention
XX
SQ   Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match              0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              |||||||||||||||||||
Db         19 GAAAAAAAAAAAAAAAAAA 1


RESULT 1041
ABS73849
ID   ABS73849 standard; DNA; 20 BP.
XX
AC   ABS73849;
XX
DT   05-DEC-2002  (first entry)
XX
DE   SCF universal oligonucleotide 220-7.
XX
KW   Stem cell factor; SCF; blood-forming system; blood cell disorder;
KW   haematopoietic system; metastatic carcinoma; acute leukaemia;
KW   multiple myeloma; Hodgkin's disease; lymphoma; malaria; vitiligo;
KW   refractory erythroblastic anaemia; miliary tuberculosis; cytostatic;
KW   disseminated fungus disease; haematopoietic; tuberculostatic;
KW   antianaemic; antifungal; antimalarial; dermatological; ss.
XX
OS   Synthetic.
XX
PN   EP1241258-A2.
XX
PD   18-SEP-2002.
XX
PF   04-OCT-1990; 2002EP-00008587.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   28-SEP-1990;   90WO-US005548.
PR   01-OCT-1990;   90US-00589701.
PR   04-OCT-1990;   90EP-00310899.
PR   04-OCT-1990;   95EP-00105391.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Zsebo KM,  Suggs SV,  Bosselman RA,  Martin FH;
XX
DR   WPI; 2002-684093/74.
XX
PT   Production of a human stem cell factor (SCF) polypeptide for treating
PT   disorders involving blood cells, such as leukemia, comprises culturing
PT   mammalian cells comprising non-human SCF promoter DNA linked to DNA
PT   encoding the human SCF.
XX
PS   Example 3; Fig 12C; 120pp; English.
XX
CC   The present invention relates to novel stem cell factors (SCFs),
CC   polynucleotide sequences encoding the SCFs, and methods of producing
CC   them. SCFs are involved in the blood-forming (haematopoietic) system in
CC   mammals, particularly humans. The method of the invention is useful for
CC   the production of human SCF. The stem cell factors are useful to treat
CC   disorders involving blood cells e.g. metastatic carcinoma, acute
CC   leukaemia, multiple myeloma, Hodgkin's disease, lymphoma, refractory
CC   erythroblastic anaemia, miliary tuberculosis, disseminated fungus
CC   disease, malaria, and vitiligo. The present sequence representing a
CC   universal oligonucleotide for SCF DNA is used in the examples of the
CC   present invention
XX
SQ   Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match              0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTA 19


RESULT 1042
ABS73850/c
ID   ABS73850 standard; DNA; 20 BP.
XX
AC   ABS73850;
XX
DT   05-DEC-2002  (first entry)
XX
DE   SCF universal oligonucleotide 220-11.
XX
KW   Stem cell factor; SCF; blood-forming system; blood cell disorder;
KW   haematopoietic system; metastatic carcinoma; acute leukaemia;
KW   multiple myeloma; Hodgkin's disease; lymphoma; malaria; vitiligo;
KW   refractory erythroblastic anaemia; miliary tuberculosis; cytostatic;
KW   disseminated fungus disease; haematopoietic; tuberculostatic;
KW   antianaemic; antifungal; antimalarial; dermatological; ss.
XX
OS   Synthetic.
XX
PN   EP1241258-A2.
XX
PD   18-SEP-2002.
XX
PF   04-OCT-1990; 2002EP-00008587.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   28-SEP-1990;   90WO-US005548.
PR   01-OCT-1990;   90US-00589701.
PR   04-OCT-1990;   90EP-00310899.
PR   04-OCT-1990;   95EP-00105391.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Zsebo KM,  Suggs SV,  Bosselman RA,  Martin FH;
```

XX
DR WPI; 2002-684093/74.
XX
PT Production of a human stem cell factor (SCF) polypeptide for treating
PT disorders involving blood cells, such as leukemia, comprises culturing
PT mammalian cells comprising non-human SCF promoter DNA linked to DNA
PT encoding the human SCF.
XX
PS Example 3; Fig 12C; 120pp; English.
XX
CC The present invention relates to novel stem cell factors (SCFs),
CC polynucleotide sequences encoding the SCFs, and methods of producing
CC them. SCFs are involved in the blood-forming (haematopoietic) system in
CC mammals, particularly humans. The method of the invention is useful for
CC the production of human SCF. The stem cell factors are useful to treat
CC disorders involving blood cells e.g. metastatic carcinoma, acute
CC leukaemia, multiple myeloma, Hodgkin's disease, lymphoma, refractory
CC erythroblastic anaemia, miliary tuberculosis, disseminated fungus
CC disease, malaria, and vitiligo. The present sequence representing a
CC universal oligonucleotide for SCF DNA is used in the examples of the
CC present invention
XX
SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAAAAAAAAA 2803
||||||||||||||||||||
Db 19 GAAAAAAAAAAAAAAAAAA 1

RESULT 1043
ABZ88618
ID ABZ88618 standard; DNA; 20 BP.
XX
AC ABZ88618;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 3860; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 19 A; 1 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 2 AAAAAAAAAAAAAAAAAAA 20

RESULT 1044
ABZ88618/c
ID ABZ88618 standard; DNA; 20 BP.
XX
AC ABZ88618;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 3860; 872pp; English.

```
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 19 A; 1 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTT 2


RESULT 1045
ABZ89678/c
ID   ABZ89678 standard; DNA; 20 BP.
XX
AC   ABZ89678;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 4920; 872pp; English.
```

```
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 19 A; 0 C; 0 G; 0 T; 0 U; 1 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              ||||||||  ||||||||||
Db         20 TTTTTTTTNTTTTTTTTTT 1


RESULT 1046
ABZ89677/c
ID   ABZ89677 standard; DNA; 20 BP.
XX
AC   ABZ89677;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 4919; 872pp; English.
```

```
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 19 A; 0 C; 0 G; 0 T; 0 U; 1 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              || |||||||||||||||||
Db         20 TTNTTTTTTTTTTTTTTTT 1


RESULT 1047
ABZ89085
ID   ABZ89085 standard; DNA; 20 BP.
XX
AC   ABZ89085;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 4327; 872pp; English.
```

```
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 19 A; 0 C; 1 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              |||||||||||||||||||
Db          2 GAAAAAAAAAAAAAAAAAA 20


RESULT 1048
ABZ88694/c
ID   ABZ88694 standard; DNA; 20 BP.
XX
AC   ABZ88694;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 3936; 872pp; English.
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XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 17 A; 0 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAA 2188
             ||||||||||||||||||| 
Db         20 TTTTTTTTTTTTTTTTTAA 2

RESULT 1049
ABZ89240/c
ID   ABZ89240 standard; DNA; 20 BP.
XX
AC   ABZ89240;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 4482; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 18 A; 1 C; 0 G; 1 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTA 2187
             ||||||||||||||||||| 
Db         20 TTTTTTTTTTTTTTTTTTA 2

RESULT 1050
ADE52462/c
ID   ADE52462 standard; DNA; 20 BP.
XX
AC   ADE52462;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stem cell factor (SCF) related DNA #33.
XX
KW   Stem cell factor; SCF; haematopoietic activity; infertility;
KW   intestinal damage; myeloproliferative disorder; leucopenia;
KW   thrombocytopenia; anaemia; bone marrow transplant; immune deficiency;
KW   neoplasia; nerve damage; osteoporosis; metastatic carcinoma; leukaemia;
KW   miliary tuberculosis; haematopoietic progenitor cell; ss.
XX
OS   Synthetic.
XX
PN   US2002031491-A1.
XX
PD   14-MAR-2002.
XX
PF   31-DEC-1998;   98US-00224683.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   01-OCT-1990;   90US-00589701.
PR   10-APR-1991;   91US-00684535.
PR   25-NOV-1992;   92US-00982255.
PR   21-DEC-1993;   93US-00172329.
PR   24-MAY-1995;   95US-00449653.
PR   12-JAN-1998;   98US-00005893.
XX
PA   (ZSEB/) ZSEBO K M.
PA   (BOSS/) BOSSELMAN R A.
PA   (SUGG/) SUGGS S V.
PA   (MART/) MARTIN F H.
XX
PI   Zsebo KM,  Bosselman RA,  Suggs SV,  Martin FH;
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XX
DR   WPI; 2003-851459/79.
XX
PT   New non-natural stem cell factor, useful for treating e.g. leucopenia or
PT   immune deficiency, also related nucleic acid and antibodies.
XX
PS   Disclosure; SEQ ID NO 34; 217pp; English.
XX
CC   The invention relates to stem cell factor (SCF) polypeptides with
CC   haematopoietic activity and the polynucleotides encoding them. The
CC   polypeptides are used for treating infertility, intestinal damage,
CC   myeloproliferative disorders, leucopenia, thrombocytopenia or anaemia,
CC   for improving engraftment of bone marrow transplants, for enhancing bone
CC   marrow recovery after radiotherapy or chemotherapy and in treatment of
CC   immune deficiency, neoplasia, nerve damage, osteoporosis, metastatic
CC   carcinoma, leukaemia and miliary tuberculosis. The SCF polypeptides are
CC   also used to expand haematopoietic progenitor cells for transplantation
CC   and to prepare such cells for transfection with a gene. The SCF
CC   polynucleotides can be used for recombinant expression of the
CC   polypeptides and also as probes for mapping of the SCF gene, for
CC   identifying SCF-related diseases and as a marker for neighbouring genes.
CC   Antibodies raised against the polypeptides are useful in diagnosis and to
CC   remove SCF from blood. This sequence represents SCF related DNA of the
CC   invention.
XX
SQ   Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              |||||||||||||||||||
Db         19 GAAAAAAAAAAAAAAAAAA 1


RESULT 1051
ADE52461
ID   ADE52461 standard; DNA; 20 BP.
XX
AC   ADE52461;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stem cell factor (SCF) related DNA #32.
XX
KW   Stem cell factor; SCF; haematopoietic activity; infertility;
KW   intestinal damage; myeloproliferative disorder; leucopenia;
KW   thrombocytopenia; anaemia; bone marrow transplant; immune deficiency;
KW   neoplasia; nerve damage; osteoporosis; metastatic carcinoma; leukaemia;
KW   miliary tuberculosis; haematopoietic progenitor cell; ss.
XX
OS   Synthetic.
XX
PN   US2002031491-A1.
XX
PD   14-MAR-2002.
XX
PF   31-DEC-1998;   98US-00224683.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   01-OCT-1990;   90US-00589701.
PR   10-APR-1991;   91US-00684535.
PR   25-NOV-1992;   92US-00982255.
PR   21-DEC-1993;   93US-00172329.
PR   24-MAY-1995;   95US-00449653.
PR   12-JAN-1998;   98US-00005893.
XX
PA   (ZSEB/) ZSEBO K M.
PA   (BOSS/) BOSSELMAN R A.
PA   (SUGG/) SUGGS S V.
PA   (MART/) MARTIN F H.
XX
PI   Zsebo KM,  Bosselman RA,  Suggs SV,  Martin FH;
XX
DR   WPI; 2003-851459/79.
XX
PT   New non-natural stem cell factor, useful for treating e.g. leucopenia or
PT   immune deficiency, also related nucleic acid and antibodies.
XX
PS   Disclosure; SEQ ID NO 33; 217pp; English.
XX
CC   The invention relates to stem cell factor (SCF) polypeptides with
CC   haematopoietic activity and the polynucleotides encoding them. The
CC   polypeptides are used for treating infertility, intestinal damage,
CC   myeloproliferative disorders, leucopenia, thrombocytopenia or anaemia,
CC   for improving engraftment of bone marrow transplants, for enhancing bone
CC   marrow recovery after radiotherapy or chemotherapy and in treatment of
CC   immune deficiency, neoplasia, nerve damage, osteoporosis, metastatic
CC   carcinoma, leukaemia and miliary tuberculosis. The SCF polypeptides are
CC   also used to expand haematopoietic progenitor cells for transplantation
CC   and to prepare such cells for transfection with a gene. The SCF
CC   polynucleotides can be used for recombinant expression of the
CC   polypeptides and also as probes for mapping of the SCF gene, for
CC   identifying SCF-related diseases and as a marker for neighbouring genes.
CC   Antibodies raised against the polypeptides are useful in diagnosis and to
CC   remove SCF from blood. This sequence represents SCF related DNA of the
CC   invention.
XX
SQ   Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTA 19


RESULT 1052
AAX26973/c
ID   AAX26973 standard; cDNA; 21 BP.
XX
AC   AAX26973;
XX
DT   25-JUN-1999  (first entry)
XX
DE   Primer used to reverse transcribe mammaglobin RNA.
XX
KW   Human; mammary-specific protein; mammaglobin; antigen; vaccine;
KW   mammaglobin-expressing cancer; breast cancer;
KW   autologous tumor lymphocyte; diagnosis; marker; primer; ss.
XX
OS   Synthetic.
XX
PN   WO9914230-A1.
XX
PD   25-MAR-1999.
XX
PF   18-SEP-1998;   98WO-US017991.
XX
PR   18-SEP-1997;   97US-00933149.
XX
PA   (UNIW ) UNIV WASHINGTON.
XX
PI   Watson MA,  Fleming TP;
XX
DR   WPI; 1999-244021/20.
XX
PT   Mammaglobin, secreted protein overexpressed in breast cancer.
XX
PS   Example 2; Page 55; 60pp; English.
XX
```

```
CC   The present primer was used to reverse transcribe RNA encoding a human
CC   mammary-specific protein, designated mammaglobin. The specification
CC   describes a protein comprising a mammaglobin antigen that is recognized
CC   by B and/or Tc cells specific for the natural, secreted and glycosylated
CC   form of mammaglobin polypeptide. This protein, or recombinant vectors
CC   that express it, are used in vaccines for treating mammaglobin-
CC   expressing cancers, specifically of the breast. Such cancers can also be
CC   treated using autologous tumor lymphocytes activated ex vivo with an
CC   mammaglobin antigen, then returned to the patient. Expression of
CC   mammaglobin is elevated in 27% of stage I primary breast cancers, so it
CC   represents a marker useful for diagnosis of this disease
XX
SQ   Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 7.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         21 AAAAAAAAAAAAAAAAAAA 3


RESULT 1053
AAZ44350/c
ID   AAZ44350 standard; DNA; 21 BP.
XX
AC   AAZ44350;
XX
DT   04-APR-2000  (first entry)
XX
DE   Protein kinase inhibiting primer #12.
XX
KW   Antimicrobial; cytostatic; immunosuppressive; protein kinase;
KW   prophylactic; therapy; treatment; cancer; autoimmune disease;
KW   pathogenic microorganism; primer; ss.
XX
OS   Unidentified.
XX
PN   US5998596-A.
XX
PD   07-DEC-1999.
XX
PF   04-APR-1995;   95US-00416214.
XX
PR   04-APR-1995;   95US-00416214.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Bergan R,  Neckers L;
XX
DR   WPI; 2000-104623/09.
XX
PT   Oligonucleotides inhibiting protein kinase, useful for treating diseases
PT   such as cancer and autoimmune disease.
XX
PS   Example 8; Col 27-28; 26pp; English.
XX
CC   This invention describes novel purified aptameric oligonucleotides which
CC   have antimicrobial, cytostatic and immunosuppressive activity. The
CC   oligonucleotides are useful for binding to and preventing or inhibiting
CC   the biological function of a protein kinase or a target molecule and for
CC   detecting the presence or absence of a target molecule in biological
CC   samples. The oligonucleotides are also useful for prophylactic and
CC   therapeutic treatment of diseases such as cancer, autoimmune diseases and
CC   diseases caused by pathogenic microorganisms. This sequence represents a
CC   primer used in the method of the invention
XX
SQ   Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 7.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         21 AAAAAAAAAAAAAAAAAAA 3


RESULT 1054
AAF99707/c
ID   AAF99707 standard; DNA; 21 BP.
XX
AC   AAF99707;
XX
DT   12-JUN-2001  (first entry)
XX
DE   Immunostimulatory nucleic acid #823.
XX
KW   Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW   immunostimulatory; tumour; viral infection; bacterial infection;
KW   fungal infection; parasitic infection; cancer; asthma;
KW   infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS   Synthetic.
XX
PN   WO200122972-A2.
XX
PD   05-APR-2001.
XX
PF   25-SEP-2000; 2000WO-US026383.
XX
PR   25-SEP-1999;   99US-0156113P.
PR   27-SEP-1999;   99US-0156135P.
PR   23-AUG-2000; 2000US-0227436P.
XX
PA   (IOWA ) UNIV IOWA RES FOUND.
PA   (COLE-) COLEY PHARM GMBH.
XX
PI   Krieg AM,  Schetter C,  Vollmer J;
XX
DR   WPI; 2001-273485/28.
XX
PT   Vaccinating against tumors, infectious diseases, allergies and asthma
PT   using immunostimulatory Py-rich and TG nucleic acids.
XX
PS   Claim 101; Page 56; 338pp; English.
XX
CC   The present invention relates to a method for stimulating an immune
CC   response. The method comprises administering an immunostimulatory nucleic
CC   acid to a non-rodent subject in sufficient quantity to stimulate an
CC   immune response. The present sequence is one such immunostimulatory
CC   nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC   (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC   against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC   and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC   haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC   staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC   also useful for preventing cancer, asthma, infectious disease, allergy or
CC   immune deficiency. The present sequence can also be used to redirect a
CC   Th2 to a Th1 immune response and to activate immune cells. Note: the
CC   present sequence may have a phosphorothioate backbone
XX
SQ   Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 7.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         21 AAAAAAAAAAAAAAAAAAA 3


RESULT 1055
AAH42480/c
```

```
ID   AAH42480 standard; DNA; 21 BP.
XX
AC   AAH42480;
XX
DT   01-OCT-2001  (first entry)
XX
DE   Oligonucleotide used to produce branched chain compounds.
XX
KW   Branched chain compound; nucleic acid synthesis; primer extension;
KW   reverse transcription; nucleic acid hybridization;
KW   nucleic acid amplification; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /note= "NH2-C6 attached"
FT   modified_base   4
FT                   /*tag=  b
FT                   /note= "NH2-C6 attached"
FT   misc_feature    6. .7
FT                   /*tag=  c
FT                   /note= "branch present"
XX
PN   EP1111068-A1.
XX
PD   27-JUN-2001.
XX
PF   21-DEC-1999;   99EP-00125484.
XX
PR   21-DEC-1999;   99EP-00125484.
XX
PA   (LION-) LION BIOSCIENCE AG.
PA   (VBCG-) VBC GENOMICS GMBH.
XX
PI   Schmidt W,  Hiller R,  Huber M,  Mueller M;
XX
DR   WPI; 2001-466959/51.
XX
PT   Branched compounds useful in e.g. nucleic acid synthesis reaction
PT   comprises nucleic acid moieties optionally extended by a polymerase.
XX
PS   Example 1; Page 10; 31pp; English.
XX
CC   The specification describes branched compounds containing nucleic acid
CC   moieties optionally extended by a polymerase. The branched chain
CC   compounds of the invention are used in nucleic acid synthesis reaction,
CC   primer extension reaction, reverse transcription reaction of RNA into
CC   DNA, nucleic acid hybridization experiment (for identifying sequence of a
CC   nucleic acid), and nucleic acid amplification experiment (for analysing
CC   the expression pattern of genes). The compounds are also used in solid-
CC   phase enzymatic reactions. The present sequence was used in the course of
CC   the invention to produce branched chain compounds
XX
SQ   Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 7.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         21 AAAAAAAAAAAAAAAAAAA 3


RESULT 1056
ABS78428/c
ID   ABS78428 standard; DNA; 21 BP.
XX
AC   ABS78428;
XX
DT   13-DEC-2002  (first entry)
XX
DE   Angiogenesis inhibitory oligonucleotide #912.
XX
KW   Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW   tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW   diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW   corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW   rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW   plaque neovascularisation; telangiectasia; haemophiliac joint;
KW   angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW   scleroderma; hypertrophic scar.
XX
OS   Synthetic.
XX
PN   WO200253141-A2.
XX
PD   11-JUL-2002.
XX
PF   14-DEC-2001; 2001WO-US048458.
XX
PR   14-DEC-2000; 2000US-0255534P.
XX
PA   (COLE-) COLEY PHARM GROUP INC.
XX
PI   Bratzler RL;
XX
DR   WPI; 2002-566690/60.
XX
PT   Inhibiting angiogenesis in a subject, involves administering at least one
PT   antiangiogenic nucleic acid molecule to the subject.
XX
PS   Claim 2; Page 35; 276pp; English.
XX
CC   The invention relates to inhibiting angiogenesis in a subject, comprising
CC   administering at least one antiangiogenic nucleic acid molecule. Also
CC   included is a kit comprising a first container housing the antiangiogenic
CC   nucleic acids, and instructions for administering them to a subject
CC   having a condition characterised by unwanted angiogenesis. The method is
CC   useful for inhibiting angiogenesis associated with solid tumour growth,
CC   tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC   diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC   corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC   rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC   neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,
CC   wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC   hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC   acid of the invention
XX
SQ   Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 7.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         21 AAAAAAAAAAAAAAAAAAA 3


RESULT 1057
ABL39404/c
ID   ABL39404 standard; DNA; 21 BP.
XX
AC   ABL39404;
XX
DT   16-APR-2002  (first entry)
XX
DE   Immunostimulatory nucleic acid SEQ ID NO: 840.
XX
KW   Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
KW   angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.
XX
OS   Synthetic.
```

```
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .21
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate backbone"
XX
PN   WO200197843-A2.
XX
PD   27-DEC-2001.
XX
PF   22-JUN-2001; 2001WO-US020154.
XX
PR   22-JUN-2000; 2000US-0213346P.
XX
PA   (IOWA ) UNIV IOWA RES FOUND.
XX
PI   Weiner G,  Hartmann G;
XX
DR   WPI; 2002-154611/20.
XX
PT   Treating or preventing cancer, such as basal cell carcinoma, comprises
PT   administering immunostimulatory nucleic acids that induce expression of
PT   cell surface antigens and antibodies to a subject having or at risk of
PT   developing cancer.
XX
PS   Disclosure; Page 309; 312pp; English.
XX
CC   The present invention relates to methods for treating or preventing
CC   cancer, involving administering to a subject having or at risk of
CC   developing cancer immunostimulatory nucleic acids that induce expression
CC   of cell surface antigens and antibodies. The methods are useful for
CC   treating or preventing cancer such as basal cell carcinoma, bladder
CC   cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC   breast cancer, cervical cancer, colon and rectum cancer, connective
CC   tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx
CC   cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
CC   Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC   cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC   cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC   present sequence is an immunostimulatory oligonucleotide described in the
CC   exemplification of the invention
XX
SQ   Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 7.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         21 AAAAAAAAAAAAAAAAAAA 3


RESULT 1058
AAD51323/c
ID   AAD51323 standard; DNA; 21 BP.
XX
AC   AAD51323;
XX
DT   16-APR-2003  (first entry)
XX
DE   Regular oligo dT primer used to illustrate the method of the invention.
XX
KW   Laminitis; viral disease; vaccine; bacterial disease; primer; epistaxis;
KW   gastritis; gastric ulcer; respiratory ailment; fracture; joint disease;
KW   musculoskeletal damage; ss.
XX
OS   Unidentified.
XX
PN   WO200290579-A1.
XX
PD   14-NOV-2002.
XX
PF   03-MAY-2002; 2002WO-AU000553.
XX
PR   04-MAY-2001; 2001AU-00004809.
PR   29-JUN-2001; 2001US-00896941.
XX
PA   (GENO-) GENOMICS RES PARTNERS PTY LTD.
XX
PI   Brandon RB;
XX
DR   WPI; 2003-120558/11.
XX
PT   Assessing condition e.g. athletic ability, stage of disease, presence of
PT   drugs, response to exercise, response to vaccines, therapies, nutritional
PT   states, of performance animal involves analyzing nucleic acid expression.
XX
PS   Disclosure; Page 46; 87pp; English.
XX
CC   The invention relates to a method for assessing a condition of a
CC   performance animal. The method involves determining in sample abundance
CC   of expressed target nucleic acid; transmitting digital sample signal to
CC   remote diagnostic server; processing digital sample signal at remotely
CC   located database to correlate digital signal with digital information and
CC   returning report of particular condition of animal. The method is useful
CC   for assessing a condition of a performance animal preferably human, dog
CC   or camel. The condition can be an athletic ability and a condition that
CC   enhances, hinders, impedes or does not change an expected ability of the
CC   performance animal; and also normal, pre-clinical, overt progress and/or
CC   stage of disease, undiagnosed of unclassified conditions, presence of
CC   drugs, response to exercise, response to vaccines, therapies, nutritional
CC   states and response to environmental conditions. Diseases assessed by the
CC   invention include laminitis, lameless, viral or bacterial disease,
CC   gastritis, gastric ulcers, respiratory ailments, fractures, epistaxis,
CC   musculoskeletal damage or disorders and joint diseases. The present
CC   sequence is a primer used to illustrate the method of the invention
XX
SQ   Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 7.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         21 AAAAAAAAAAAAAAAAAAA 3


RESULT 1059
ACH03246/c
ID   ACH03246 standard; DNA; 21 BP.
XX
AC   ACH03246;
XX
DT   25-SEP-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #881.
XX
KW   Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW   antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW   psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW   inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS   Synthetic.
XX
PN   US2003050268-A1.
XX
PD   13-MAR-2003.
XX
PF   29-MAR-2002; 2002US-00112653.
XX
PR   29-MAR-2001; 2001US-0279642P.
XX
PA   (KRIE/) KRIEG A M.
```

```
PA   (BERG/) BERG D J.
XX
PI   Krieg AM,  Berg DJ;
XX
DR   WPI; 2003-521815/49.
XX
PT   Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT   allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT   disease by administering an immunostimulatory nucleic acid.
XX
PS   Disclosure; Page 33; 229pp; English.
XX
CC   The invention describes a method of treating non-allergic inflammatory
CC   disease comprising administering to a subject having or at risk of
CC   developing a non-allergic inflammatory disease an immunostimulatory
CC   nucleic acid for prevention or treatment of the disease. The method is
CC   useful for treating non-allergic inflammatory diseases, such as
CC   psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC   inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC   This sequence represents an immunostimulatory nucleic acid
XX
SQ   Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 7.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         21 AAAAAAAAAAAAAAAAAAA 3


RESULT 1060
ADB37209/c
ID   ADB37209 standard; DNA; 21 BP.
XX
AC   ADB37209;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #823.
XX
KW   ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW   hypo-responsive subject; immunostimulatory.
XX
OS   Synthetic.
XX
PN   US2003087848-A1.
XX
PD   08-MAY-2003.
XX
PF   02-FEB-2001; 2001US-00776479.
XX
PR   03-FEB-2000; 2000US-0179991P.
XX
PA   (BRAT/) BRATZLER R L.
PA   (PETE/) PETERSEN D M.
PA   (FOUR/) FOURON Y.
XX
PI   Bratzler RL,  Petersen DM,  Fouron Y;
XX
DR   WPI; 2003-657977/62.
XX
PT   Treating and/or preventing allergy or asthma using an immunostimulatory
PT   nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS   Disclosure; Page 17; 221pp; English.
XX
CC   The invention relates to a method of treating or preventing allergy or
CC   asthma which comprises administering to a subject a poly-G nucleic acid
CC   in an aerosol formulation. The methods and compositions of the present
CC   invention are useful for diagnosing and/or treating asthma and allergy
CC   especially in a hypo-responsive subject. The present sequence represents
CC   an immunostimulatory nucleic acid of the invention.
XX
SQ   Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 7.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         21 AAAAAAAAAAAAAAAAAAA 3


RESULT 1061
AAQ90391
ID   AAQ90391 standard; DNA; 21 BP.
XX
AC   AAQ90391;
XX
DT   08-JAN-1996  (first entry)
XX
DE   CP-1 (synthetic DNA probe with 3'ribonucleoside terminal #2).
XX
KW   CP-1; HLA; dQa; 3' ribonucleoside; self-addressable electronic device;
KW   SAED; hybridisation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    21
FT                   /*tag=  a
FT                   /note= "3' ribonucleoside terminal"
XX
PN   WO9512808-A1.
XX
PD   11-MAY-1995.
XX
PF   26-OCT-1994;   94WO-US012270.
XX
PR   01-NOV-1993;   93US-00146504.
XX
PA   (NANO-) NANOGEN INC.
XX
PI   Heller MJ,  Tu E;
XX
DR   WPI; 1995-185870/24.
XX
PT   New self-addressable electronic devices - used for multi-step and
PT   multiplex reactions such as DNA hybridisation(s), clinical diagnostics
PT   and bio:polymer synthesis.
XX
PS   Example 1; Page 40; 86pp; English.
XX
CC   The sequences represented by, AAQ90390-90401 are synthetic DNA probes
CC   containing 3' ribonucleoside termini. The sequences shown in AAQ90402-15
CC   are synthetic DNA probes with 5' amino termini. These sequences were
CC   specific for the polymorphisms of HLA gene dQa. The sequences were used
CC   in the device of the invention. This is a self-addressable electronic
CC   device (SAED) that can be used to carry out multi-step and multiplex
CC   reactions, such as nucleic acid hybridisations. The advantages of this
CC   method are that these reactions can be carried out with complete and
CC   precise electronic control, and that the rate, specificity and
CC   sensitivity of these reactions are greatly improved at micro-locations
XX
SQ   Sequence 21 BP; 20 A; 0 C; 0 G; 0 T; 1 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 7.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19
```

```
RESULT 1062
AAT10743
ID   AAT10743 standard; RNA; 21 BP.
XX
AC   AAT10743;
XX
DT   09-SEP-1996  (first entry)
XX
DE   Oligonucleotide probe, CP-1.
XX
KW   Electronically self-addressable device; ED; electrode; current source;
KW   attachment layer; permeable; counterion; genetic typing; probe;
KW   detection; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   21
FT                   /*tag=  a
FT                   /note= "3'-ribonucleoside terminus"
XX
PN   WO9601836-A1.
XX
PD   25-JAN-1996.
XX
PF   05-JUL-1995;   95WO-US008570.
XX
PR   07-JUL-1994;   94US-00271882.
XX
PA   (NANO-) NANOGEN INC.
XX
PI   Heller MJ,  Tu E,  Evans GA,  Sosnowski RG;
XX
DR   WPI; 1996-097582/10.
XX
PT   Electronically self-addressable device - used for electronic control of,
PT   e.g. nucleic acid hybridisation.
XX
PS   Example 1; Page 60; 155pp; English.
XX
CC   The sequences given in AAT10742-67 are synthetic oligonucleotides which
CC   are used in the construction of the electronically self- addressable
CC   device (ED) of the invention. The ED comprises a substrate, an electrode
CC   or opt. a number of electrodes supported by the substrate, a current
CC   source operatively connected to the electrode and an attachment layer
CC   adjacent to the electrode which is permeable to a counterion but not
CC   permeable to a molecule capable of insulating or binding to the
CC   electrode. The attachment layer is capable of attaching a macromolecule.
CC   The ED is used for genetic typing and comprises a number of
CC   electronically addressable locations each comprising an electrode, and a
CC   binding entity, such as one of these probes, attached to each of the
CC   locations capable of detecting the presence of a genetic sequence
XX
SQ   Sequence 21 BP; 20 A; 0 C; 0 G; 0 T; 1 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 7.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 1063
AAX81302
ID   AAX81302 standard; DNA; 21 BP.
XX
AC   AAX81302;
XX
DT   20-AUG-1999  (first entry)
XX
DE   3' ribonucleoside oligonucleotide probe CP-1.
XX
KW   Microelectronic device; multi-step reaction; microscopic format;
KW   ion-permeable permeation layer; electrode; electrical control; transport;
KW   attachment; binding; DNA/RNA hybrid; probe; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        21
FT                   /*tag=  a
XX
PN   WO9929711-A1.
XX
PD   17-JUN-1999.
XX
PF   01-DEC-1998;   98WO-US025475.
XX
PR   05-DEC-1997;   97US-00986065.
XX
PA   (NANO-) NANOGEN INC.
XX
PI   Sosnowski RG,  Butler WF,  Tu E,  Nerenberg MI,  Heller MJ,  Edman CF;
XX
DR   WPI; 1999-385567/32.
XX
PT   New microelectronic device designed to carry out and control multi-step
PT   and multiplex molecular biological reactions in microscopic format.
XX
PS   Example 1; Page 89; 179pp; English.
XX
CC   The specification describes a self-addressable, self-assembling
CC   microelectronic device which is designed to actively carry out and
CC   control multi-step and multiplex molecular biological reactions in
CC   microscopic formats. A key aspect of this inventions is played by the ion
CC   -permeable permeation layer which overlies the electrode. This permeation
CC   layer allows attachment of nucleic acids to permit immobilization but
CC   also separates the attached oligonucleotides and hybridized target DNA
CC   sequences from the highly reactive electrochemical environment generated
CC   immediately at the electrode surface. The microelectronic device is
CC   designed and fabricated to actively carry out and control reactions such
CC   as nucleic acid hybridizations, antibody/antigen reactions, sample
CC   preparation, diagnostics and biopolymer synthesis. The device can
CC   electronically control the transport and attachment of specific binding
CC   entities, such as nucleic acids and polypeptides, to specific micro-
CC   locations. The device can subsequently control the transport and reaction
CC   of analytes or reactants at the addressed specific micro-locations. The
CC   device is able to concentrate analytes and reactants, remove non-
CC   specifically bound molecules, provide stringency control for DNA
CC   hybridization reactions and improve the detection of analytes. The
CC   present sequence represents a probe used to exemplify the invention
XX
SQ   Sequence 21 BP; 20 A; 0 C; 0 G; 0 T; 1 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 7.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 1064
AAQ75724
ID   AAQ75724 standard; DNA; 21 BP.
XX
AC   AAQ75724;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
```

```
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 4 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 7.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAA 2188
                ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTAA 19


RESULT 1065
AAQ75752/c
ID   AAQ75752 standard; DNA; 21 BP.
XX
AC   AAQ75752;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 7.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAA 2802
                ||||||||||||||||||
Db         19 TGAAAAAAAAAAAAAAAAA 1


RESULT 1066
AAQ75762/c
ID   AAQ75762 standard; DNA; 21 BP.
XX
AC   AAQ75762;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 7.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAA 2802
                ||||||||||||||||||
Db         19 TGAAAAAAAAAAAAAAAAA 1
```

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RESULT 1067
AAQ75719
ID   AAQ75719 standard; DNA; 21 BP.
XX
AC   AAQ75719;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 7.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAA 2188
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTAA 19


RESULT 1068
AAQ75730
ID   AAQ75730 standard; DNA; 21 BP.
XX
AC   AAQ75730;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 7.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAA 2188
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTAA 19


RESULT 1069
AAQ75763/c
ID   AAQ75763 standard; DNA; 21 BP.
XX
AC   AAQ75763;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
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SQ   Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 7.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||||
Db         19 TGAAAAAAAAAAAAAAAAA 1


RESULT 1070
AAQ75728
ID   AAQ75728 standard; DNA; 21 BP.
XX
AC   AAQ75728;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 3 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 7.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAA 2188
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTAA 19


RESULT 1071
AAQ75727
ID   AAQ75727 standard; DNA; 21 BP.
XX
AC   AAQ75727;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 7.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAA 2188
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTAA 19


RESULT 1072
AAQ75764/c
ID   AAQ75764 standard; DNA; 21 BP.
XX
AC   AAQ75764;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
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XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 7.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||||
Db         19 TGAAAAAAAAAAAAAAAAA 1


RESULT 1073
AAQ75722
ID   AAQ75722 standard; DNA; 21 BP.
XX
AC   AAQ75722;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 7.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAA 2188
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTAA 19


RESULT 1074
AAQ75723
ID   AAQ75723 standard; DNA; 21 BP.
XX
AC   AAQ75723;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 3 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 7.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAA 2188
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTAA 19


RESULT 1075
AAQ75760/c
ID   AAQ75760 standard; DNA; 21 BP.
XX
AC   AAQ75760;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
```

```
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 7.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAA 2802
                ||||||||||||||||||
Db         19 TGAAAAAAAAAAAAAAAAA 1


RESULT 1076
AAQ75751/c
ID   AAQ75751 standard; DNA; 21 BP.
XX
AC   AAQ75751;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 7.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAA 2802
                ||||||||||||||||||
Db         19 TGAAAAAAAAAAAAAAAAA 1


RESULT 1077
AAQ75754/c
ID   AAQ75754 standard; DNA; 21 BP.
XX
AC   AAQ75754;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 7.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAA 2802
                ||||||||||||||||||
Db         19 TGAAAAAAAAAAAAAAAAA 1


RESULT 1078
AAQ75759/c
ID   AAQ75759 standard; DNA; 21 BP.
XX
AC   AAQ75759;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
```

```
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match              0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 7.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||||
Db         19 TGAAAAAAAAAAAAAAAAA 1


RESULT 1079
AAQ75720
ID   AAQ75720 standard; DNA; 21 BP.
XX
AC   AAQ75720;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 3 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match              0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 7.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAA 2188
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTAA 19


RESULT 1080
AAQ75766/c
ID   AAQ75766 standard; DNA; 21 BP.
XX
AC   AAQ75766;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 3 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match              0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 7.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||||
Db         19 TGAAAAAAAAAAAAAAAAA 1


RESULT 1081
```

```
AAV35395
ID   AAV35395 standard; DNA; 21 BP.
XX
AC   AAV35395;
XX
DT   13-OCT-1998  (first entry)
XX
DE   HIV-1 gag protein DNA primer #8.
XX
KW   Hypervariable region; ENV protein; vaccinia virus; gag gene; retrovirus;
KW   vaccines; infection; protection; primer; ss.
XX
OS   Synthetic.
XX
PN   WO9822596-A1.
XX
PD   28-MAY-1998.
XX
PF   19-NOV-1997;   97WO-JP004216.
XX
PR   19-NOV-1996;   96JP-00323412.
XX
PA   (NINA-) JAPAN NAT INST INFECTIOUS DISEASES.
PA   (JAPG ) NIPPON ZEON KK.
XX
PI   Kojima A,  Kurata T,  Yasuda A;
XX
DR   WPI; 1998-312481/27.
XX
PT   Recombinant vaccinia virus containing fusion HIB gag gene - for
PT   production in host cells of gag protein for use as vaccine.
XX
PS   Example 1; Page 66; 84pp; Japanese.
XX
CC   AAV35388-V35414 are primers used in a method which results in a
CC   recombinant vaccinia virus comprising of a gag gene from a retrovirus
CC   such as HIV-1 or HIV-2, fused to a DNA fragment containing an epitope
CC   region (30-300 bases in length) of a retroviral gene other than the gag
CC   gene. The gag gene may be altered so as to produce a gag protein modified
CC   from the natural sequence by the addition, deletion or substitution of at
CC   least 1 amino acid residue. The fusion gene is inserted into a region of
CC   a vaccinia virus not essential to its propagation, to give a recombinant
CC   vaccinia virus vector which is used to transform a host cell (such as
CC   HeLa, Vero, VEF, rabbit kidney RK13 or human myeloma TK-143 cells). Upon
CC   culturing the host cell produces particulate structures containing the
CC   fusion gag protein. The recombinant vaccinia virus or the fusion gag
CC   protein particles may be used in the production of vaccines for
CC   protecting against infection with retroviruses such as HIV
XX
SQ   Sequence 21 BP; 19 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 7.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          3 AAAAAAAAAAAAAAAAAAA 21


RESULT 1082
AAV35395/c
ID   AAV35395 standard; DNA; 21 BP.
XX
AC   AAV35395;
XX
DT   13-OCT-1998  (first entry)
XX
DE   HIV-1 gag protein DNA primer #8.
XX
KW   Hypervariable region; ENV protein; vaccinia virus; gag gene; retrovirus;
KW   vaccines; infection; protection; primer; ss.
XX
OS   Synthetic.
XX
PN   WO9822596-A1.
XX
PD   28-MAY-1998.
XX
PF   19-NOV-1997;   97WO-JP004216.
XX
PR   19-NOV-1996;   96JP-00323412.
XX
PA   (NINA-) JAPAN NAT INST INFECTIOUS DISEASES.
PA   (JAPG ) NIPPON ZEON KK.
XX
PI   Kojima A,  Kurata T,  Yasuda A;
XX
DR   WPI; 1998-312481/27.
XX
PT   Recombinant vaccinia virus containing fusion HIB gag gene - for
PT   production in host cells of gag protein for use as vaccine.
XX
PS   Example 1; Page 66; 84pp; Japanese.
XX
CC   AAV35388-V35414 are primers used in a method which results in a
CC   recombinant vaccinia virus comprising of a gag gene from a retrovirus
CC   such as HIV-1 or HIV-2, fused to a DNA fragment containing an epitope
CC   region (30-300 bases in length) of a retroviral gene other than the gag
CC   gene. The gag gene may be altered so as to produce a gag protein modified
CC   from the natural sequence by the addition, deletion or substitution of at
CC   least 1 amino acid residue. The fusion gene is inserted into a region of
CC   a vaccinia virus not essential to its propagation, to give a recombinant
CC   vaccinia virus vector which is used to transform a host cell (such as
CC   HeLa, Vero, VEF, rabbit kidney RK13 or human myeloma TK-143 cells). Upon
CC   culturing the host cell produces particulate structures containing the
CC   fusion gag protein. The recombinant vaccinia virus or the fusion gag
CC   protein particles may be used in the production of vaccines for
CC   protecting against infection with retroviruses such as HIV
XX
SQ   Sequence 21 BP; 19 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 7.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db         21 TTTTTTTTTTTTTTTTTTT 3


RESULT 1083
AAQ64724
ID   AAQ64724 standard; cDNA to mRNA; 22 BP.
XX
AC   AAQ64724;
XX
DT   25-MAR-2003  (revised)
DT   04-JAN-1995  (first entry)
XX
DE   2',5'-linked tetraadenylate-anti(dT)18 oligonucleotide chimeric mol.
XX
KW   antisense; 2',5'-tetraadenylate; 2-5A dependent RNase activator;
KW   RNA cleavage; antiviral therapy; chimeric molecule; PKR;
KW   protein synthesis regulation; phosphorylation; eIF-2alpha;
KW   eukaryotic translation initiation factor; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .4
FT                   /*tag=  a
FT                   /label= 2',5'-linked_tetraadenylate
FT                   /note= "nucleotides linked through phosphodiester bonds
FT                   at hydroxyl groups of 2' and 5' carbons"
FT   misc_feature    4. .5
```

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FT                   /*tag=  b
FT                   /note= "the 2-5A moiety (*tag = a) and the antisense DNA
FT                   sequence (*tag = c) are linked by two 1,4-butanediol
FT                   molecules linked through phosphodiester bonds"
FT   misc_feature    5. .22
FT                   /*tag=  c
FT                   /note= "antisense region, complementary to oligo dT"
XX
PN   WO9409129-A2.
XX
PD   28-APR-1994.
XX
PF   20-OCT-1993;   93WO-US010103.
XX
PR   21-OCT-1992;   92US-00965666.
PR   17-SEP-1993;   93US-00123449.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA   (CLEV-) CLEVELAND CLINIC RES INST.
XX
PI   Torrence P,  Silverman R,  Maitra R,  Lesiak K;
XX
DR   WPI; 1994-151315/18.
XX
PT   Specific cleavage of RNA, useful partic. for treating viral infection,
PT   cancers, etc. - by using anti-sense oligo:nucleotide coupled to activator
PT   of 2-5A dependent RNase.
XX
PS   Example 9; Page 66; 86pp; English.
XX
CC   This sequence was used to determine whether 2-5A-antisense chimeric
CC   molecules are inhibitory to cell growth. The molecules AAQ64709, AAQ64711
CC   and AAQ64724 all lacked cytotoxicity. In the novel 2-5A-antisense
CC   oligonucleotide chimeric molecules, the antisense region targets the
CC   chimeric molecule to a particular region of RNA to be specifically
CC   cleaved and the 2',5'-linked tetraadenylate tail activates the 2-5A
CC   RNase. Typical applications are treatment of viral infections (esp. for
CC   cleavage of an RNA virus genome), cancer; leukaemia, cardiovascular
CC   disorders (e.g. restenosis after angioplasty), genetic disorders,
CC   osteoarthritis or rheumatoid arthritis. (Updated on 25-MAR-2003 to
CC   correct PN field.)
XX
SQ   Sequence 22 BP; 22 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 8e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 1084
AAF17413
ID   AAF17413 standard; DNA; 22 BP.
XX
AC   AAF17413;
XX
DT   09-MAR-2001  (first entry)
XX
DE   L1 cleavage site related sequence #3.
XX
KW   Retrotransposon; genetic defect; cystic fibrosis; ds.
XX
OS   Unidentified.
XX
PN   US6150160-A.
XX
PD   21-NOV-2000.
XX
PF   28-APR-1997;   97US-00847844.
XX
PR   16-NOV-1995;   95US-0006831P.
PR   15-NOV-1996;   96US-00749805.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
PA   (UYPE-) UNIV PENNSYLVANIA.
XX
PI   Moran JV,  Dombroski BA,  Kazazian HH,  Boeke JD;
XX
DR   WPI; 2001-060015/07.
XX
PT   DNAc comprising a promoter P and an L1 cassette sequence having a core
PT   retrotransposon element, useful for random insertion of a heterologous or
PT   homologous DNA sequence into a cell genome and for correcting genetic
PT   defects.
XX
PS   Disclosure; Fig 14; 87pp; English.
XX
CC   The present invention relates to DNA for a promoter and an L1 cassette
CC   sequence having a core retrotransposon element. The invention is useful
CC   for random insertion of a heterologous or homologous DNA sequence into a
CC   cell genome, and for correction of a genetic defect in the cell into
CC   which the insertion is made. Genetic defects which may be corrected
CC   includes cystic fibrosis, mutations in the dystrophin gene, genetic
CC   defects associated with blood clotting and other genetic defects
XX
SQ   Sequence 22 BP; 22 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 8e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 1085
AAT92356
ID   AAT92356 standard; DNA; 22 BP.
XX
AC   AAT92356;
XX
DT   26-JAN-1998  (first entry)
XX
DE   Amino modified oligodeoxyribonucleotide.
XX
KW   Amino modified oligodeoxyribonucleotide; oligonucleotide;
KW   achiral linker reagent; 5-(aminomethyl)-1,3-benzenedimethanol;
KW   N-flureseinyl-(5-aminomethyl)-1,3-benzenedimethanol;
KW   hybridisation probe; PCR primer; nucleic acid sequencing;
KW   affinity matrix; cloning recombinant DNA; in-vitro mutagenesis; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 11
FT                   /*tag=  a
FT                   /note= "n =  5-(aminomethyl)-1,3-benzenedimethanol"
FT   misc_difference 12
FT                   /*tag=  b
FT                   /note= "n =  5-(aminomethyl)-1,3-benzenedimethanol"
XX
PN   WO9705156-A1.
XX
PD   13-FEB-1997.
XX
PF   26-JUL-1996;   96WO-DK000330.
XX
PR   27-JUL-1995;   95DK-00000863.
XX
PA   (BEHR/) BEHRENS C.
PA   (PETE/) PETERSEN K H.
PA   (EGHO/) EGHOLM M.
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PA   (NIEL/) NIELSEN J.
PA   (DAHL/) DAHL O.
XX
PI   Behrens C,  Petersen KH,  Egholm M,  Nielsen J,  Dahl O;
XX
DR   WPI; 1997-145615/13.
XX
PT   New achiral linker reagents - useful for incorporation of multiple amino
PT   gps. or reporter gps. into oligo:nucleotide(s).
XX
PS   Disclosure; Page 20; 42pp; English.
XX
CC   Achiral linker reagents have been developed for the incorporation of
CC   multiple amino groups into oligonucleotides. The present sequence
CC   represents a modified oligodeoxyribonucleotide. The achiral linker
CC   reagents can be used for incorporation of multiple primary amino groups
CC   or reporter groups into oligonucleotides. They are compatible with
CC   conventional DNA synthesis following the phosphoramidite methodology, and
CC   can be incorporated in good yields. The linker reagents may be used for
CC   labelling of oligonucleotides. They may also be used for preparation of
CC   oligonucleotides, e.g. for use as hybridisation probes, for use as
CC   primers in the polymerase chain reaction or in nucleic acid sequencing
CC   reactions, for production of affinity matrices for purification of DNA
CC   binding proteins or other biomolecules, for production of affinity
CC   matrices for detection of nucleic acid sequences, for cloning recombinant
CC   DNA or for in-vitro mutagenesis
XX
SQ   Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 2 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 22;
  Best Local Similarity   90.5%;  Pred. No. 8e+02;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||  |||||||||
Db          1 TTTTTTTTTTNNTTTTTTTT 21


RESULT 1086
AAC62450/c
ID   AAC62450 standard; DNA; 23 BP.
XX
AC   AAC62450;
XX
DT   07-FEB-2001  (first entry)
XX
DE   Cleavage of nucleic acids from solid supports assay oligonucleotide #1.
XX
KW   Nucleic acid cleavage; solid support; DNA-RNA hybrid;
KW   affinity chromatography; sequencing; mutagenesis; DNA preparation;
KW   nucleic acid purification; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        23
FT                   /*tag=  a
XX
PN   WO200058329-A1.
XX
PD   05-OCT-2000.
XX
PF   28-MAR-2000; 2000WO-GB001190.
XX
PR   29-MAR-1999;   99GB-00007245.
XX
PA   (GOLD/) GOLDSBOROUGH A.
XX
DR   WPI; 2000-664908/64.
XX
PT   Detaching nucleic acid molecule comprising unconventional nucleotide
PT   incorporated at predetermined site from a solid support involves cleaving
PT   the nucleic acid molecule at the site of unconventional nucleotide.
XX
PS   Disclosure; Page 16; 47pp; English.
XX
CC   The present invention is concerned with the cleavage of nucleic acids
CC   from solid supports. This is carried out by adding a non-conventional
CC   nucleotide into the nucleic acid attached to the support, so that it is
CC   recognised and cleaved by a specific DNA glycosylase and the sequence is
CC   released. This is useful in many molecular biological procedures such as
CC   sequencing, in vitro amplifications, cDNA and template preparation, DNA-
CC   based assays, mutagenesis procedures, nucleic acid purification and
CC   affinity chromatography. The present sequence is an oligonucleotide used
CC   in assays to demonstrate the methods of the invention
XX
SQ   Sequence 23 BP; 0 A; 0 C; 0 G; 22 T; 1 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 8.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         23 AAAAAAAAAAAAAAAAAAA 5


RESULT 1087
AAC62451/c
ID   AAC62451 standard; RNA; 23 BP.
XX
AC   AAC62451;
XX
DT   07-FEB-2001  (first entry)
XX
DE   Cleavage of nucleic acids from solid supports assay oligonucleotide #2.
XX
KW   Nucleic acid cleavage; solid support; affinity chromatography;
KW   sequencing; mutagenesis; DNA preparation; nucleic acid purification; ss.
XX
OS   Synthetic.
XX
PN   WO200058329-A1.
XX
PD   05-OCT-2000.
XX
PF   28-MAR-2000; 2000WO-GB001190.
XX
PR   29-MAR-1999;   99GB-00007245.
XX
PA   (GOLD/) GOLDSBOROUGH A.
XX
DR   WPI; 2000-664908/64.
XX
PT   Detaching nucleic acid molecule comprising unconventional nucleotide
PT   incorporated at predetermined site from a solid support involves cleaving
PT   the nucleic acid molecule at the site of unconventional nucleotide.
XX
PS   Example 1; Page 32; 47pp; English.
XX
CC   The present invention is concerned with the cleavage of nucleic acids
CC   from solid supports. This is carried out by adding a non-conventional
CC   nucleotide into the nucleic acid attached to the support, so that it is
CC   recognised and cleaved by a specific DNA glycosylase and the sequence is
CC   released. This is useful in many molecular biological procedures such as
CC   sequencing, in vitro amplifications, cDNA and template preparation, DNA-
CC   based assays, mutagenesis procedures, nucleic acid purification and
CC   affinity chromatography. The present sequence is an oligonucleotide used
CC   in assays to demonstrate the methods of the invention
XX
SQ   Sequence 23 BP; 0 A; 0 C; 0 G; 0 T; 23 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 8.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

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Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         23 AAAAAAAAAAAAAAAAAAA 5


RESULT 1088
AAF16627/c
ID   AAF16627 standard; DNA; 23 BP.
XX
AC   AAF16627;
XX
DT   13-MAR-2001  (first entry)
XX
DE   Gastric acid production inhibiting oligonucleotide SEQ ID NO: 114.
XX
KW   Gastric acid disturbance; gastric reflux; gastritis; dyspepsia;
KW   stomach ulcer; duodenal ulcer; Helicobacter pylori; antisense;
KW   DNA-RNA hybrid; ss.
XX
OS   Homo sapiens.
XX
PN   WO200071164-A1.
XX
PD   30-NOV-2000.
XX
PF   24-MAY-2000; 2000WO-AU000498.
XX
PR   24-MAY-1999;   99AU-00000510.
XX
PA   (TACH/) TACHAS G.
XX
PI   Tachas G;
XX
DR   WPI; 2001-025093/03.
XX
PT   Treating gastric acid disturbance by administering an oligonucleotide
PT   which modulates the activity of a polypeptide involved in gastric acid
PT   production or secretion.
XX
PS   Example 3; Page 152; 164pp; English.
XX
CC   The present invention provides oligonucleotides, and methods for their
CC   use, which are useful in modulating the action of proteins involved in
CC   gastric acid production. The target protein is preferably the histamine
CC   H2 receptor or one of the proteins which form part of the gastric proton
CC   pump. The sequences and methods of the invention are useful in the
CC   treatment of gastric reflux, gastritis, dyspepsia, stomach ulcers,
CC   duodenal ulcers and other gastric acid disturbances, most of which are
CC   caused by Helicobacter pylori
XX
SQ   Sequence 23 BP; 1 A; 0 C; 0 G; 22 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 8.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         23 AAAAAAAAAAAAAAAAAAA 5


RESULT 1089
AAT33701
ID   AAT33701 standard; DNA; 23 BP.
XX
AC   AAT33701;
XX
DT   19-MAY-1997  (first entry)
XX
DE   Primer #1 for tissue or cell derived RNA.
XX
KW   PCR; polymerase chain reaction; primer; amplify; reverse-transcription;
KW   molecular indexing; class IIS restriction enzyme; cancer; causative gene;
KW   viral infection; hereditary disease; agricultural gene; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1
FT                   /*tag=  a
FT                   /note= "hydroxylated"
XX
PN   EP735144-A1.
XX
PD   02-OCT-1996.
XX
PF   26-MAR-1996;   96EP-00104817.
XX
PR   28-MAR-1995;   95JP-00069695.
PR   20-JUL-1995;   95JP-00184006.
PR   12-SEP-1995;   95JP-00234122.
XX
PA   (SHKJ ) RES DEV CORP JAPAN.
XX
PI   Kato K;
XX
DR   WPI; 1996-435619/44.
XX
PT   Molecular indexing of DNA - using restriction enzymes, PCR amplification
PT   and electrophoresis to analyse DNA fragments.
XX
PS   Claim 3; Page 14; 20pp; English.
XX
CC   AAT33701-T33703 represent amplification primers used in the reverse-
CC   transcription of tissue or cell derived mRNA, in the method of the
CC   invention. The method of the invention is a molecular indexing method,
CC   and comprises digesting the cDNA amplified by these sequences with a
CC   class IIS restriction enzyme. Each resultant cDNA fragment is then
CC   ligated to a biotinylated adaptor (selected from a pool of 64 adaptors
CC   cohesive to all possible overhangs), and digesting the products with two
CC   further class IIS restriction enzymes. These steps are repeated (but the
CC   enzyme used for the first step is different in each) to produce two
CC   further cDNA samples. The ligation samples are then recovered using
CC   streptavidin-coated paramagnetic beads, removing the strand complementary
CC   to an adaptor-primer. The adaptor primer and an anchored oligo-dT primer
CC   (such as this sequence) are then used to amplify the cDNA samples. The
CC   amplified products are separated, and the sizes of the fragments obtained
CC   is recorded. The method can be used for the analysis and diagnosis or
CC   diseases such as cancers or viral infections, for the search and
CC   isolation of the genes of physiologically active substances that are
CC   potential pharmaceuticals, or causative genes of hereditary diseases, as
CC   well as for the isolation of genes for improving agricultural products.
CC   Using this method, it is possible to classify (index) DNA into groups in
CC   a short period of time without duplication
XX
SQ   Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 8.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTT 2181
              |||||||||||||||||||
Db          4 TCCTTTTTTTTTTTTTTTT 22


RESULT 1090
AAV61554
ID   AAV61554 standard; DNA; 23 BP.
XX
AC   AAV61554;
XX
DT   08-DEC-1998  (first entry)
XX
DE   Double-anchored oligo-dT primer, used to synthesise apolipoprotein cDNA.
XX
```

```
KW   Primer; PCR; amplification; RT-PCR; quantitate; amount ratio; liver;
KW   apolipoprotein; kidney; ATAC-PCR; Adaptor-tagged Competitive PCR;
KW   gene expression; internal standard; calibration curve; ss.
XX
OS   Synthetic.
OS   Mus sp.
XX
PN   EP870842-A2.
XX
PD   14-OCT-1998.
XX
PF   07-APR-1998;   98EP-00302726.
XX
PR   07-APR-1997;   97JP-00088495.
XX
PA   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI   Kato K;
XX
DR   WPI; 1998-523164/45.
XX
PT   Determination of gene expression levels - using combinations of different
PT   cDNA samples tagged with different PCR adaptors.
XX
PS   Example 2; Page 9; 22pp; English.
XX
CC   The present sequence represents a primer which was used to synthesise
CC   Apolipoprotein cDNA in a RT-PCR reaction. This primer as well as primers
CC   AAV61555 and AAV61556 were added to both mouse liver-derived and mouse
CC   kidney-derived total RNA to generate single-stranded cDNA. These primers
CC   were used in the method of the invention to determine the amount ratio
CC   between a cDNA coding for mouse liver-derived Apolipoprotein and a cDNA
CC   that codes for the mouse kidney-derived Apolipoprotein by using Adaptor-
CC   tagged Competitive PCR (ATAC-PCR). This method allows gene expression to
CC   be quantitatively determined, and because internal standards are not
CC   required to prepare a calibration curve, it is a quicker and less
CC   laborious process
XX
SQ   Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 8.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTT 2181
              ||||||||||||||||||
Db          4 TCCTTTTTTTTTTTTTTTT 22


RESULT 1091
AAA29753
ID   AAA29753 standard; DNA; 23 BP.
XX
AC   AAA29753;
XX
DT   15-AUG-2000  (first entry)
XX
DE   Synthetic oligonucleotide #1.
XX
KW   Primer; destabilise non-specific duplex formation; PCR; detection;
KW   purification; sequencing; genetic marker; RACE; DNA synthesis; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   8
FT                   /*tag=  a
FT                   /mod_base= i
FT                   /note= "inosine"
FT   modified_base   18
FT                   /*tag=  b
FT                   /mod_base= i
FT                   /note= "inosine"
XX
PN   WO200020630-A1.
XX
PD   13-APR-2000.
XX
PF   06-OCT-1999;   99WO-CA000933.
XX
PR   07-OCT-1998;   98CA-02246623.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Pelletier J,  Das M;
XX
DR   WPI; 2000-328943/28.
XX
PT   Novel method of stabilizing duplex formation, or destabilizing non-
PT   specific duplex formation using primer containing modified nucleotide
PT   analogs, useful for preventing mispriming during PCR, RACE, DNA synthesis
PT   or sequencing.
XX
PS   Example 1; Page 25; 46pp; English.
XX
CC   The present invention describes a method for destabilising non-specific
CC   duplex formation, between an oligonucleotide and a target nucleic acid
CC   (NA), comprising incubating the target NA with a modified oligonucleotide
CC   (I) comprising a homopolymeric sequence having a modification which
CC   decreases or abrogates H-bonding between the modified oligonucleotide and
CC   the non-specific target NA. The modified oligonucleotide is used to
CC   improve discrimination between the targeted homopolymeric sequence and a
CC   non-homopolymeric target sequence. It is used to increase the proportion
CC   of full length cDNA clones for a library, to reduce mispriming during
CC   sequencing, 5' or 3' RACE (rapid amplification of cDNA ends) or DNA
CC   synthesis or to generate bona fide genetic markers. The present sequence
CC   represents an oligonucleotide which is used in the exemplification of the
CC   present invention
XX
SQ   Sequence 23 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 2 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 23;
  Best Local Similarity   90.5%;  Pred. No. 8.9e+02;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |||||||| |||
Db          1 TTTTTTNTTTTTTTTTNTTT 21


RESULT 1092
AAA08407
ID   AAA08407 standard; DNA; 23 BP.
XX
AC   AAA08407;
XX
DT   13-JUL-2000  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO:1.
XX
KW   Detection; primer; adapter; probe; hybridisation; gene cluster;
KW   fractionation; ss.
XX
OS   Synthetic.
XX
PN   JP2000055914-A.
XX
PD   25-FEB-2000.
XX
PF   13-AUG-1998;   98JP-00228944.
XX
PR   13-AUG-1998;   98JP-00228944.
XX
PA   (TAIS ) TAISHO PHARM CO LTD.
XX
DR   WPI; 2000-368733/32.
```

```
XX
PT   Gene detection method involves hybridizing probe opposite to objective
PT   gene out of fractional gene cluster.
XX
PS   Example 1; Page 9; 11pp; Japanese.
XX
CC   The present invention describes a gene detection method which comprises
CC   fractionating using a probe opposite to the objective gene which is
CC   hybridised out of fractioned gene cluster. The objective gene detected
CC   belongs to the group of objective genes contained in the sample. The
CC   method is used for gene detection by fractionation of cDNA by molecular
CC   index method using specific primer. It provides high detection
CC   sensitivity of objective gene. AAA08407 to AAA08414 represent
CC   oligonucleotides used in the exemplification of the present invention
XX
SQ   Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 8.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTT 2181
              ||||||||||||||||||
Db          4 TCCTTTTTTTTTTTTTTTT 22


RESULT 1093
ABA99682
ID   ABA99682 standard; DNA; 23 BP.
XX
AC   ABA99682;
XX
DT   31-MAY-2002  (first entry)
XX
DE   Murine osteoporosis/arthro-rheumatism associated gene PCR primer DAPA1.
XX
KW   Osteoporosis; murine; treatment; arthro-rheumatism; PCR; primer; ss.
XX
OS   Mus musculus.
XX
PN   JP2002051782-A.
XX
PD   19-FEB-2002.
XX
PF   09-AUG-2000; 2000JP-00241413.
XX
PR   09-AUG-2000; 2000JP-00241413.
XX
PA   (SANY ) SANKYO CO LTD.
XX
DR   WPI; 2002-288360/33.
XX
PT   Preventing or treating an agent for osteoporosis or arthro-rheumatism.
XX
PS   Example 2; Page 38; 44pp; Japanese.
XX
CC   This invention describes a novel method for testing the effect of a
CC   substance as a preventive or treating agent for osteoporosis or arthro-
CC   rheumatism. This sequence represents a PCR primer used in the
CC   amplification of a gene encoding a protein associated with osteoporosis
CC   or arthro-rheumatism which is described in the disclosure of the
CC   invention
XX
SQ   Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 8.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTT 2181
              ||||||||||||||||||
Db          4 TCCTTTTTTTTTTTTTTTT 22


RESULT 1094
ABK86172/c
ID   ABK86172 standard; DNA; 24 BP.
XX
AC   ABK86172;
XX
DT   24-SEP-2002  (first entry)
XX
DE   Oligo dT primer #4 used in method to study gene expression.
XX
KW   Oligo dT primer; gene expression analysis; primer; ss.
XX
OS   Synthetic.
XX
PN   WO200236828-A2.
XX
PD   10-MAY-2002.
XX
PF   01-NOV-2001; 2001WO-US045401.
XX
PR   01-NOV-2000; 2000US-0244933P.
XX
PA   (GENO-) GENOMIC SOLUTIONS INC.
XX
PI   Kane MD,  Dombkowski AA,  Nagel AC;
XX
DR   WPI; 2002-508123/54.
XX
PT   Identifying and characterizing gene expression in samples, for
PT   identifying mRNAs expressed at different levels, comprises employing an
PT   identimer having a oligo-dT primer of a specific sequence and a
PT   detectable marker at its 5' end.
XX
PS   Example 1; Page 15; 45pp; English.
XX
CC   The invention relates to systems for identification and characterisation
CC   of gene expression in one or more samples, comprising an identimer having
CC   a specific oligo-dT primer sequence, where the identimer comprises a
CC   detectable marker at its 5' end. The system is useful for identifying any
CC   or all genes expressed in a given in vivo or in vitro RNA sample, as well
CC   as the relative differences in mRNA between 2 or more samples, where
CC   desired, for supporting discovery of new genes, and for identifying mRNAs
CC   that are expressed at different levels between 2 or more samples. The new
CC   system or method addresses limitations of prior methods by comprising
CC   compositions and systems that incorporate new strategies where molecular
CC   or biochemical assay compositions and systems are linked to DNA or RNA
CC   sequence databases for optimal resource efficiency in assaying gene
CC   expression. The system has the following advantages over existing
CC   methods: (a) prior sequence information or clone library construction is
CC   not needed to enable the assay; (b) provides immediate sequence
CC   information in addition to information concerning changes or differences
CC   in mRNA level, to determine mRNA expression level and mRNA identification
CC   in one assay; (c) generates cDNA fragments from all mRNAs present in the
CC   sample for subsequent investigation by common molecular biology
CC   techniques; and (d) does not require prior knowledge of the sequence of
CC   the genome of the organism under investigation and can be employed in
CC   organisms lacking significant genomic sequence in formation. The present
CC   sequence represents an oligo dT primer used in the method of the
CC   invention
XX
SQ   Sequence 24 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 4 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||||||||||||
Db         24 AAAAAAAAAAAAAAAAAAA 6


RESULT 1095
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AAT68615
ID   AAT68615 standard; DNA; 24 BP.
XX
AC   AAT68615;
XX
DT   20-FEB-1998  (first entry)
XX
DE   DNA probe used in fingerprinting technique.
XX
KW   probe; screening; fingerprinting; assay; 3' termini; hybridisation; ss.
XX
OS   Synthetic.
XX
PN   EP778351-A2.
XX
PD   11-JUN-1997.
XX
PF   26-NOV-1996;   96EP-00118921.
XX
PR   30-NOV-1995;   95JP-00311949.
XX
PA   (HITA ) HITACHI LTD.
XX
PI   Kambara H,  Okano K,  Uematsu C;
XX
DR   WPI; 1997-300347/28.
XX
PT   Nucleic acid assay methods - based on restriction fragment length
PT   determination.
XX
PS   Example 1; Page 7; 21pp; English.
XX
CC   The present sequence is a DNA probe used in a novel method of analysis or
CC   assay for nucleotides, which comprises: (i) digesting DNA with a
CC   restriction enzyme; (ii) discriminating a difference in sequences of the
CC   DNA fragments obtained around the 3' termini with a DNA probe and
CC   extending the DNA probe by a complementary strand synthesis to
CC   fractionate the DNA fragments into groups; and (iii) measuring lengths of
CC   the DNA fragments which belong to the groups, or length of the extended
CC   DNA probe, and using the lengths obtained for the fragments around the 3'
CC   termini as fingerprints. Where polyA is present, the presence of
CC   recognition sequence GCG is critical for clarifying the terminal site,
CC   this is because the length of polyA cannot be controlled. The method is
CC   useful for assaying a large number of cDNA molecules or DNA fragments and
CC   for assaying long DNA sequences
XX
SQ   Sequence 24 BP; 0 A; 2 C; 1 G; 19 T; 0 U; 2 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 1096
ABL55130/c
ID   ABL55130 standard; DNA; 24 BP.
XX
AC   ABL55130;
XX
DT   31-MAY-2002  (first entry)
XX
DE   Human gonadotropin-releasing hormone 10 RT-PCR primer, SEQ ID NO:4.
XX
KW   Human; gonadotropin-releasing hormone 10; recombinant production; cancer;
KW   HIV infection; human immunodeficiency virus; gene therapy; cytostatic;
KW   anti-HIV; reverse transcription-PCR; RT-PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1325900-A.
XX
PD   12-DEC-2001.
XX
PF   31-MAY-2000; 2000CN-00116266.
XX
PR   31-MAY-2000; 2000CN-00116266.
XX
PA   (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-196660/26.
XX
PT   Polypeptide-human gonadotropin-releasing hormone 10 and polynucleotide
PT   encoding it.
XX
PS   Example 2; Page 17 (Disclosure); 32pp; Chinese.
XX
CC   The invention relates to human gonadotropin-releasing hormone 10
CC   (AAM49158) and to nucleic acids encoding it (ABL55128). The protein has a
CC   molecular weight of 10 kD. The invention also relates to a method for the
CC   recombinant production of the protein, an antagonist of the protein, and
CC   the use of the protein, gene and antagonist in therapeutic applications.
CC   Gonadotropin-releasing hormone 10 can be used in the treatment of a
CC   variety of diseases such as cancer and HIV (human immunodeficiency virus)
CC   infection. Sequences ABL55129-ABL55130 represent reverse transcription-
CC   PCR (RT-PCR) primers used in an exemplification of the invention to
CC   isolate human gonadotropin-releasing hormone 10 cDNA
XX
SQ   Sequence 24 BP; 1 A; 1 C; 3 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 1097
AAD34264
ID   AAD34264 standard; DNA; 25 BP.
XX
AC   AAD34264;
XX
DT   16-JUL-2002  (first entry)
XX
DE   Human CYP2D6 gene polymorphic site 385 detecting sense 5' oligo.
XX
KW   Human; cytochrome P450 2D6; CYP2D6; enzyme; detection; xenobiotic;
KW   ligase-based sequenced determination; drug metabolism; chromosome 22; ss.
XX
OS   Homo sapiens.
XX
PN   WO200218638-A2.
XX
PD   07-MAR-2002.
XX
PF   27-AUG-2001; 2001WO-IB001544.
XX
PR   30-AUG-2000; 2000GB-00021286.
XX
PA   (GEMI-) GEMINI GENOMICS PLC.
XX
PI   Risinger C,  Andersson MK,  Lewander T,  Oliasson E;
XX
DR   WPI; 2002-329785/36.
XX
PT   New sequence determination oligonucleotides, useful for detecting
PT   polymorphic sites in a 5' flanking region of a CYP2D6 gene, as
PT   hybridization probes, as components of diagnostic assays, or in ligase-
```

```
PT   based sequence determination.
XX
PS   Claim 2; Page 23; 63pp; English.
XX
CC   The invention relates to sequence determination oligonucleotides for
CC   detecting polymorphic sites in a 5' flanking region of cytochrome P450
CC   2D6 (CYP2D6) gene. CYP2D6 enzymes are involved in the metabolism of many
CC   different xenobiotics. Human CYP2D6 gene is located on chromosome 22. The
CC   oligonucleotides may be used as in situ hybridisation probes, in ligase-
CC   based sequenced determination, as components of diagnostic assays, as
CC   probes in sequence determination methods based on mismatches, as
CC   hybridisation-based diagnostic assays, and as components of diagnostic
CC   microarray. CYP2D6 is useful to predict variations in an individual's
CC   ability to metabolise certain drugs. The present sequence is a sense
CC   oligonucleotide used for detecting of human CYP2D6 gene 5' flanking
CC   region single nucleotide polymorphism (SNP)
XX
SQ   Sequence 25 BP; 22 A; 2 C; 1 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          3 AAAAAAAAAAAAAAAAAAA 21


RESULT 1098
AAH38515/c
ID   AAH38515 standard; DNA; 25 BP.
XX
AC   AAH38515;
XX
DT   14-AUG-2001  (first entry)
XX
DE   SNP specific SNPE primer SEQ ID 1311.
XX
KW   Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW   SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
KW   Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW   polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW   acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW   inflammation; forensic investigation; paternity analysis; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200129262-A2.
XX
PD   26-APR-2001.
XX
PF   13-OCT-2000; 2000WO-US028436.
XX
PR   15-OCT-1999;   99US-0160096P.
XX
PA   (ORCH-) ORCHID BIOSCIENCES INC.
XX
PI   Picoult-Newburg L,  Pohl M;
XX
DR   WPI; 2001-290930/30.
XX
PT   New genotyping oligonucleotide, useful for detecting the presence,
PT   absence or identity of single polynucleotide polymorphism in a nucleic
PT   acid sample.
XX
PS   Claim 1; Page 56; 83pp; English.
XX
CC   Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC   primer extension (SNPE) primers, and the sequences of regions flanking
CC   sites of single nucleotide polymorphisms SNPs. The present invention
CC   includes kits for determining the presence or absence of a SNP, using the
CC   oligonucleotides of the invention. The PCR primers are used to amplify a
CC   SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC   The oligonucleotides are useful for genotyping a nucleic acid sample by
CC   performing a single-nucleotide primer extension reaction. The
CC   oligonucleotides are useful for determining the presence, absence or
CC   identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC   assess by association analysis the genotype of an individual or group of
CC   individuals, having a pathological phenotypic trait suspected of being
CC   caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC   agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC   dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC   osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC   traits also include symptoms of or susceptibility to multifactorial
CC   disease of which a component is or may be genetic such as autoimmune
CC   diseases, including, rheumatoid arthritis, multiple sclerosis,
CC   inflammation, cancer, nervous system diseases and infection by pathogenic
CC   microorganism. The method is also useful in forensic investigations and
CC   paternity analysis. The present sequence represents a single nucleotide
CC   primer extension (SNPE) primer specific for a human SNP containing DNA
CC   sequence
XX
SQ   Sequence 25 BP; 1 A; 1 C; 0 G; 23 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         25 AAAAAAAAAAAAAAAAAAA 7


RESULT 1099
AAV57477
ID   AAV57477 standard; DNA; 25 BP.
XX
AC   AAV57477;
XX
DT   14-DEC-1998  (first entry)
XX
DE   Cytochrome P450ox monooxygenase PCR primer SEQ ID NO:11.
XX
KW   Cytochrome P450 monooxygenase; P450ox; Sorghum bicolor (L.) Moench;
KW   Sinapis alba; biosynthetic conversion; aldoxime; nitrile; cyanohydrin;
KW   cyanogenic glycoside; transgenic plant; resistance; PCR primer; ss.
XX
OS   Synthetic.
OS   Sorghum bicolor.
XX
PN   WO9840470-A2.
XX
PD   17-SEP-1998.
XX
PF   05-MAR-1998;   98WO-EP001253.
XX
PR   07-MAR-1997;   97EP-00810132.
PR   08-DEC-1997;   97EP-00810954.
XX
PA   (NOVS ) NOVARTIS AG.
PA   (UYRO-) UNIV ROYAL VETERINARY & AGRIC.
XX
PI   Halkier BA,  Bak S,  Kahn RA,  Moeller BL;
XX
DR   WPI; 1998-520808/44.
XX
PT   Cytochrome P450 monooxygenase of the cyanogenic glycoside pathway -
PT   useful for the production of plants with improved nutritive value or pest
PT   resistance.
XX
PS   Example 5; Page 29; 32pp; English.
XX
CC   The present sequence represents a PCR primer for cytochrome P450
CC   monooxygenase from Sorghum bicolor (L.) Moench, designated P450ox.
CC   Cytochrome P450 monooxygenase catalyses: (i) the conversion of aldoxime
CC   to a nitrile; and (ii) the nitrile to the corresponding cyanohydrin. DNA
```

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CC   encoding cytochrome P450 monooxygenase can be used to obtain transgenic
CC   plants, for the purpose of improving the nutritive value or pest
CC   resistance of the plant. Cytochrome P450 monooxygenase catalyses the
CC   conversion of aldoximes to nitriles to cyanohydrins, which are the
CC   precursors of toxic cyanogenic glycosides, so staple food such as cassava
CC   and lima beans, as well as animal feed such as white clover, can be
CC   rendered less toxic by blocking the cytochrome P450 monooxygenase
CC   activity. Introducing the enzyme to plants or to certain tissues could
CC   help reduce crop damage since the product is also toxic to insects,
CC   acarids and nematodes
XX
SQ   Sequence 25 BP; 1 A; 3 C; 3 G; 17 T; 0 U; 1 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTT 2181
              ||||||||||||||||||||
Db          6 TCCTTTTTTTTTTTTTTTT 24


RESULT 1100
AAA57855
ID   AAA57855 standard; DNA; 28 BP.
XX
AC   AAA57855;
XX
DT   11-OCT-2000  (first entry)
XX
DE   Deoxy-A22-tagged substrate oligonucleotide.
XX
KW   Ribozyme; catalytic RNA; analyte detection; effector molecule;
KW   nucleic acid substrate; in vitro selection; ribozyme ligase;
KW   conformation dependent activity; allosteric activation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        23. .28
FT                   /*tag=  a
FT   misc_binding    24. .28
FT                   /*tag=  b
FT                   /bound_moiety= "Bases 13-17 of N90 RNA pool (AAA57851)"
XX
PN   WO200024931-A2.
XX
PD   04-MAY-2000.
XX
PF   22-OCT-1999;   99WO-IL000557.
XX
PR   23-OCT-1998;   98IL-00126731.
XX
PA   (INTE-) INTELLIGENE LTD.
XX
PI   Nathan A,  Ellington A;
XX
DR   WPI; 2000-350763/30.
XX
PT   Detecting an analyte in a sample comprises providing nucleic acid
PT   sequence which is catalytically active in presence of analyte, contacting
PT   catalytic nucleic acid with substrate and amplifying catalytic product.
XX
PS   Disclosure; Page; 36pp; English.
XX
CC   The invention relates to a method of detecting an analyte in a sample.
CC   The method comprises providing a nucleic acid sequence which is initially
CC   catalytically inactive, but which becomes catalytically active in the
CC   presence of an analyte (the effector); providing a nucleic acid substrate
CC   for the catalytic activity of the nucleic acid sequence; and contacting
CC   the nucleic acid sequence and the substrate with the sample under
CC   conditions allowing catalytic activity of nucleic acid sequences. The
CC   catalytic nucleic acid sequence will be able to convert the nucleic acid
CC   substrate into a nucleic acid product only if the analyte of interest is
CC   present. The nucleic acid catalytic product is then amplified, and a
CC   significant increase in the amount of product indicates the presence of
CC   the analyte in the sample. The method is useful for the qualitative or
CC   quantitative determination of an analyte in a sample in diagnostic
CC   assays. The invention describes the in vitro selection of a ribozyme
CC   ligase (L1; AAA57859, AAA57860) which is catalytically active only in the
CC   presence of an oligonucleotide effector (AAA57854). The L1 ribozyme
CC   ligase was selected from a pool of RNA molecules comprising a central
CC   randomised region 90 nucleotides in length flanked on both sides by
CC   constant sequence regions (the N90 RNA pool; AAA57851). In the presence
CC   of the effector, selection was performed using one of the tagged
CC   substrate molecules AAA57855-A57857. RNAs with ligase activity (i.e.,
CC   those which have become ligated to the substrate molecule) were reverse
CC   transcribed using the effector oligo, and then PCR amplified using the
CC   effector and a DNA primer identical in sequence to the substrate used for
CC   the selection. A ribozyme ligase, L1, was selected via this procedure. L1
CC   can only adopt its active conformation (AAA57859) in the presence of the
CC   effector oligo (analyte). In the absence of the effector, L1 adopts an
CC   inactive conformation (AAA57860). The present sequence represents the
CC   deoxy-A22-tagged substrate oligonucleotide. The dA22 tag enables
CC   successfully ligated products to be isolated using oligo(dT)12-18
CC   cellulose. Note: The present sequence is not given in the specification,
CC   but is created from the inforamtion given on page 11
XX
SQ   Sequence 28 BP; 23 A; 2 C; 1 G; 0 T; 2 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 1101
AAL43065
ID   AAL43065 standard; RNA; 28 BP.
XX
AC   AAL43065;
XX
DT   25-SEP-2002  (first entry)
XX
DE   Regulatable, catalytically active nucleic acid substrate #1.
XX
KW   Regulatable catalytically active nucleic acid; RCANA; ribozyme;
KW   gene therapy; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "5' biotinylated"
XX
PN   WO200196559-A2.
XX
PD   20-DEC-2001.
XX
PF   14-JUN-2001; 2001WO-US019302.
XX
PR   15-JUN-2000; 2000US-0212097P.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Ellington AD,  Hesselberth J,  Marshall K,  Robertson M,  Sooter L;
PI   Davidson E,  Cox JC,  Reidel T;
XX
DR   WPI; 2002-122216/16.
XX
PT   New regulatable, catalytically active nucleic acids (RCANA), useful in
```

PT gene therapy (particularly for regulating gene expression), or in assays
PT for detecting the presence of ligands or activation of an effector of
PT RCANA.
XX
PS Example 6; Page 75; 126pp; English.
XX
CC The present invention relates to regulatable, catalytically active
CC nucleic acids (RCANAs) which are regulated by polypeptides. These are
CC useful for regulating gene expression, in assays for detecting the
CC presence of ligands, for activation of an effector of RCANA, and in gene
CC therapy. The present sequence is an oligonucleotide substrate used in the
CC construction of an RCANA
XX
SQ Sequence 28 BP; 23 A; 2 C; 1 G; 0 T; 2 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAAA 19

RESULT 1102
ADA39569
ID ADA39569 standard; RNA; 28 BP.
XX
AC ADA39569;
XX
DT 20-NOV-2003 (first entry)
XX
DE Substrate RNA related oligonucleotide SEQ ID NO:25.
XX
KW regulatable catalytically active nucleic acid; RCANA; catalytic domain;
KW regulation; screening; gene therapy; biological pathway regulation;
KW regulatory element; metabolic pathway; ribozyme; ss.
XX
OS Synthetic.
XX
PN WO2003027310-A2.
XX
PD 03-APR-2003.
XX
PF 24-SEP-2002; 2002WO-US030458.
XX
PR 24-SEP-2001; 2001US-0324715P.
XX
PA (ARCH-) ARCHEMIX CORP.
XX
PI Wilson C, Cload ST, Keefe AD;
XX
DR WPI; 2003-354657/33.
XX
PT Regulating production of a product in a cell, comprises inserting a
PT regulatable catalytically active nucleic acid into a gene that produces
PT the product or regulates the production of the product in the cell.
XX
PS Example 6; Page 76; 128pp; English.
XX
CC The present invention describes a method for regulating production of a
CC product in a cell. The method comprises inserting a regulatable
CC catalytically active nucleic acid (RCANA) into a gene that produces the
CC product or regulates the production of the product in the cell, where the
CC RCANA comprises a catalytic domain which modifies a transcript to alter
CC its coding potential and a regulatory domain that recognises an effector
CC that alters the function of the catalytic domain, and contacting the
CC regulatory domain with an effector to regulate production of the product.
CC Also described: (1) regulating a biological pathway in cell; and (2)
CC screening a population of cells for a cell that produces a bioproduct.
CC The methods are useful for regulating a biological pathway in cell, or
CC regulating production of a product in a cell. The RCANAs are useful as
CC regulatory elements to control the expression of genes in a metabolic
CC pathway, or as regulated selectable markers to increase a selective
CC pressure favouring or disfavouring production of a targeted bioproduct.
CC The RCANAs are also useful for in vitro or in vivo sensing or detection,
CC and in gene therapy. The present sequence represents an RNA substrate
CC oligonucleotide, which is used in an example from the present invention.
XX
SQ Sequence 28 BP; 23 A; 2 C; 1 G; 0 T; 2 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAAA 19

RESULT 1103
AAS11744
ID AAS11744 standard; DNA; 28 BP.
XX
AC AAS11744;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human haemoglobin alpha 2 transcript (extreme 3' end).
XX
KW Peptide-based cDNA characterisation; haemoglobin alpha 2; human; ds.
XX
OS Homo sapiens.
XX
PN WO200161051-A1.
XX
PD 23-AUG-2001.
XX
PF 16-FEB-2001; 2001WO-US005305.
XX
PR 16-FEB-2000; 2000US-0182983P.
XX
PA (SEQU-) SEQUEL GENETICS INC.
XX
PI Jarvik JW;
XX
DR WPI; 2001-514778/56.
XX
PT Transcript, genetic, and especially nucleic acid sequence analysis
PT comprises analysis of hybrid peptide products.
XX
PS Example 11; Page 30; 48pp; English.
XX
CC The invention relates to a method of peptide-based transcript or genetic
CC analysis comprising: (a) providing multiple polynucleotides (I) derived
CC from mRNAs from a biological sample, where (I) has homology to a known
CC reference sequence (II); (b) expressing (I); and (c) assessing a physical
CC property of the expression products to determine the sequences of (I) by
CC comparison with the predicted properties of polypeptides encoded by (II).
CC The method is useful for transcript or genetic analysis, especially
CC nucleic acid analysis where the method comprises expressing polypeptides
CC from two or more reading frames and determining the masses to create a
CC peptide mass signature characteristic of the nucleic acid molecule. The
CC peptide is considerably smaller than the DNA molecule that encodes it
CC (individual amino acids averages about 110 Daltons each whereas the
CC trinucleotides (triplets) that encode them average N Daltons each). Also,
CC the peptides are much more diverse in composition than nucleic acids, as
CC they are composed of combinations of 20 different amino acids instead of
CC combinations of 4 different nucleotides, e.g., two random DNA fragments
CC of identical composition (e.g., with 10 adenines, 10 thymines, 15
CC guanines, and 15 cytosines) are extremely unlikely to encode peptides of
CC identical composition. This means that whereas the two nucleic acids have
CC identical masses and cannot be distinguished on the basis of mass, the
CC peptides that they encode will, except in statistically very rare cases,
CC have different masses and can be readily distinguished in the basis of
CC mass. The present sequence represents the coding sequence of human

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CC   haemoglobin alpha 2 transcript (extreme 3' end) used in an example to
CC   demonstrate the method of the invention
XX
SQ   Sequence 28 BP; 23 A; 2 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          6 AAAAAAAAAAAAAAAAAAA 24


RESULT 1104
AAV61015
ID   AAV61015 standard; DNA; 28 BP.
XX
AC   AAV61015;
XX
DT   03-DEC-1998  (first entry)
XX
DE   HS/HIP reverse transcriptase PCR primer #4.
XX
KW   Human; heparan sulfate/heparin interacting protein; HIP; diagnosis;
KW   blood coagulation; antithrombin-3; bleeding; wound; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9838214-A1.
XX
PD   03-SEP-1998.
XX
PF   27-FEB-1998;   98WO-US003788.
XX
PR   28-FEB-1997;   97US-00810609.
XX
PA   (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
PI   Carson DD,  Hoeoek M,  Liu S;
XX
DR   WPI; 1998-495388/42.
XX
PT   Use of heparin sulphate/heparin interacting protein - for modulating
PT   blood coagulation, e.g. for neutralising heparin, treating diseases
PT   involving excessive bleeding or administration to wound sites.
XX
PS   Example 1; Page 78; 148pp; English.
XX
CC   A method has been developed for identifying a heparin (Hp) component that
CC   binds to antithrombin-3 (AT-3). The method comprises:(a) contacting a Hp
CC   sample suspected of containing a Hp component that binds to AT-3 with a
CC   heparan sulphate (HS)/Hp interacting protein (HIP) to allow binding of
CC   the Hp component; and (b) detecting the binding of the Hp component to
CC   the HS/HIP. The present sequence represents a primer for reverse
CC   transcriptase PCR of heparan sulfate/heparin interacting protein
CC   (HS/HIP). Products from the present invention can be used for modulating
CC   blood coagulation. They can be used for neutralising heparin, treating
CC   diseases characterised by excessive bleeding or administration to wound
CC   sites. The HS/HIPs can also be used for the production of antibodies and
CC   in diagnostic applications
XX
SQ   Sequence 28 BP; 0 A; 6 C; 4 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTT 2183
              |||||||||||||||||||
Db         10 CTTTTTTTTTTTTTTTTTT 28


RESULT 1105
AAZ61254
ID   AAZ61254 standard; DNA; 28 BP.
XX
AC   AAZ61254;
XX
DT   30-MAY-2000  (first entry)
XX
DE   Oligo dT primer for honey bee venom PX3.101 cDNA.
XX
KW   Protein PX3.101; honey bee; venom; interleukin-8; IL-8; receptor; CXCR1;
KW   CXCR2; cyclooxygenase; lipoxygenase; phospholipase; protease;
KW   inflammatory disease; gene therapy; cancer; autoimmune disease; pain;
KW   chemokine imbalance; rheumatoid arthritis; multiple sclerosis; psoriasis;
KW   systemic lupus erythematosus; Crohn's disease; vasculitis; scleroderma;
KW   metastatic cancer; Alzheimer's disease; wound healing; aging process;
KW   antigen; primer; ss.
XX
OS   Apis mellifera.
XX
PN   GB2341389-A.
XX
PD   15-MAR-2000.
XX
PF   13-SEP-1999;   99GB-00021605.
XX
PR   14-SEP-1998;   98US-0100172P.
XX
PA   (PANP-) PAN PACIFIC PHARM INC.
XX
PI   Chi X,  Lu Y;
XX
DR   WPI; 2000-185368/17.
XX
PT   Isolated nucleic acids encoding the bee venom protein PX3.101 useful for
PT   treating autoimmune and inflammatory disorders such as rheumatoid
PT   arthritis.
XX
PS   Example 3; Page 43; 83pp; English.
XX
CC   The present primer was used for cDNA encoding the protein PX3.101, which
CC   is a honey bee venom isolated Apis mellifera. PX3.101 inhibits the
CC   binding of interleukin-8 (IL-8) to its receptor (e.g. CXCR1 and CXCR2)
CC   and inhibits a variety of enzymes (e.g. cyclooxygenases, lipoxygenases,
CC   phospholipases and proteases) associated with inflammatory diseases. The
CC   nucleic acids may be used for the recombinant production of PX3.101
CC   proteins either in vivo (as part of a gene therapy protocol) or in vitro
CC   (as a fermentation culture). The nucleic acids may also be used as probes
CC   to identify similar sequences in samples. The PX3.101 protein may be used
CC   for the treatment of inflammatory diseases, cancers, autoimmune diseases,
CC   pain and/or diseases associated with chemokine (especially IL-8)
CC   imbalances such as rheumatoid arthritis, multiple sclerosis, psoriasis,
CC   systemic lupus erythematosus (SLE), Crohn's disease, vasculitis,
CC   scleroderma, metastatic cancer and Alzheimer's disease in humans. It is
CC   also disclosed that the proteins may be used to accelerate wound healing,
CC   reduce several aging processes and protect against ultraviolet light. The
CC   proteins may also be used as antigens in the production of antibodies
CC   specific for PX3.101. The antibodies may be used as diagnostic agents to
CC   detect PX3.101 protein in samples and to down regulate PX3.101 activity
XX
SQ   Sequence 28 BP; 0 A; 4 C; 4 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTT 2183
              |||||||||||||||||||
Db         10 CTTTTTTTTTTTTTTTTTT 28


RESULT 1106
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AAI71210
ID   AAI71210 standard; DNA; 28 BP.
XX
AC   AAI71210;
XX
DT   22-JAN-2002  (first entry)
XX
DE   Single stranded DNA PCR primer SEQ ID NO:5.
XX
KW   Single stranded DNA primer; PCR primer; amplification; ss.
XX
OS   Synthetic.
XX
PN   JP2001204472-A.
XX
PD   31-JUL-2001.
XX
PF   21-JAN-2000; 2000JP-00012535.
XX
PR   21-JAN-2000; 2000JP-00012535.
XX
PA   (SUME ) SUMITOMO ELECTRIC IND CO.
XX
DR   WPI; 2001-609513/70.
XX
PT   New polynucleotide for the amplification of a one-side single-stranded
PT   DNA and the production of a double-stranded cDNA comprises a single-
PT   stranded DNA primer.
XX
PS   Disclosure; Page 11; 13pp; Japanese.
XX
CC   The present invention describes a single-stranded DNA primer comprising a
CC   single-stranded DNA having a dTn sequence, which hybridises with the
CC   polyA site of an mRNA at the 3'-terminal, and has a blocking group at the
CC   5'-terminal in which the other part constitutes an adapter double-
CC   stranded DNA connected to the double-stranded cDNA. The terminal of the
CC   side of the DNA is not connected to the double-stranded cDNA, which
CC   consists of a base sequence having full homology to the single-stranded
CC   DNA corresponding to the 5'-terminal. A method is also described for the
CC   preparation of a double-stranded cDNA in which the above single-stranded
CC   DNA primer is hybridised with the polyA site of an mRNA and said single-
CC   stranded DNA primer is used as the primer to reverse-transcribe said mRNA
CC   and further it is converted to a double-stranded cDNA by a DNA
CC   polymerase. The primer is used for the uniform amplification of DNAs. The
CC   present sequence represents a PCR primer which is given in the
CC   exemplification of the present invention
XX
SQ   Sequence 28 BP; 3 A; 3 C; 2 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTT 2183
             |||||||||||||||||||
Db         10 CTTTTTTTTTTTTTTTTTT 28


RESULT 1107
AAQ79096/c
ID   AAQ79096 standard; DNA; 29 BP.
XX
AC   AAQ79096;
XX
DT   25-MAR-2003  (revised)
DT   07-AUG-1995  (first entry)
XX
DE   Tobacco PMT PCR primer P-23.
XX
KW   Tobacco; transgenic plant; putrescine-N-methyltransferase; PMT; alkaloid;
KW   nicotine; primer; polymerase chain reaction; PCR; Nicotiana tabacum; ss.
XX
OS   Synthetic.
XX
PN   WO9428142-A1.
XX
PD   08-DEC-1994.
XX
PF   01-JUN-1994;   94WO-US006106.
XX
PR   01-JUN-1993;   93US-00076681.
XX
PA   (PHIM ) PHILIP MORRIS PROD INC.
XX
PI   Wahab SZ,  Malik VS;
XX
DR   WPI; 1995-022814/03.
XX
PT   Recombinant DNA encoding tobacco protein, PMT - useful for producing
PT   transgenic tobacco plants with decreased alkaloid content.
XX
PS   Disclosure; Page 57; 69pp; English.
XX
CC   Forward primer P-18 (AAQ79095), based on an N-terminal methionine and
CC   amino acids 1-7 of a CNBr fragment (AAR67579) of tobacco putrescine-N-
CC   methyltransferase (PMT), and reverse primer P-23 (AAQ79096), were used to
CC   amplify RNA derived from tobacco var. Burley 21 root extract. Clone Q7
CC   was obtained. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 29 BP; 2 A; 1 C; 1 G; 25 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
             |||||||||||||||||||
Db         29 AAAAAAAAAAAAAAAAAAA 11


RESULT 1108
AAQ68614
ID   AAQ68614 standard; cDNA; 29 BP.
XX
AC   AAQ68614;
XX
DT   25-MAR-2003  (revised)
DT   19-JAN-1995  (first entry)
XX
DE   tRNAPolyU reverse tRNA primer.
XX
KW   cDNA; RNA template; reverse-transcriptase; primer; tRNAPolyU;
KW   tRNA template; pUC18; ss.
XX
OS   Synthetic.
XX
PN   WO9413689-A1.
XX
PD   23-JUN-1994.
XX
PF   09-DEC-1993;   93WO-US012029.
XX
PR   09-DEC-1992;   92US-00989851.
XX
PA   (MILL/) MILLER J E.
XX
PI   Miller JE;
XX
DR   WPI; 1994-217796/26.
XX
PT   In vivo cDNA synthesis - by using synthetic polynucleotide(s) which bind
PT   in vivo to RNA templates as primers for reverse transcriptase.
XX
PS   Example 1; Page 33; 102pp; English.
XX
CC   DNA encoding the modified tRNA primer, tRNAPolyU (AAQ68616), was obtained
```

```
CC   using the primer pair given in AAQ68612-13. The DNA was cloned in pUC18.
CC   PCR was used to amplify a promoter-tRNA-polyU fragment and to define the
CC   end of the tRNAPolyU coding template. A reverse tRNA primer (AAQ68614)
CC   was used. The 5' base of this primer was also the last 3' base of the
CC   encoded tRNAPolyU template, as shown in AAQ68617. For in vitro production
CC   of tRNAPolyU, a DraI-sensitive T7-tRNAPolyU cassette was linearized and
CC   used as template for in vitro transcription using oligomers AAQ68612 and
CC   AAQ68515. The tRNA primer is used for in vivo cDNA synthesis. (Updated on
CC   25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 29 BP; 22 A; 3 C; 4 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 1109
AAT09934
ID   AAT09934 standard; cDNA; 29 BP.
XX
AC   AAT09934;
XX
DT   07-AUG-1996  (first entry)
XX
DE   Reverse tRNA primer #5.
XX
KW   Polymerase chain reaction: PCR; primer; amplify; murine; tRNAproGGG; RT;
KW   DNA polymerase I; bacteriophage T7; RNA polymerase promoter; synthesis;
KW   Moloney Murine Leukaemia Virus; MoMuMLV; reverse transcriptase; analysis;
KW   covalently-linked cDNA; subtractive cDNA library; light sensitive cDNA;
KW   cytotoxic sensitive cDNA; cDNA probe; diagnosis; DNA sequencing; ss.
XX
OS   Synthetic.
XX
PN   WO9535369-A1.
XX
PD   28-DEC-1995.
XX
PF   22-JUN-1995;   95WO-US007968.
XX
PR   22-JUN-1994;   94US-00264038.
XX
PA   (MILL/) MILLER J E.
XX
PI   Miller JE;
XX
DR   WPI; 1996-058406/06.
XX
PT   Method for synthesising covalently linked complementary DNA - uses
PT   primers which can bind reverse transcriptase and anneal to a distinct
PT   template, allowing synthesis to occur.
XX
PS   Example 1; Page 43; 140pp; English.
XX
CC   This sequence represents a reverse tRNA primer and is used to amplify the
CC   sequence represented by AAT09937. The amplified sequence is used in the
CC   method of the invention, along with the sequence amplified by AAT09930
CC   and AAT09931. The sequence amplified by AAT09930 and AAT09931 is a
CC   recombinant tRNAproGGG primer operatively linked to the bacteriophage T7
CC   RNA polymerase promoter which is capable of binding to the Moloney Murine
CC   Leukaemia Virus (MoMuMLV) reverse transcriptase (RT) and can then be used
CC   in the method of the invention. The method is for synthesising a
CC   covalently-linked cDNA copy of a plurality of polynucleotide template
CC   molecules. In this method, a polynucleotide template primer molecule
CC   (such as the amplified sequence) is used in a mixture with a RT enzyme or
CC   complex. The mixture is then incubated under conditions which permit the
CC   synthesis of a DNA molecule which comprises regions complementary to the
CC   polynucleotide template molecule. The primers and DNA molecules can be
CC   used in the construction of subtractive cDNA libraries, production of
CC   specific cytotoxic or light sensitive cDNA products, and cDNA probes for
CC   analytical, diagnostic or preparative use. Also, they can be used in in
CC   vivo DNA sequencing. The method of cDNA synthesis utilises structure-
CC   specific analogues to the natural target site of the RT enzyme or complex
XX
SQ   Sequence 29 BP; 22 A; 3 C; 4 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 1110
AAQ97396/c
ID   AAQ97396 standard; DNA; 29 BP.
XX
AC   AAQ97396;
XX
DT   25-MAR-2003  (revised)
DT   01-APR-1996  (first entry)
XX
DE   Rat type I steroid 5-alpha reductase cDNA PCR primer.
XX
KW   Steroid 5-alpha reductase; sexual development; differentiation; probe;
KW   recombinant; inhibit; prostatic hyperplasia; acne; hirsutism;
KW   male pattern baldness; endometriosis; prostate cancer; testosterone;
KW   dihydroxytestosterone; ss.
XX
OS   Rattus sp.
XX
PN   US5422262-A.
XX
PD   06-JUN-1995.
XX
PF   18-NOV-1991;   91US-00795859.
XX
PR   30-APR-1990;   90US-00517661.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Andersson S,  Russell DW;
XX
DR   WPI; 1995-214658/28.
XX
PT   Steroid 5 alpha-reductase nucleic acid segments and recombinant vectors -
PT   where the sequences are useful in e.g. analysis of normal and abnormal
PT   sexual differentiation.
XX
PS   Example 1; Col 21; 72pp; English.
XX
CC   5-alpha reductase enzymes catalyse the conversion of testosterone to
CC   dihydroxytestosterone. The rat steroid 5-alpha reductase I (SRD5A-I) cDNA
CC   sequence has been isolated and purified using the PCR primer AAQ97396.
CC   The rat enzyme cDNA can be used in the prepn. of genetic constructs for
CC   the large scale production of SRD5A or as probes for enzyme-encoding
CC   sequences from alternative sources. The sequences are also useful in the
CC   analysis of normal and abnormal sexual differentiation, benign prostatic
CC   hyperplasia, male pattern baldness; acne; hirsutism and endometriosis.
CC   (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 29 BP; 1 A; 4 C; 4 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
```

```
Db         29 AAAAAAAAAAAAAAAAAAA 11


RESULT 1111
AAT99803/c
ID   AAT99803 standard; DNA; 29 BP.
XX
AC   AAT99803;
XX
DT   20-MAR-1998  (first entry)
XX
DE   Primer for rat steroid 5alpha-reductase coding sequence.
XX
KW   Steroid 5alpha-reductase; enzyme; testosterone conversion; inhibitor;
KW   rat; PCR primer; amplify; ss.
XX
OS   Synthetic.
OS   Rattus sp.
XX
PN   US5679521-A.
XX
PD   21-OCT-1997.
XX
PF   01-JUN-1995;   95US-00457616.
XX
PR   30-APR-1990;   90US-00517661.
PR   18-NOV-1991;   91US-00795859.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Russell DW,  Andersson S;
XX
DR   WPI; 1997-525718/48.
XX
PT   Production of recombinant steroid 5alpha-reductase enzyme - by culturing
PT   cell containing DNA encoding the enzyme.
XX
PS   Example 1; Col 20; 70pp; English.
XX
CC   This sequence is a primer for the DNA encoding rat steroid 5alpha-
CC   reductase. The encoded enzyme can be produced by the method of the
CC   invention. The method is for producing a steroid 5alpha-reductase, and
CC   comprises preparing a recombinant host cell containing a DNA segment
CC   encoding a steroid 5alpha-reductase and culturing the cell under
CC   conditions such that the steroid 5alpha-reductase is produced by the
CC   cell. The steroid 5alpha-reductase produced by the method is used for
CC   identifying substances that affect the enzymatic activity of steroid
CC   5alpha-reductase. Substances identified as inhibiting steroid 5alpha-
CC   reductase activity can be used for inhibiting the conversion of
CC   testosterone
XX
SQ   Sequence 29 BP; 1 A; 4 C; 4 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         29 AAAAAAAAAAAAAAAAAAA 11


RESULT 1112
AAI69697
ID   AAI69697 standard; DNA; 29 BP.
XX
AC   AAI69697;
XX
DT   10-JAN-2002  (first entry)
XX
DE   Hepatitis E virus HEV-T1 sequence related PCR primer #62.
XX
KW   Hepatitis E virus; HEV-T1; hepatitis infection; PCR primer; ss.
XX
OS   Unidentified.
XX
PN   CN1300771-A.
XX
PD   27-JUN-2001.
XX
PF   23-DEC-1999;   99CN-00125741.
XX
PR   23-DEC-1999;   99CN-00125741.
XX
PA   (CHME-) CHINESE MEDICINE & BIOLOGIC PROD APPRAIS.
XX
PI   Wang Y,  Zhang H,  Li H;
XX
DR   WPI; 2001-550442/62.
XX
PT   Hepatitis E virus gene sequence and its application.
XX
PS   Example 1; Page 15(Disclosure); 34pp; Chinese.
XX
CC   The present invention relates to a novel nucleotide sequence and protein
CC   of a new hepatitis E virus HEV-T1 and the application of the nucleotide
CC   sequence and protein in diagnosing, preventing and treating hepatitis.
CC   The present sequence is a PCR primer described in the exemplification of
CC   the invention
XX
SQ   Sequence 29 BP; 3 A; 3 C; 3 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTT 2183
              |||||||||||||||||||
Db         11 CTTTTTTTTTTTTTTTTTT 29


RESULT 1113
ADA26182
ID   ADA26182 standard; DNA; 29 BP.
XX
AC   ADA26182;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Rice semi-dwarf (sd-1) DNA fragment SEQ ID NO:27.
XX
KW   genotype; plant; rice; semi-dwarf; sd-1; polymorphism; detection;
KW   characteristic; single nucleotide polymorphism; SNP; genotyping;
KW   chromosome 1; gene; ds.
XX
OS   Synthetic.
OS   Oryza sativa.
XX
PN   WO2003070934-A1.
XX
PD   28-AUG-2003.
XX
PF   07-FEB-2003; 2003WO-JP001317.
XX
PR   25-FEB-2002; 2002JP-00048115.
XX
PA   (PLAN-) PLANT GENOME CENT CO LTD.
XX
PI   Minobe Y,  Monna L,  Kitazawa N,  Yoshino R,  Suzuki J;
XX
DR   WPI; 2003-697617/66.
XX
PT   Judging the genotype of a region around a plant sd-1 gene with
PT   polymorphism-obtained markers isolated by positional cloning, useful in
PT   genotyping for examination of semi-dwarf character of rice.
XX
```

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PS   Disclosure; Page 15; 104pp; Japanese.
XX
CC   The present invention describes a method for judging the genotype of a
CC   region around a plant semi-dwarf (sd-1) gene in which polymorphisms are
CC   present, by detecting the polymorphisms. Also described: (1) examining
CC   semi-dwarf characteristics of a plant using the judgment method with
CC   detection of polymorphisms; (2) oligonucleotides for amplifying sd-1 DNA
CC   regions, which are primers for judging the genotype of a region around a
CC   plant sd-1 gene; (3) reagents for judging the genotype of a region around
CC   a plant sd-1 gene containing these oligonucleotides; and (4) reagents for
CC   examining the semi-dwarf character of a plant containing the
CC   oligonucleotides. The method is for judging the genotype of a region
CC   around a plant sd-1 gene, which is applicable in genotyping by (d)CAPS
CC   ((derived) cleaved amplified polymorphic sequence) for examination of the
CC   semi-dwarf character of rice to identify desirable strains e.g. with high
CC   crop yield, pest resistance and resistance to flooded water. The method
CC   is easy and quick, in which a seedling is required for studying single
CC   nucleotide polymorphisms (SNPs) for genotyping, without needing
CC   cultivation of seedling to fully-grown plant for judging heterozygote and
CC   distinguishing morphology. The present sequence represents a rice sd-1
CC   DNA fragment, which is given in the exemplification of the present
CC   invention. Rice sd-1 is located on chromosome 1.
XX
SQ   Sequence 29 BP; 0 A; 6 C; 0 G; 23 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 29;
  Best Local Similarity   81.5%;  Pred. No. 1.5e+03;
  Matches   22;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTT 2181
                ||||| | | |||| ||| ||||||||
Db          3 TTTTTCTTTTCTTTCTTTCTTTTTTT 29


RESULT 1114
AAF26222/c
ID   AAF26222 standard; DNA; 30 BP.
XX
AC   AAF26222;
XX
DT   26-APR-2001  (first entry)
XX
DE   APC binding protein associated primer ON-AT- SEQ ID 7.
XX
KW   APC binding protein; cell proliferation; adenomatous polyposis coli;
KW   tumor cell detection; primer; ss.
XX
OS   Unidentified.
XX
PN   DE19933237-A1.
XX
PD   18-JAN-2001.
XX
PF   15-JUL-1999;   99DE-01033237.
XX
PR   15-JUL-1999;   99DE-01033237.
XX
PA   (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI   Mueller O;
XX
DR   WPI; 2001-148321/16.
XX
PT   Determining proliferative capacity of cells, useful e.g. for detecting
PT   tumor cells, by measuring concentration and subcellular localization of
PT   adenomatous polyposis coli protein.
XX
PS   Claim 10; Page 13; 26pp; German.
XX
CC   This invention describes a novel method for determining the proliferative
CC   activity of cells, comprising detecting, in a sample, the concentration
CC   and/or subcellular localization of APC (adenomatous polyposis coli)
CC   protein (I). The invention also describes (1) determining function of (I)
CC   in a sample by detecting presence of the C-terminal, DNA-binding domain
CC   of (I); (2) detecting mutations in (I)-encoding nucleic acid by detecting
CC   the DNA-binding domain of (I); (3) purifying, enriching and/or detecting
CC   (I) or its fragments by reaction with a probe; (4) double-stranded DNA
CC   (II) that contains the sequence GGCCGCA_2_3G (S1) and/or GATCCT_2_3GC
CC   (S2); (5) peptide fragment of (I) containing at least the DNA-binding
CC   domain; (6) antibodies (Ab) directed against an epitope of positions 1340
CC   -1901, 2219-2580 or 2581-2843 of (I); (7) set of two or more antibodies,
CC   one of which is Ab and the other directed against the N-terminal region
CC   (1-1299) of (I); and (8) kit for detecting DNA-binding capacity of (I) or
CC   its fragments in a sample consisting of (II), Ab or the set of (7). The
CC   method is used to detect proliferative, especially tumor (precursor),
CC   cells, to detect function of (I) and mutations in (I), and to purify
CC   and/or enrich (I), or its fragments, from a sample. The method allows
CC   simple, rapid and reliable detection of proliferation, without the need
CC   for polymerase chain reaction or sequencing
XX
SQ   Sequence 30 BP; 1 A; 3 C; 2 G; 24 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
                |||||||||||||||||||
Db         28 AAAAAAAAAAAAAAAAAAA 10


RESULT 1115
AAS63441
ID   AAS63441 standard; DNA; 30 BP.
XX
AC   AAS63441;
XX
DT   29-JAN-2002  (first entry)
XX
DE   Oligonucleotide-nanoparticle probe #63.
XX
KW   Oligonucleotide-nanoparticle probe; diagnostic; forensic analysis;
KW   nucleic acid detection; nanostructure; biochip; biofilter; drug delivery;
KW   ss.
XX
OS   Synthetic.
XX
PN   WO200173123-A2.
XX
PD   04-OCT-2001.
XX
PF   28-MAR-2001; 2001WO-US010071.
XX
PR   28-MAR-2000; 2000US-0192699P.
PR   26-APR-2000; 2000US-0200161P.
PR   26-JUN-2000; 2000US-00603830.
PR   26-JUN-2000; 2000US-0213906P.
PR   08-DEC-2000; 2000US-0254392P.
PR   11-DEC-2000; 2000US-0255235P.
PR   12-JAN-2001; 2001US-00760500.
PR   28-MAR-2001; 2001US-00820279.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA,  Park S,  Li Z;
XX
DR   WPI; 2001-656926/75.
XX
PT   Detecting and separating nucleic acid, useful e.g. for diagnosis,
PT   comprises reaction with nanoparticles that carry oligonucleotides
PT   complementary to parts of the target.
XX
PS   Example 24; Fig 44; 404pp; English.
XX
CC   The invention relates to a method for detection of nucleic acid (I)
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CC   having at least 2 portions, comprising treatment with nanoparticles that
CC   carry oligonucleotides complementary to at least 2 parts of (I), where
CC   detectable change caused by hybridisation of the oligonucleotide to (I)
CC   is observed. The method is used to detect (or to separate) specific (I),
CC   e.g. for diagnosing a wide variety of diseases, sequencing, in forensic
CC   analysis etc., and generally to detect analytes other than (I). The
CC   oligonucleotide-derivatised nanoparticles are also useful for preparing
CC   nanostructures useful, for example, as biochips, biofilters, mechanical
CC   devices, separation membranes, chemical sensors, in computers, and for
CC   drug delivery. Very stable nanoparticle-oligonucleotide conjugates can be
CC   produced, allowing their direct use (as probes) in polymerase chain
CC   reaction, i.e. they survive multiple heating/cooling cycles so do not
CC   need to be added after amplification. (I) are detected by simple colour
CC   change, without the need for special equipment, making possible rapid
CC   field testing for e.g. pathogens. AAS63374-AAS63448 represent
CC   oligonucleotide-nanoparticle probes, and related sequences, used in the
CC   method of the invention
XX
SQ   Sequence 30 BP; 23 A; 4 C; 2 G; 1 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 1116
AAS10385
ID   AAS10385 standard; DNA; 30 BP.
XX
AC   AAS10385;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Oligonucleotide-cyclic disulphide linker, c1 #2.
XX
KW   Nanoparticle; cyclic disulphide-oligonucleotide; DNA detection;
KW   DNA isolation; genetic disease; bacterial disease; viral disease;
KW   forensic science; paternity testing; gene therapy; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1
FT                   /*tag=  a
FT                   /note= "A is covalently linked to a cyclic-disulphide
FT                   moiety"
XX
PN   WO200151665-A2.
XX
PD   19-JUL-2001.
XX
PF   12-JAN-2001; 2001WO-US001190.
XX
PR   13-JAN-2000; 2000US-0176409P.
PR   26-APR-2000; 2000US-0200161P.
PR   26-JUN-2000; 2000US-00603830.
PR   12-JAN-2001; 2001US-00760500.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA,  Li Z;
XX
DR   WPI; 2001-451868/48.
XX
PT   Detecting a nucleic acid useful in e.g. diagnosing genetic, bacterial or
PT   viral diseases, by contacting the nucleic acid with oligonucleotides
PT   attached to nanoparticles and having sequences complementary a portion of
PT   the nucleic acid.
XX
PS   Example 24; Fig 44; 323pp; English.
XX
CC   The sequence represents a cyclic disulphide linked oligonucleotide which
CC   may be coupled with colloidal gold particles (nanoparticles) and used to
CC   demonstrate the method of the invention. The invention relates to
CC   isolating or detecting a nucleic acid of interest, in a mixture of
CC   nucleic acids, by binding it to 2 or more complimentary nucleotides which
CC   have a nanoparticle attached to their 5' ends. The nanoparticles (e.g.
CC   colloidal gold) are used to both isolate and detect (e.g. by linking the
CC   particle to a fluorescent probe) the resultant complex. The methods are
CC   useful for detecting nucleic acids, natural or synthetic, and modified or
CC   unmodified. The methods may also be applied in the diagnosis of genetic,
CC   bacterial and viral diseases, in forensics, in DNA sequencing, for
CC   paternity testing, for cell line authentication, and for monitoring gene
CC   therapy. The methods are further useful in research and analytical
CC   laboratories in DNA sequencing, in the field to detect the presence of
CC   specific pathogens, for quick identification of an infection to assist in
CC   drug prescription, and in homes and health centres for inexpensive first-
CC   line screening. The methods, which are based on observing colour change
CC   with the naked eye, are cheap, fast, simple, robust (reagents are
CC   stable), do not require specialised or expensive equipment, and little or
CC   no instrumentation is required
XX
SQ   Sequence 30 BP; 23 A; 4 C; 2 G; 1 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 1117
ABK65048
ID   ABK65048 standard; DNA; 30 BP.
XX
AC   ABK65048;
XX
DT   02-JUL-2002  (first entry)
XX
DE   Nanoparticle-oligonucleotide #68.
XX
KW   Nanoparticle-oligonucleotide; nanofabrication; nucleic acid detection;
KW   ss.
XX
OS   Synthetic.
XX
PN   WO200218643-A2.
XX
PD   07-MAR-2002.
XX
PF   10-AUG-2001; 2001WO-US025237.
XX
PR   11-AUG-2000; 2000US-0224631P.
PR   08-DEC-2000; 2000US-0254392P.
PR   11-DEC-2000; 2000US-0255235P.
PR   12-JAN-2001; 2001US-00760500.
PR   28-MAR-2001; 2001US-00820279.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA,  Garimella V,  Li Z,  Park S;
XX
DR   WPI; 2002-258024/30.
XX
PT   Detecting nucleic acid, useful for diagnosis of genetic, viral or
PT   bacterial disease, comprises hybridizing nanoparticles with attached
PT   oligonucleotides to nucleic acid and detecting change brought about by
PT   hybridization.
```

```
XX
PS   Example 24; Fig 44; 412pp; English.
XX
CC   The invention relates to a method of detecting a nucleic acid (NA) having
CC   at least 2 portions comprising: (a) providing nanoparticles (NP) with
CC   attached oligonucleotides (OGN), where OGN has a sequence complementary
CC   to the sequence of NA; (b) contacting NA and NP under conditions
CC   effective to allow hybridisation of OGN with NA; and (c) observing a
CC   detectable change brought about by hybridisation of OGN with NA. The
CC   method is useful for detecting a nucleic acid, separating a selected
CC   nucleic acid from others and methods of nanofabrication. Detecting
CC   analytes such as nucleic acids and proteins are useful for the diagnosis
CC   of genetic, bacterial and viral diseases. The OGN-NP conjugates that use
CC   cyclic disulphide linkers improve the sensitivity of diagnostic assays.
CC   In particular assays using OGN-NP conjugates prepared using linkers
CC   comprising a steroid residue attached to a cyclic disulphide have been
CC   found to be approximately 10 times more sensitive than assays employing
CC   conjugates prepared using alkanethiols or acyclic disulphides as the
CC   linker. The OGN-NP conjugates are stable allowing them to be used
CC   directly in PCR solutions. Therefore conjugates added as probes to a DNA
CC   target to be PCR amplified can be carried through the 30 or 40 heating
CC   cooling cycles of the PCR and are still able to detect the amplicons
CC   without opening the tubes and causing contamination. ABK64981-ABK65055
CC   represent nanoparticle-oligonucleotides of the invention
XX
SQ   Sequence 30 BP; 23 A; 4 C; 2 G; 1 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 1118
ABS64686
ID   ABS64686 standard; DNA; 30 BP.
XX
AC   ABS64686;
XX
DT   15-NOV-2002  (first entry)
XX
DE   Nucleic acid detection method associated polynucleotide #68.
XX
KW   Nucleic acid detection method; nanoparticle-oligonucleotide conjugate;
KW   nanoparticle; viral RNA detection; bacterial DNA detection;
KW   fungal DNA detection; nanoprobe conjugate; ss.
XX
OS   Synthetic.
XX
PN   WO200246472-A2.
XX
PD   13-JUN-2002.
XX
PF   07-DEC-2001; 2001WO-US046418.
XX
PR   08-DEC-2000; 2000US-0254392P.
PR   08-DEC-2000; 2000US-0254418P.
PR   11-DEC-2000; 2000US-0255235P.
PR   11-DEC-2000; 2000US-0255236P.
PR   12-JAN-2001; 2001US-00760500.
PR   28-MAR-2001; 2001US-00820279.
PR   09-APR-2001; 2001US-0282640P.
PR   10-AUG-2001; 2001US-00927777.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA,  Garimella V,  Li Z,  Park S;
XX
DR   WPI; 2002-608256/65.
XX
PT   Detecting nucleic acid having two portions, by providing nanoparticles
PT   having oligonucleotides attached to it, contacting nucleic acid and
PT   nanoparticles to allow hybridization, and observing detectable change.
XX
PS   Example 24; Fig 44; 442pp; English.
XX
CC   The invention describes a method of detecting (M1) a nucleic acid having
CC   two portions, involving providing nanoparticles having oligonucleotides
CC   attached to it, which has a sequence complementary to sequence of two
CC   portions of nucleic acid, contacting nucleic acid and nanoparticles, to
CC   allow hybridisation of oligonucleotides with two or more portions of
CC   nucleic acid, and observing a detectable change brought about by
CC   hybridisation. (M1), nanoparticles (I), nanoparticle-oligonucleotide
CC   conjugates (II) and the aggregate probe are useful for detecting two or
CC   more nucleic acids (from a biological source) having at least two
CC   portions, such as viral RNA, bacterial or fungal DNA, a gene associated
CC   with a disease, synthetic, or structurally-modified natural or synthetic
CC   RNA or DNA, or a product of a polymerase chain reaction amplification.
CC   (II) is useful for preparing a nanoprobe conjugate for detecting an
CC   analyte, and for detecting a nucleic acid bound to an electrode surface.
CC   (I) and (II) are useful for fabrication, and for separating a selected
CC   nucleic acid having two portions from other nucleic acids. (I), (II) and
CC   the aggregate probe are useful for detecting an analyte (especially
CC   polyvalent analyte) in a sample. This sequence represents a
CC   polynucleotide used to demonstrate the method of the invention
XX
SQ   Sequence 30 BP; 23 A; 4 C; 2 G; 1 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 1119
AAL61658
ID   AAL61658 standard; DNA; 30 BP.
XX
AC   AAL61658;
XX
DT   22-SEP-2003  (first entry)
XX
DE   Oligonucleotide #19 used in the nucleic acid detection method.
XX
KW   Nucleic acid detection; fabrication; ss.
XX
OS   Unidentified.
XX
PN   WO2003035829-A2.
XX
PD   01-MAY-2003.
XX
PF   08-OCT-2002; 2002WO-US032088.
XX
PR   09-OCT-2001; 2001US-0327864P.
PR   07-DEC-2001; 2001US-00008978.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Park S,  Taton TA,  Mirkin CA;
XX
DR   WPI; 2003-430409/40.
XX
PT   Detecting nucleic acid having two portions, by providing nanoparticles
PT   having oligonucleotides attached to it, contacting nucleic acid and
PT   nanoparticles to allow hybridization, and observing detectable change.
XX
PS   Example 24; Fig 44; 467pp; English.
XX
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CC The invention relates to a method of detecting a nucleic acid having two
CC portions. The method involves providing nanoparticles having
CC oligonucleotides attached to it which has a sequence complementary to
CC sequence of two portions of nucleic acid, contacting nucleic acid and
CC nanoparticles to allow hybridisation of oligonucleotides with two or more
CC portions of nucleic acid and observing a detectable change brought about
CC by hybridisation. The method and aggregate probes are useful for
CC detecting two or more nucleic acids (from a biological source) having at
CC least two portions such as viral RNA, bacterial or fungal DNA, a gene
CC associated with a disease, synthetic or structurally modified natural or
CC synthetic RNA or DNA, or a product of a polymerase chain reaction
CC amplification. The invention is useful for preparing a nanoprobe
CC conjugate for detecting an analyte and for detecting a nucleic acid bound
CC to an electrode surface. It is also useful for fabrication and for
CC separating a selected nucleic acid having two portions from other nucleic
CC acids. The present sequence is an oligo used to illustrate the method of
CC the invention
XX
SQ Sequence 30 BP; 23 A; 4 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19
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RESULT 1120
AAX77343/c
ID AAX77343 standard; DNA; 30 BP.
XX
AC AAX77343;
XX
DT 09-AUG-1999 (first entry)
XX
DE Sindbis virus mRNA amplifying RT-PCR 3' primer.
XX
KW Nucleic acid identification; exogenous protein; gene sorting;
KW growth factor; membrane receptor; sindbis virus; RT-PCR; primer; ss.
XX
OS Synthetic.
OS Sindbis virus.
XX
PN WO9925876-A1.
XX
PD 27-MAY-1999.
XX
PF 17-NOV-1998; 98WO-US024520.
XX
PR 17-NOV-1997; 97US-00972218.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY GMBH.
XX
PI Bailey JE, Renner WA, Orberger GH, Koller D;
XX
DR WPI; 1999-357620/30.
XX
PT Isolating genes encoding proteins with selected properties, useful for
PT identifying therapeutic agents or targets.
XX
PS Disclosure; Page 66; 136pp; English.
XX
CC The invention relates to the identification of a recombinant nucleic acid
CC encoding an exogenous protein having a selected property. The method
CC comprises preparing a population of eukaryotic host cells, culturing the
CC cells under suitable conditions and identifying cells that contain the
CC recombinant nucleic acid. The method is used to sort genes according to
CC the type of proteins they express, and also to identify new ligand/
CC receptor interactions. Typical applications of the nucleic acid and the
CC exogenous protein are in isolation of new growth factors, cytokines,
CC membrane receptors, cytoplasmic, organelle or nuclear proteins, all of
CC which may be useful as therapeutic agents or therapeutic targets, e.g.
CC apoptosis-promoting or tumour suppressing proteins, regulators of cell
CC proliferation or metabolic processes etc. The protein can also be used to
CC screen for specific modulators. The nucleic acid can also be used as
CC sources of therapeutic antisense or ribozyme sequences. The method allows
CC the protein (rather than a partial DNA sequence) to be isolated and,
CC since a wide range of cells can be used, they can be expressed with the
CC correct glycosylation pattern
XX
SQ Sequence 30 BP; 0 A; 5 C; 5 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         30 AAAAAAAAAAAAAAAAAAA 12
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RESULT 1121
AAA90394/c
ID AAA90394 standard; DNA; 30 BP.
XX
AC AAA90394;
XX
DT 10-JAN-2001 (first entry)
XX
DE Sindbis virus 3' RT-PCR primer.
XX
KW Nucleic acid identification; exogenous protein; drug screening;
KW recombinant expression; pSinRep5 vector; mammalian expression system;
KW reverse transcription-PCR; RT-PCR primer; ss.
XX
OS Sindbis virus.
OS Synthetic.
XX
PN JP2000189173-A.
XX
PD 11-JUL-2000.
XX
PF 23-AUG-1999; 99JP-00236220.
XX
PR 17-NOV-1998; 98US-00193707.
PR 17-NOV-1998; 98WO-US024520.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY GMBH.
XX
DR WPI; 2000-551637/51.
XX
PT Identifying a recombinant nucleic acid to identify and isolate various
PT cellular proteins, comprises culturing a composition comprising
PT eukaryotic host cells and identifying a cell comprising recombinant
PT nucleic acid.
XX
PS Example; Page 35; 56pp; Japanese.
XX
CC The invention relates to the identification of a recombinant nucleic acid
CC encoding an exogenous protein having a selected property.The method
CC comprises preparing populations of eukaryotic host cells, where each cell
CC comprises an expression vector encoding a different exogenous protein.
CC The host cells are cultured under suitable conditions and the nucleic
CC acid which encodes the exogenous protein is identified. The method is
CC useful for the identification and isolation of proteins with a selected
CC property. Typical applications of the nucleic acid and the exogenous
CC protein are in isolation of new growth factors, cytokines, membrane
CC receptors, cytoplasmic, organelle or nuclear proteins, all of which may
CC be useful as therapeutic agents or therapeutic targets, e.g., pro-
CC apoptotic or tumour suppressing proteins, regulators of cell
CC proliferation or of metabolic processes. The protein can also be used to
CC screen for ligands and specific modulators of activity. The method of the
CC invention allows the direct cloning of full length cDNAs in one step. It
CC facilitates direct expression of the protein without the need to perform

```
CC   further procedures such as subcloning and establishment of a cell line
CC   for protein production. The method allows a protein of interest (rather
CC   than a partial DNA sequence) to be isolated and, since a wide range of
CC   cell types can be used, they can be expressed in a correctly folded and
CC   glycosylated form. Sequences AAA90394-A90395 represent Sindbis virus
CC   reverse transcription-PCR (RT-PCR) primers used in the exemplifications
CC   of the invention. This patent is related to WO9925876
XX
SQ   Sequence 30 BP; 0 A; 5 C; 5 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         30 AAAAAAAAAAAAAAAAAAA 12


RESULT 1122
AAF26221
ID   AAF26221 standard; DNA; 30 BP.
XX
AC   AAF26221;
XX
DT   26-APR-2001  (first entry)
XX
DE   APC binding protein associated primer ON-AT+ SEQ ID 6.
XX
KW   APC binding protein; cell proliferation; adenomatous polyposis coli;
KW   tumor cell detection; primer; ss.
XX
OS   Unidentified.
XX
PN   DE19933237-A1.
XX
PD   18-JAN-2001.
XX
PF   15-JUL-1999;   99DE-01033237.
XX
PR   15-JUL-1999;   99DE-01033237.
XX
PA   (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI   Mueller O;
XX
DR   WPI; 2001-148321/16.
XX
PT   Determining proliferative capacity of cells, useful e.g. for detecting
PT   tumor cells, by measuring concentration and subcellular localization of
PT   adenomatous polyposis coli protein.
XX
PS   Claim 10; Page 12; 26pp; German.
XX
CC   This invention describes a novel method for determining the proliferative
CC   activity of cells, comprising detecting, in a sample, the concentration
CC   and/or subcellular localization of APC (adenomatous polyposis coli)
CC   protein (I). The invention also describes (1) determining function of (I)
CC   in a sample by detecting presence of the C-terminal, DNA-binding domain
CC   of (I); (2) detecting mutations in (I)-encoding nucleic acid by detecting
CC   the DNA-binding domain of (I); (3) purifying, enriching and/or detecting
CC   (I) or its fragments by reaction with a probe; (4) double-stranded DNA
CC   (II) that contains the sequence GGCCGCA_2_3G (S1) and/or GATCCT_2_3GC
CC   (S2); (5) peptide fragment of (I) containing at least the DNA-binding
CC   domain; (6) antibodies (Ab) directed against an epitope of positions 1340
CC   -1901, 2219-2580 or 2581-2843 of (I); (7) set of two or more antibodies,
CC   one of which is Ab and the other directed against the N-terminal region
CC   (1-1299) of (I); and (8) kit for detecting DNA-binding capacity of (I) or
CC   its fragments in a sample consisting of (II), Ab or the set of (7). The
CC   method is used to detect proliferative, especially tumor (precursor),
CC   cells, to detect function of (I) and mutations in (I), and to purify
CC   and/or enrich (I), or its fragments, from a sample. The method allows
CC   simple, rapid and reliable detection of proliferation, without the need
CC   for polymerase chain reaction or sequencing
XX
SQ   Sequence 30 BP; 23 A; 3 C; 4 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          7 AAAAAAAAAAAAAAAAAAA 25


RESULT 1123
AAQ43410/c
ID   AAQ43410 standard; DNA; 31 BP.
XX
AC   AAQ43410;
XX
DT   25-MAR-2003  (revised)
DT   29-OCT-1993  (first entry)
XX
DE   Structural production oligonucleotide S-Strand-1.
XX
KW   Molecular scaffolding; molecule orientation; orient; juxtaposition;
KW   functional artificial components; one; two; three; dimensional;
KW   structure formation; therapeutic; analytical; industrial; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .15
FT                   /*tag= a
FT                   /note= "exposed/exposable sticky end"
FT   misc_feature    1
FT                   /*tag= b
FT                   /note= "PO4-Cytosine"
FT   misc_feature    31
FT                   /*tag= c
FT                   /note= "Thymine - Teflon based solid support"
XX
PN   WO9312244-A1.
XX
PD   24-JUN-1993.
XX
PF   03-DEC-1992;   92WO-US010431.
XX
PR   12-DEC-1991;   91US-00805564.
XX
PA   (UYNY ) UNIV NEW YORK STATE.
XX
PI   Seeman NC,  Zhang Y;
XX
DR   WPI; 1993-214185/26.
XX
PT   Prodn. of structure including double stranded polynucleotide - comprises
PT   cleavage of loop in core structure of 1st polynucleotide with restriction
PT   enzyme and ligation to 2nd polynucleotide, used to orient mols., etc.
XX
PS   Example; Page 34; 58pp; English.
XX
CC   The sequence is that of the oligonucleotide S-Strand-1 which can be used
CC   in the formation or modification of one-, two- and three- dimensional
CC   structures. It may be used as molecular scaffolding to orient and
CC   juxtapose other molecules. It has analytical, industrial or therapeutical
CC   potential. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 31 BP; 2 A; 4 C; 2 G; 23 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              ||||||||||||||||||
Db         31 AAAAAAAAAAAAAAAAAA 13


RESULT 1124
AAF60568/c
ID   AAF60568 standard; DNA; 32 BP.
XX
AC   AAF60568;
XX
DT   27-APR-2001  (first entry)
XX
DE   Neuraminidase PCR primer #6.
XX
KW   PCR primer; virucide; vaccine; gene therapy; neuraminidase; vaccine;
KW   immune response; ss.
XX
OS   Influenza virus.
XX
PN   WO200109291-A1.
XX
PD   08-FEB-2001.
XX
PF   28-JUL-2000; 2000WO-GB002933.
XX
PR   30-JUL-1999;   99GB-00017981.
PR   30-JUL-1999;   99US-0146145P.
XX
PA   (ISIS-) ISIS INNOVATION LTD.
XX
PI   Brownlee GG,  Fodor E,  Poon L;
XX
DR   WPI; 2001-159859/16.
XX
PT   New negative-sense single stranded RNA virus, e.g. influenza virus,
PT   attenuated by replacing the poly U track with a poly A track, useful as a
PT   vaccine and in gene therapy.
XX
PS   Example 7; Page 28; 49pp; English.
XX
CC   The present invention relates to an attenuated influenza virus. The virus
CC   is attenuated by replacement of the poly U track in a genomic nucleic
CC   acid by a poly A track capable of being copied to provide a poly U tail
CC   for mRNA transcribed from the nucleic acid. The attenuated virus is
CC   useful as a vaccine, for immunisation against diseases caused by the
CC   equivalent wild type viruses. The present sequence is a PCR primer used
CC   to generate the virus of the present invention
XX
SQ   Sequence 32 BP; 1 A; 6 C; 4 G; 21 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              ||||||||||||||||||
Db         32 AAAAAAAAAAAAAAAAAA 14


RESULT 1125
AAV03988/c
ID   AAV03988 standard; DNA; 32 BP.
XX
AC   AAV03988;
XX
DT   13-MAY-1998  (first entry)
XX
DE   Primer B for Non-A non-B hepatitis viral peptide coding sequence.
XX
KW   Non-A non-B hepatitis virus; antibody production; infection diagnosis;
KW   PCR primer; amplify; ss.
XX
OS   Synthetic.
OS   Hepatitis virus.
XX
PN   JP04084887-A.
XX
PD   18-MAR-1992.
XX
PF   25-JUL-1990;   90JP-00198588.
XX
PR   25-JUL-1990;   90JP-00198588.
XX
PA   (KAGA ) KAGAKU OYOBI KESSEI RYOHO.
XX
DR   WPI; 1992-145501/18.
XX
PT   Nucleic acid fragment coding peptide of non-A non-B hepatitis virus - for
PT   the early diagnosis of non-A non-B hepatitis by ELISA or agglutination
PT   methods.
XX
PS   Example 2; Page 7; 12pp; Japanese.
XX
CC   This sequence represents a primer for the coding sequence for a non-A non
CC   -B hepatitis virus peptide. The protein encoded by the amplified sequence
CC   can be used to prepare an antibody specific for non-A non-B hepatitis
CC   virus. The peptide and antibody can be used in both ELISA and
CC   agglutination methods and is useful in the early diagnosis of non-A non-B
CC   hepatitis
XX
SQ   Sequence 32 BP; 1 A; 5 C; 5 G; 21 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              ||||||||||||||||||
Db         32 AAAAAAAAAAAAAAAAAA 14


RESULT 1126
AAT77235/c
ID   AAT77235 standard; DNA; 32 BP.
XX
AC   AAT77235;
XX
DT   12-FEB-1998  (first entry)
XX
DE   Rat fibroblast growth factor FGF-10 RACE primer X.
XX
KW   Fibroblast growth factor; rat; human; recombinant DNA; bone disease;
KW   wound healing; cartilage; RACE primer; ss.
XX
OS   Synthetic.
OS   Rattus rattus.
XX
PN   WO9720929-A1.
XX
PD   12-JUN-1997.
XX
PF   06-DEC-1996;   96WO-JP003579.
XX
PR   07-DEC-1995;   95JP-00345689.
PR   28-MAR-1996;   96JP-00103240.
PR   24-JUL-1996;   96JP-00214378.
XX
PA   (SUMU ) SUMITOMO PHARM CO LTD.
XX
PI   Itoh N,  Negoro T,  Katsumata T,  Tagashira S;
XX
DR   WPI; 1997-319776/29.
XX
PT   Recombinant fibroblast growth factor FGF-10 and related DNA - useful for
PT   the treatment of bone disease and for wound healing.
```

```
XX
PS   Example 1; Page 36; 51pp; Japanese.
XX
CC   The present sequence represents a RACE primer involved in the
CC   amplification of rat fibroblast growth factor FGF-10. Recombinant FGF-10,
CC   vectors, containing the DNA, and host cells, containing the vectors, are
CC   useful for the recombinant production of FGF-10. The recombinant FGF-10
CC   is useful for the treatment of diseases and injury of bone or cartilage,
CC   and as a wound healing promoter
XX
SQ   Sequence 32 BP; 3 A; 4 C; 4 G; 21 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         32 AAAAAAAAAAAAAAAAAAA 14


RESULT 1127
AAS63424
ID   AAS63424 standard; DNA; 32 BP.
XX
AC   AAS63424;
XX
DT   29-JAN-2002  (first entry)
XX
DE   Oligonucleotide-nanoparticle probe #48.
XX
KW   Oligonucleotide-nanoparticle probe; diagnostic; forensic analysis;
KW   nucleic acid detection; nanostructure; biochip; biofilter; drug delivery;
KW   ss.
XX
OS   Synthetic.
XX
PN   WO200173123-A2.
XX
PD   04-OCT-2001.
XX
PF   28-MAR-2001; 2001WO-US010071.
XX
PR   28-MAR-2000; 2000US-0192699P.
PR   26-APR-2000; 2000US-0200161P.
PR   26-JUN-2000; 2000US-00603830.
PR   26-JUN-2000; 2000US-0213906P.
PR   08-DEC-2000; 2000US-0254392P.
PR   11-DEC-2000; 2000US-0255235P.
PR   12-JAN-2001; 2001US-00760500.
PR   28-MAR-2001; 2001US-00820279.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA,  Park S,  Li Z;
XX
DR   WPI; 2001-656926/75.
XX
PT   Detecting and separating nucleic acid, useful e.g. for diagnosis,
PT   comprises reaction with nanoparticles that carry oligonucleotides
PT   complementary to parts of the target.
XX
PS   Example 18; Page 148; 404pp; English.
XX
CC   The invention relates to a method for detection of nucleic acid (I)
CC   having at least 2 portions, comprising treatment with nanoparticles that
CC   carry oligonucleotides complementary to at least 2 parts of (I), where
CC   detectable change caused by hybridisation of the oligonucleotide to (I)
CC   is observed. The method is used to detect (or to separate) specific (I),
CC   e.g. for diagnosing a wide variety of diseases, sequencing, in forensic
CC   analysis etc., and generally to detect analytes other than (I). The
CC   oligonucleotide-derivatised nanoparticles are also useful for preparing
CC   nanostructures useful, for example, as biochips, biofilters, mechanical
CC   devices, separation membranes, chemical sensors, in computers, and for
CC   drug delivery. Very stable nanoparticle-oligonucleotide conjugates can be
CC   produced, allowing their direct use (as probes) in polymerase chain
CC   reaction, i.e. they survive multiple heating/cooling cycles so do not
CC   need to be added after amplification. (I) are detected by simple colour
CC   change, without the need for special equipment, making possible rapid
CC   field testing for e.g. pathogens. AAS63374-AAS63448 represent
CC   oligonucleotide-nanoparticle probes, and related sequences, used in the
CC   method of the invention
XX
SQ   Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 1128
AAS10367
ID   AAS10367 standard; DNA; 32 BP.
XX
AC   AAS10367;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Alkanethiol-modified oligonucleotide, SA2012F.
XX
KW   Nanoparticle; alkanethiol-modified oligonucleotide; DNA detection;
KW   DNA isolation; genetic disease; bacterial disease; viral disease;
KW   forensic science; paternity testing; gene therapy; ss; SA2012F.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1
FT                   /*tag=  a
FT                   /note= "A is covalently linked to a hexythiol moiety"
FT   misc_feature    12
FT                   /*tag=  b
FT                   /note= "T is covalently linked to a fluorescein moiety"
XX
PN   WO200151665-A2.
XX
PD   19-JUL-2001.
XX
PF   12-JAN-2001; 2001WO-US001190.
XX
PR   13-JAN-2000; 2000US-0176409P.
PR   26-APR-2000; 2000US-0200161P.
PR   26-JUN-2000; 2000US-00603830.
PR   12-JAN-2001; 2001US-00760500.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA,  Li Z;
XX
DR   WPI; 2001-451868/48.
XX
PT   Detecting a nucleic acid useful in e.g. diagnosing genetic, bacterial or
PT   viral diseases, by contacting the nucleic acid with oligonucleotides
PT   attached to nanoparticles and having sequences complementary a portion of
PT   the nucleic acid.
XX
PS   Example 18; Page 320; 323pp; English.
XX
CC   The sequence represents an alkanethiol-modified oligonucleotide which may
CC   be coupled with colloidal gold particles (nanoparticles) and used to
```

CC demonstrate the method of the invention. The invention relates to
CC isolating or detecting a nucleic acid of interest, in a mixture of
CC nucleic acids, by binding it to 2 or more complimentary nucleotides which
CC have a nanoparticle attached to their 5' ends. The nanoparticles (e.g.
CC colloidal gold) are used to both isolate and detect (e.g. by linking the
CC particle to a fluorescent probe) the resultant complex. The methods are
CC useful for detecting nucleic acids, natural or synthetic, and modified or
CC unmodified. The methods may also be applied in the diagnosis of genetic,
CC bacterial and viral diseases, in forensics, in DNA sequencing, for
CC paternity testing, for cell line authentication, and for monitoring gene
CC therapy. The methods are further useful in research and analytical
CC laboratories in DNA sequencing, in the field to detect the presence of
CC specific pathogens, for quick identification of an infection to assist in
CC drug prescription, and in homes and health centres for inexpensive first-
CC line screening. The methods, which are based on observing colour change
CC with the naked eye, are cheap, fast, simple, robust (reagents are
CC stable), do not require specialised or expensive equipment, and little or
CC no instrumentation is required
XX
SQ Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAAA 19

RESULT 1129
ABK65031
ID ABK65031 standard; DNA; 32 BP.
XX
AC ABK65031;
XX
DT 02-JUL-2002 (first entry)
XX
DE Nanoparticle-oligonucleotide #51.
XX
KW Nanoparticle-oligonucleotide; nanofabrication; nucleic acid detection;
KW ss.
XX
OS Synthetic.
XX
PN WO200218643-A2.
XX
PD 07-MAR-2002.
XX
PF 10-AUG-2001; 2001WO-US025237.
XX
PR 11-AUG-2000; 2000US-0224631P.
PR 08-DEC-2000; 2000US-0254392P.
PR 11-DEC-2000; 2000US-0255235P.
PR 12-JAN-2001; 2001US-00760500.
PR 28-MAR-2001; 2001US-00820279.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA, Garimella V, Li Z, Park S;
XX
DR WPI; 2002-258024/30.
XX
PT Detecting nucleic acid, useful for diagnosis of genetic, viral or
PT bacterial disease, comprises hybridizing nanoparticles with attached
PT oligonucleotides to nucleic acid and detecting change brought about by
PT hybridization.
XX
PS Example 18; Page 162; 412pp; English.
XX
CC The invention relates to a method of detecting a nucleic acid (NA) having
CC at least 2 portions comprising: (a) providing nanoparticles (NP) with
CC attached oligonucleotides (OGN), where OGN has a sequence complementary
CC to the sequence of NA; (b) contacting NA and NP under conditions
CC effective to allow hybridisation of OGN with NA; and (c) observing a
CC detectable change brought about by hybridisation of OGN with NA. The
CC method is useful for detecting a nucleic acid, separating a selected
CC nucleic acid from others and methods of nanofabrication. Detecting
CC analytes such as nucleic acids and proteins are useful for the diagnosis
CC of genetic, bacterial and viral diseases. The OGN-NP conjugates that use
CC cyclic disulphide linkers improve the sensitivity of diagnostic assays.
CC In particular assays using OGN-NP conjugates prepared using linkers
CC comprising a steroid residue attached to a cyclic disulphide have been
CC found to be approximately 10 times more sensitive than assays employing
CC conjugates prepared using alkanethiols or acyclic disulphides as the
CC linker. The OGN-NP conjugates are stable allowing them to be used
CC directly in PCR solutions. Therefore conjugates added as probes to a DNA
CC target to be PCR amplified can be carried through the 30 or 40 heating
CC cooling cycles of the PCR and are still able to detect the amplicons
CC without opening the tubes and causing contamination. ABK64981-ABK65055
CC represent nanoparticle-oligonucleotides of the invention
XX
SQ Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAAA 19

RESULT 1130
ABS64669
ID ABS64669 standard; DNA; 32 BP.
XX
AC ABS64669;
XX
DT 15-NOV-2002 (first entry)
XX
DE Nucleic acid detection method associated polynucleotide #51.
XX
KW Nucleic acid detection method; nanoparticle-oligonucleotide conjugate;
KW nanoparticle; viral RNA detection; bacterial DNA detection;
KW fungal DNA detection; nanoprobe conjugate; ss.
XX
OS Synthetic.
XX
PN WO200246472-A2.
XX
PD 13-JUN-2002.
XX
PF 07-DEC-2001; 2001WO-US046418.
XX
PR 08-DEC-2000; 2000US-0254392P.
PR 08-DEC-2000; 2000US-0254418P.
PR 11-DEC-2000; 2000US-0255235P.
PR 11-DEC-2000; 2000US-0255236P.
PR 12-JAN-2001; 2001US-00760500.
PR 28-MAR-2001; 2001US-00820279.
PR 09-APR-2001; 2001US-0282640P.
PR 10-AUG-2001; 2001US-00927777.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA, Garimella V, Li Z, Park S;
XX
DR WPI; 2002-608256/65.
XX
PT Detecting nucleic acid having two portions, by providing nanoparticles
PT having oligonucleotides attached to it, contacting nucleic acid and
PT nanoparticles to allow hybridization, and observing detectable change.
XX

```
PS   Example 18; Page 436; 442pp; English.
XX
CC   The invention describes a method of detecting (M1) a nucleic acid having
CC   two portions, involving providing nanoparticles having oligonucleotides
CC   attached to it, which has a sequence complementary to sequence of two
CC   portions of nucleic acid, contacting nucleic acid and nanoparticles, to
CC   allow hybridisation of oligonucleotides with two or more portions of
CC   nucleic acid, and observing a detectable change brought about by
CC   hybridisation. (M1), nanoparticles (I), nanoparticle-oligonucleotide
CC   conjugates (II) and the aggregate probe are useful for detecting two or
CC   more nucleic acids (from a biological source) having at least two
CC   portions, such as viral RNA, bacterial or fungal DNA, a gene associated
CC   with a disease, synthetic, or structurally-modified natural or synthetic
CC   RNA or DNA, or a product of a polymerase chain reaction amplification.
CC   (II) is useful for preparing a nanoprobe conjugate for detecting an
CC   analyte, and for detecting a nucleic acid bound to an electrode surface.
CC   (I) and (II) are useful for fabrication, and for separating a selected
CC   nucleic acid having two portions from other nucleic acids. (I), (II) and
CC   the aggregate probe are useful for detecting an analyte (especially
CC   polyvalent analyte) in a sample. This sequence represents a
CC   polynucleotide used to demonstrate the method of the invention
XX
SQ   Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 1131
ACD27316
ID   ACD27316 standard; DNA; 32 BP.
XX
AC   ACD27316;
XX
DT   15-OCT-2003  (first entry)
XX
DE   Nanotechnology nucleic acid detection method associated #50.
XX
KW   Nanotechnology; ss; nucleic acid detection; nanoparticle;
KW   virus detection; human immunodeficiency virus; HIV; hepatitis; herpes;
KW   cytomegalovirus; Epstein-Barr virus; bacterial disease; DNA sequencing;
KW   sexually transmitted disease; inherited disorder; forensic;
KW   paternity testing; cell line authentication.
XX
OS   Synthetic.
XX
PN   US2002155461-A1.
XX
PD   24-OCT-2002.
XX
PF   12-OCT-2001; 2001US-00976378.
XX
PR   29-JUL-1996;   96US-0031809P.
PR   21-JUL-1997;   97WO-US012783.
PR   29-JAN-1999;   99US-00240755.
PR   25-JUN-1999;   99US-00344667.
PR   26-APR-2000; 2000US-0200161P.
PR   26-JUN-2000; 2000US-00603830.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA;
XX
DR   WPI; 2003-228115/22.
XX
PT   Detecting nucleic acids having 2 portions e.g. for detecting disease,
PT   comprises use of nanoparticles which have oligonucleotides attached to
PT   them that are complementary to portions of the nucleic acid sequence.
XX
PS   Example 18; Page 40; 130pp; English.
XX
CC   This invention relates to a novel method for detecting a nucleic acid
CC   having 2 portions. The method comprises providing nanoparticles having
CC   oligonucleotides attached, where the oligonucleotide on each nanoparticle
CC   has a sequence complementary to a sequence of 2 portions of nucleic acid.
CC   The nucleic acid and nanoparticle are contacted to allow hybridisation of
CC   the oligonucleotide on the nanoparticle with two or more portions of
CC   nucleic acid and observing a detectable change brought about by the
CC   hybridisation. The method of the invention is useful for separating a
CC   selected nucleic acid having 2 portions, from other nucleic acids, and
CC   for detecting nucleic acids having 2 portions. The method of the
CC   invention is useful for detecting any type of nucleic acids which may be
CC   used for diagnosis of disease and in sequencing of nucleic acids.
CC   Preferably, the method is useful for detecting nucleic acids for
CC   diagnosis and/or monitoring of viral diseases (human immunodeficiency
CC   virus, hepatitis virus, herpes virus, cytomegalovirus and Epstein-Barr
CC   virus), bacterial diseases, sexually transmitted diseases, inherited
CC   disorders, in forensics, in DNA sequencing, for paternity testing, for
CC   cell line authentication, for monitoring gene therapy, etc. This method
CC   involves detecting nucleic acids based on observing a colour change with
CC   the naked eye so is cheap, fast, simple and robust, and does not require
CC   specialised expensive equipment. The present sequence represents an
CC   oligonucleotide used to demonstrate the method of the invention
XX
SQ   Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 1132
AAL61641
ID   AAL61641 standard; DNA; 32 BP.
XX
AC   AAL61641;
XX
DT   22-SEP-2003  (first entry)
XX
DE   Thiol-modified oligo #2 used in the nucleic acid detection method.
XX
KW   Nucleic acid detection; fabrication; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1
FT                   /*tag=  a
FT                   /note= "Linked to HS(CH2)6 group"
FT   misc_feature    32
FT                   /*tag=  b
FT                   /note= "Linked to (CH2)6-F (fluorescein)"
XX
PN   WO2003035829-A2.
XX
PD   01-MAY-2003.
XX
PF   08-OCT-2002; 2002WO-US032088.
XX
PR   09-OCT-2001; 2001US-0327864P.
PR   07-DEC-2001; 2001US-00008978.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Park S,  Taton TA,  Mirkin CA;
XX
```

DR WPI; 2003-430409/40.
XX
PT Detecting nucleic acid having two portions, by providing nanoparticles
PT having oligonucleotides attached to it, contacting nucleic acid and
PT nanoparticles to allow hybridization, and observing detectable change.
XX
PS Example 18; Page 167; 467pp; English.
XX
CC The invention relates to a method of detecting a nucleic acid having two
CC portions. The method involves providing nanoparticles having
CC oligonucleotides attached to it which has a sequence complementary to
CC sequence of two portions of nucleic acid, contacting nucleic acid and
CC nanoparticles to allow hybridisation of oligonucleotides with two or more
CC portions of nucleic acid and observing a detectable change brought about
CC by hybridisation. The method and aggregate probes are useful for
CC detecting two or more nucleic acids (from a biological source) having at
CC least two portions such as viral RNA, bacterial or fungal DNA, a gene
CC associated with a disease, synthetic or structurally modified natural or
CC synthetic RNA or DNA, or a product of a polymerase chain reaction
CC amplification. The invention is useful for preparing a nanoprobe
CC conjugate for detecting an analyte and for detecting a nucleic acid bound
CC to an electrode surface. It is also useful for fabrication and for
CC separating a selected nucleic acid having two portions from other nucleic
CC acids. The present sequence is an oligo used to illustrate the method of
CC the invention
XX
SQ Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAAA 19

RESULT 1133
ABX79177
ID ABX79177 standard; DNA; 32 BP.
XX
AC ABX79177;
XX
DT 15-APR-2003 (first entry)
XX
DE Fluorescein-labelled alkanethiol-modified oligonucleotide #2.
XX
KW Nanoparticle; ss; nucleic acid detection; viral disease;
KW human immunodeficiency virus infection; hepatitis virus infection;
KW herpes virus infection; cytomegalovirus infection; forensic science;
KW Epstein-Barr virus infection; bacterial disease; gene therapy;
KW sexually transmitted disease; inherited disorder; DNA sequencing;
KW paternity testing; cell line authentication.
XX
OS Synthetic.
XX
PN US2002155462-A1.
XX
PD 24-OCT-2002.
XX
PF 12-OCT-2001; 2001US-00976577.
XX
PR 29-JUL-1996; 96US-0031809P.
PR 21-JUL-1997; 97WO-US012783.
PR 29-JAN-1999; 99US-00240755.
PR 25-JUN-1999; 99US-00344667.
PR 26-APR-2000; 2000US-0200161P.
PR 26-JUN-2000; 2000US-00603830.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA;
XX
DR WPI; 2003-198491/19.
XX
PT Detecting nucleic acids having at least 2 portions comprises use of
PT nanoparticles which have oligonucleotides attached to them that are
PT complementary to portions of the nucleic acid sequence.
XX
PS Example 18; Page 40; 130pp; English.
XX
CC The invention relates to detecting a nucleic acid (NA) having at least 2
CC portions, comprises providing a type of nanoparticles (NP) having
CC attached to oligonucleotides (O) ((O) on each NP has a sequence
CC complementary to sequence of at least 2 portions of NA), contacting NA
CC and NP to allow hybridisation of (O) on NP with 2 or more portions of NA,
CC and observing a detectable change brought about by hybridisation of (O)
CC on NP with NA. The nanoparticle is useful for separating a selected
CC nucleic acid having at least 2 portions, from other nucleic acids, and
CC for detecting nucleic acids having at least 2 portions. The method of
CC using NP is useful for detecting any type of nucleic acids which may be
CC used for diagnosis of disease and in sequencing of nucleic acids.
CC Preferably, the method is useful for detecting nucleic acids for
CC diagnosis and/or monitoring of viral diseases (human immunodeficiency
CC virus, hepatitis virus, herpes virus, cytomegalovirus and Epstein-Barr
CC virus), bacterial diseases, sexually transmitted diseases, inherited
CC disorders, in forensics, in DNA sequencing, for paternity testing, for
CC cell line authentication and for monitoring gene therapy. The method is
CC useful in research and analytical laboratories in DNA sequencing and in
CC the field to detect the presence of specific pathogens. Detecting nucleic
CC acids based on observing a colour change with the naked eye is cheap,
CC fast, simple and robust, and do not require specialised expensive
CC equipment. The present sequence is a fluorescein labelled oligonucleotide
CC used to demonstrate the method of the invention
XX
SQ Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAAA 19

RESULT 1134
ABX92173
ID ABX92173 standard; DNA; 32 BP.
XX
AC ABX92173;
XX
DT 12-MAY-2003 (first entry)
XX
DE Nanoparticle-associated oligonucleotide SEQ ID 51.
XX
KW Nonoparticle; nucleic acid detection; hybridisation; diagnosis;
KW sequencing; viral infection; human immunodeficiency virus; HIV;
KW hepatitis virus; herpes virus; cytomegalovirus; Epstein-Barr virus;
KW bacterial infection; sexually transmitted disease; inherited disorder;
KW forensic; paternity testing; cell line authentication; gene therapy; ss.
XX
OS Synthetic.
XX
PN US2002155458-A1.
XX
PD 24-OCT-2002.
XX
PF 28-SEP-2001; 2001US-00967409.
XX
PR 29-JUL-1996; 96US-0031809P.
PR 21-JUL-1997; 97WO-US012783.
PR 29-JAN-1999; 99US-00240755.
PR 25-JUN-1999; 99US-00344667.
PR 26-APR-2000; 2000US-0200161P.

PR 26-JUN-2000; 2000US-00603830.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA;
XX
DR WPI; 2003-182627/18.
XX
PT Detecting nucleic acids having at least two portions involves use of
PT nanoparticles which have oligonucleotides attached to them that are
PT complementary to portions of the nucleic acid sequence.
XX
PS Example 18; Page 59; 130pp; English.
XX
CC This invention describes a novel method of detecting nucleic acid having
CC at least two portions. The method involves providing nanoparticles
CC attached to oligonucleotides, where the oligonucleotide on each
CC nanoparticle have a sequence complementary to a sequence of at least two
CC portions of nucleic acid, contacting nucleic acid and nanoparticle to
CC allow hybridisation of the oligonucleotide on the nanoparticle with two
CC or more portions of nucleic acid and observing a detectable change
CC brought about by hybridisation of the oligonucleotide nanoparticle with
CC nucleic acid. The method is useful for separating a selected nucleic acid
CC having at least two portions, from other nucleic acids and for detecting
CC nucleic acids having at least two portions. The method is useful for
CC detecting any type of nucleic acids which may be used for diagnosis of
CC disease and in sequencing of nucleic acids. Preferably, the method is
CC useful for detecting nucleic acids for diagnosis and/or monitoring of
CC viral infections (human immunodeficiency virus (HIV), hepatitis virus,
CC herpes virus, cytomegalovirus and Epstein-Barr virus), bacterial
CC diseases, sexually transmitted diseases, inherited disorders, in
CC forensics, in DNA sequencing, for paternity testing, for cell line
CC authentication, and for monitoring gene therapy. The method is useful in
CC research and analytical laboratories in DNA sequencing, in the field to
CC detect the presence of specific pathogens. Detecting nucleic acids based
CC on observing a colour change with the naked eye is cheap, fast, simple
CC and robust and does not require specialised expensive equipment. ABX92123
CC -ABX92186 and ABQ77356 represent oligonucleotides used to illustrate the
CC method of the invention
XX
SQ Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAAA 19

RESULT 1135
ACD27251
ID ACD27251 standard; DNA; 32 BP.
XX
AC ACD27251;
XX
DT 15-OCT-2003 (first entry)
XX
DE Nanotechnology nucleic acid detection method associated #50.
XX
KW Nanotechnology; ss; nucleic acid detection; nanoparticle;
KW virus detection; human immunodeficiency virus; HIV; hepatitis; herpes;
KW cytomegalovirus; Epstein-Barr virus; bacterial disease; DNA sequencing;
KW sexually transmitted disease; inherited disorder; forensic;
KW paternity testing; cell line authentication.
XX
OS Synthetic.
XX
PN US2002155459-A1.
XX
PD 24-OCT-2002.
XX
PF 11-OCT-2001; 2001US-00975062.
XX
PR 29-JUL-1996; 96US-0031809P.
PR 21-JUL-1997; 97WO-US012783.
PR 29-JAN-1999; 99US-00240755.
PR 25-JUN-1999; 99US-00344667.
PR 26-APR-2000; 2000US-0200161P.
PR 26-JUN-2000; 2000US-00603830.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA;
XX
DR WPI; 2003-228114/22.
XX
PT Detecting nucleic acids having 2 portions e.g. for detecting disease,
PT comprises use of nanoparticles which have oligonucleotides attached to
PT them that are complementary to portions of the nucleic acid sequence.
XX
PS Example 18; Page 40; 129pp; English.
XX
CC This invention relates to a novel method for detecting a nucleic acid
CC having 2 portions. The method comprises providing nanoparticles having
CC oligonucleotides attached, where the oligonucleotide on each nanoparticle
CC has a sequence complementary to a sequence of 2 portions of nucleic acid.
CC The nucleic acid and nanoparticle are contacted to allow hybridisation of
CC the oligonucleotide on the nanoparticle with two or more portions of
CC nucleic acid and observing a detectable change brought about by the
CC hybridisation. The method of the invention is useful for separating a
CC selected nucleic acid having 2 portions, from other nucleic acids, and
CC for detecting nucleic acids having 2 portions. The method of the
CC invention is useful for detecting any type of nucleic acids which may be
CC used for diagnosis of disease and in sequencing of nucleic acids.
CC Preferably, the method is useful for detecting nucleic acids for
CC diagnosis and/or monitoring of viral diseases (human immunodeficiency
CC virus, hepatitis virus, herpes virus, cytomegalovirus and Epstein-Barr
CC virus), bacterial diseases, sexually transmitted diseases, inherited
CC disorders, in forensics, in DNA sequencing, for paternity testing, for
CC cell line authentication, for monitoring gene therapy, etc. This method
CC involves detecting nucleic acids based on observing a colour change with
CC the naked eye so is cheap, fast, simple and robust, and does not require
CC specialised expensive equipment. The present sequence represents an
CC oligonucleotide used to demonstrate the method of the invention
XX
SQ Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAAA 19

RESULT 1136
ACD27121
ID ACD27121 standard; DNA; 32 BP.
XX
AC ACD27121;
XX
DT 15-OCT-2003 (first entry)
XX
DE Nanotechnology nucleic acid detection method oligonucleotide #50.
XX
KW Nanotechnology; nucleic acid detection; nanoparticle; ss; forensic;
KW DNA sequencing; paternity testing; cell line authentication.
XX
OS Synthetic.
XX
PN US2002164605-A1.

```
XX
PD   07-NOV-2002.
XX
PF   28-SEP-2001; 2001US-00966312.
XX
PR   29-JUL-1996;   96US-0031809P.
PR   21-JUL-1997;   97WO-US012783.
PR   29-JAN-1999;   99US-00240755.
PR   25-JUN-1999;   99US-00344667.
PR   26-APR-2000; 2000US-0200161P.
PR   26-JUN-2000; 2000US-00603830.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA;
XX
DR   WPI; 2003-247253/24.
XX
PT   Detecting nucleic acid having two portions, by providing nanoparticles
PT   having oligonucleotides attached to it, contacting nucleic acid and
PT   nanoparticles to allow hybridization, and observing detectable change,
PT   useful in forensics.
XX
PS   Example 18; Page 40; 130pp; English.
XX
CC   This invention relates to a novel method for detecting nucleic acid
CC   sequences having two portions. The method involves providing
CC   nanoparticles having oligonucleotides attached to them, which has a
CC   sequence complementary to sequence of two portions of nucleic acid,
CC   contacting nucleic acid and nanoparticles, to allow hybridisation of
CC   oligonucleotides with two or more portions of nucleic acid, and observing
CC   a detectable change brought about by hybridisation. The method of the
CC   invention and the aggregate probes are useful for detecting two or more
CC   nucleic acids (from a biological source) having at least two portions,
CC   such as viral RNA or DNA, bacterial or fungal DNA, a gene associated with
CC   a disease, synthetic, or structurally- modified natural or synthetic RNA
CC   or DNA, or a product of a polymerase chain reaction amplification.
CC   Nanoparticles and nanoparticle- oligonucleotide conjugates of the
CC   invention are useful for nanofabrication, and for separating a selected
CC   nucleic acid having two portions from other nucleic acids. The method of
CC   the invention is useful in forensics, DNA sequencing, for paternity
CC   testing, cell line authentication, and monitoring gene therapy.
CC   Diagnostic assays employing the nanoparticle-oligonucleotide conjugates
CC   of the invention improve the sensitivity of the nucleic acid detection
CC   assay. The present sequence represents an oligonucleotide used to
CC   demonstrate the method of the invention
XX
SQ   Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 1137
ACD27381
ID   ACD27381 standard; DNA; 32 BP.
XX
AC   ACD27381;
XX
DT   15-OCT-2003  (first entry)
XX
DE   Nanotechnology nucleic acid detection method associated #50.
XX
KW   Nanoparticle; ss; nucleic acid detection; DNA sequencing;
KW   pathogen detection.
XX
OS   Synthetic.
XX
PN   US2002182611-A1.
XX
PD   05-DEC-2002.
XX
PF   28-SEP-2001; 2001US-00966491.
XX
PR   29-JUL-1996;   96US-0031809P.
PR   21-JUL-1997;   97WO-US012783.
PR   29-JAN-1999;   99US-00240755.
PR   25-JUN-1999;   99US-00344667.
PR   26-APR-2000; 2000US-0200161P.
PR   26-JUN-2000; 2000US-00603830.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA;
XX
DR   WPI; 2003-596264/56.
XX
PT   Detection of nucleic acid for, e.g. research and analytical laboratories
PT   in deoxyribonucleic acid sequencing, involves contacting nucleic acid
PT   with nanoparticles having oligonucleotides.
XX
PS   Example 18; Page 40; 109pp; English.
XX
CC   This invention relates to a novel method for detecting a nucleic acid by
CC   contacting a nucleic acid with at least two types of nanoparticles having
CC   oligonucleotides attached, allowing hybridisation of the oligonucleotides
CC   on the nanoparticles, and observing a detectable change. The
CC   oligonucleotides on each nanoparticle have a sequence complementary to
CC   its respective portion of the sequence of the nucleic acid to be
CC   detected. The method of the invention may be used for the detection of a
CC   nucleic acid used in, e.g. research and analytical laboratories in DNA
CC   sequencing, in the field to detect the presence of specific pathogens, in
CC   the doctor's office for quick identification of an infection to assist in
CC   prescribing a drug for treatment, and in homes and health centres for
CC   inexpensive first-line screening. The method of the invention detects
CC   nucleic acids based on observing a colour change with the naked eye. This
CC   method is cheap, fast, simple, robust and does not require specialised or
CC   expensive equipment. The present sequence represents an oligonucleotide
CC   used to demonstrate the method of the invention
XX
SQ   Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 1138
ACD27186
ID   ACD27186 standard; DNA; 32 BP.
XX
AC   ACD27186;
XX
DT   15-OCT-2003  (first entry)
XX
DE   Nanotechnology nucleic acid detection method associated #50.
XX
KW   Nanoparticle; ss; nucleic acid detection; DNA sequencing.
XX
OS   Synthetic.
XX
PN   US2002182613-A1.
XX
PD   05-DEC-2002.
XX
```

PF 12-OCT-2001; 2001US-00976971.
XX
PR 29-JUL-1996; 96US-0031809P.
PR 21-JUL-1997; 97WO-US012783.
PR 29-JAN-1999; 99US-00240755.
PR 25-JUN-1999; 99US-00344667.
PR 26-APR-2000; 2000US-0200161P.
PR 26-JUN-2000; 2000US-00603830.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA;
XX
DR WPI; 2003-596265/56.
XX
PT Detection of nucleic acid for, e.g. research and analytical laboratories
PT in deoxyribonucleic acid sequencing, involves contacting nucleic acid
PT with nanoparticles having oligonucleotides.
XX
PS Example 18; Page 40; 107pp; English.
XX
CC This invention relates to a novel method for detecting a nucleic acid by
CC contacting nucleic acid with at least two types of nanoparticles having
CC oligonucleotides, allowing hybridisation of the oligonucleotides on the
CC nanoparticles, and observing a detectable change. The oligonucleotides on
CC each nanoparticle have a sequence complementary to its respective portion
CC of the sequence of the nucleic acid. The method of the invention may be
CC used for the detection of a nucleic acid used in, e.g. research and
CC analytical laboratories in DNA sequencing, in the field to detect the
CC presence of specific pathogens, in the doctor's office for quick
CC identification of an infection to assist in prescribing a drug for
CC treatment, and in homes and health centres for inexpensive first-line
CC screening. The inventive method of detecting nucleic acids based on
CC observing a colour change with the naked eye are cheap, fast, simple,
CC robust (the reagents are stable), do not require specialised or expensive
CC equipment, and little or no instrumentation is required. The present
CC sequence represents an oligonucleotide used to demonstrate the method of
CC the invention
XX
SQ Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAAA 19

RESULT 1139
ACD27056
ID ACD27056 standard; DNA; 32 BP.
XX
AC ACD27056;
XX
DT 15-OCT-2003 (first entry)
XX
DE Nanotechnology nucleic acid detection method oligonucleotide #50.
XX
KW Nanotechnology; nucleic acid detection; nanofabrication; nanoprobe; ss.
XX
OS Synthetic.
XX
PN US2003044805-A1.
XX
PD 06-MAR-2003.
XX
PF 15-OCT-2001; 2001US-00981344.
XX
PR 29-JUL-1996; 96US-0031809P.
PR 21-JUL-1997; 97WO-US012783.
PR 29-JAN-1999; 99US-00240755.
PR 25-JUN-1999; 99US-00344667.
PR 26-APR-2000; 2000US-0200161P.
PR 26-JUN-2000; 2000US-00603830.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA;
XX
DR WPI; 2003-521746/49.
XX
PT Detection of nucleic acid having -2 portions used to prepare biomaterials
PT and in nanofabrication methods, comprises providing nanoparticles,
PT contacting nucleic acid and nanoparticles, and observing change.
XX
PS Example 18; Page 40; 130pp; English.
XX
CC This invention relates to a novel method for detecting nucleic acids. The
CC method comprises providing nanoparticles with oligonucleotides attached
CC to them, which have a sequence complementary to a sequence of two
CC portions of nucleic acid, contacting the nucleic acid and nanoparticles
CC to allow hybridisation of the oligonucleotides with two or more portions
CC of the nucleic acid, and observing a detectable change brought about by
CC the hybridisation. The nucleic acid to be detected must have at least two
CC portions and the distances between these are chosen so that when the
CC nanoparticle-oligonucleotide conjugate binds the target sequence a
CC detectable change occurs. The method of the invention is useful for
CC detecting two or more nucleic acids (from a biological source) having at
CC least two portions, such as viral RNA, bacterial or fungal DNA, a gene
CC associated with a disease, synthetic, or structurally- modified natural
CC or synthetic RNA or DNA, or a product of a polymerase chain reaction
CC amplification. Nanoparticle-oligonucleotide conjugates of the invention
CC are useful for preparing a nanoprobe conjugate for detecting an analyte,
CC and for detecting a nucleic acid bound to an electrode surface.
CC Nanoparticles and nanoparticle conjugates of the invention are useful for
CC nanofabrication and for separating a selected nucleic acid having two
CC portions from other nucleic acids. Diagnostic assays employing
CC nanoparticle-oligonucleotide conjugates improve the sensitivity of
CC nucleic acid detection methods and can be used to detect nucleic acids
CC that are present in only small amounts in a sample. The invention also
CC provides highly desirable nanoparticle-oligonucleotide conjugates. These
CC conjugates are stable with tailored hybridisation abilities. The present
CC sequence represents an oligonucleotide used to demonstrate the method of
CC the invention
XX
SQ Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAAA 19

RESULT 1140
ACH00060
ID ACH00060 standard; DNA; 32 BP.
XX
AC ACH00060;
XX
DT 15-OCT-2003 (first entry)
XX
DE Nanotechnology nucleic acid detection method oligonucleotide #50.
XX
KW Nanotechnology; nucleic acid detection; nanofabrication; nanoprobe; ss.
XX
OS Synthetic.
XX
PN US2003049631-A1.
XX

```
PD   13-MAR-2003.
XX
PF   10-OCT-2001; 2001US-00974500.
XX
PR   29-JUL-1996;   96US-0031809P.
PR   21-JUL-1997;   97WO-US012783.
PR   29-JAN-1999;   99US-00240755.
PR   25-JUN-1999;   99US-00344667.
PR   26-APR-2000; 2000US-0200161P.
PR   26-JUN-2000; 2000US-00603830.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA;
XX
DR   WPI; 2003-634854/60.
XX
PT   Detection of nucleic acid having at least two portions, by contacting
PT   nucleic acid and nanoparticles under conditions, which allows
PT   hybridization of oligonucleotides on nanoparticles with at least two
PT   portions of nucleic acid.
XX
PS   Example 18; Page 40; 108pp; English.
XX
CC   This invention relates to a novel method for detecting nucleic acids. The
CC   method comprises providing nanoparticles with oligonucleotides attached
CC   to them, which have a sequence complementary to a sequence of two
CC   portions of nucleic acid, contacting the nucleic acid and nanoparticles
CC   to allow hybridisation of the oligonucleotides with two or more portions
CC   of the nucleic acid, and observing a detectable change brought about by
CC   the hybridisation. The nucleic acid to be detected must have at least two
CC   portions and the distances between these are chosen so that when the
CC   nanoparticle-oligonucleotide conjugate binds the target sequence a
CC   detectable change occurs. The method of the invention is useful for
CC   detecting two or more nucleic acids (from a biological source) having at
CC   least two portions, such as viral RNA, bacterial or fungal DNA, a gene
CC   associated with a disease, synthetic, or structurally- modified natural
CC   or synthetic RNA or DNA, or a product of a polymerase chain reaction
CC   amplification. Nanoparticle-oligonucleotide conjugates of the invention
CC   are useful for preparing a nanoprobe conjugate for detecting an analyte,
CC   and for detecting a nucleic acid bound to an electrode surface.
CC   Nanoparticles and nanoparticle conjugates of the invention are useful for
CC   nanofabrication and for separating a selected nucleic acid having two
CC   portions from other nucleic acids. Diagnostic assays employing
CC   nanoparticle-oligonucleotide conjugates improve the sensitivity of
CC   nucleic acid detection methods and can be used to detect nucleic acids
CC   that are present in only small amounts in a sample. The invention also
CC   provides highly desirable nanoparticle-oligonucleotide conjugates. These
CC   conjugates are stable with tailored hybridisation abilities. The present
CC   sequence represents an oligonucleotide used to demonstrate the method of
CC   the invention
XX
SQ   Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 1141
ADA06155
ID   ADA06155 standard; DNA; 32 BP.
XX
AC   ADA06155;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Nanoparticle labelled oligonucleotides, spacer DNA #1.
XX
KW   ss; nanoparticle; colloidal gold; semiconductor; nanomaterial;
KW   nanostructure; viral disease; human immunodeficiency virus infection;
KW   hepatitis virus infection; herpes virus infection;
KW   cytomegalovirus virus infection; Epstein-Barr virus; bacterial disease;
KW   sexually transmitted disease; inherited disorders; paternity testing;
KW   cell line authentication; gene therapy.
XX
OS   Synthetic.
XX
PN   US2003068622-A1.
XX
PD   10-APR-2003.
XX
PF   12-OCT-2001; 2001US-00976863.
XX
PR   29-JUL-1996;   96US-0031809P.
PR   21-JUL-1997;   97WO-US012783.
PR   29-JAN-1999;   99US-00240755.
PR   25-JUN-1999;   99US-00344667.
PR   26-APR-2000; 2000US-0200161P.
PR   26-JUN-2000; 2000US-00603830.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA;
XX
DR   WPI; 2003-576420/54.
XX
PT   Detecting nucleic acids having at least 2 portions comprises use of
PT   nanoparticles which have oligonucleotides attached to them that are
PT   complementary to portions of the target nucleic acid sequence.
XX
PS   Example 18; Page 40; 130pp; English.
XX
CC   The invention relates to detecting a nucleic acid (NA) having at least 2
CC   portions comprises providing a type of nanoparticles (NP. e.g. colloidal
CC   gold) having oligonucleotides (O) attached (where (O) on each NP has a
CC   sequence complementary to sequence of at least two portions of NA),
CC   contacting NA and NP to allow hybridisation of (O) on NP with 2 or more
CC   portions of NA, and observing a detectable change brought about by
CC   hybridization of (O) on NP with NA. Also included are aggregate probes,
CC   core probes, substrate having NP attached to it, a metallic or
CC   semiconductor NP having (O) attached to it, nanomaterials/nanostructures
CC   comprising nanoparticles and methods of nanofabrication utilising
CC   nanoparticles and satellite probes. The methods, probes nucleic acids,
CC   nanoparticles and oligonucleotides are useful for separating a selected
CC   nucleic acid having at least two portions, from other nucleic acids, and
CC   for detecting nucleic acids having at least two portions, for detecting
CC   NA having at least two portions. The method is useful for detecting any
CC   type of nucleic acids which may be used for diagnosis of disease and in
CC   sequencing of nucleic acids. Preferably, the method is useful for
CC   detecting nucleic acids for diagnosis and/or monitoring of viral diseases
CC   (human immunodeficiency virus, hepatitis virus, herpes virus,
CC   cytomegalovirus and Epstein-Barr virus), bacterial diseases, sexually
CC   transmitted diseases, inherited disorders, in forensics, in DNA
CC   sequencing, for paternity testing, for cell line authentication, for
CC   monitoring gene therapy, etc. The method is useful in research and
CC   analytical laboratories in DNA sequencing, in the field to detect the
CC   presence of specific pathogens, etc. Detecting nucleic acids based on
CC   observing a colour change with the naked eye is cheap, fast, simple and
CC   robust, and do not require specialised expensive equipment. The present
CC   sequence is a spacer oligonucleotide used to illustrate the method of the
CC   invention.
XX
SQ   Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
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                    ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 1142
ACD26991
ID   ACD26991 standard; DNA; 32 BP.
XX
AC   ACD26991;
XX
DT   15-OCT-2003  (first entry)
XX
DE   Nanotechnology nucleic acid detection method oligonucleotide #50.
XX
KW   Nanotechnology; nucleic acid detection; nanofabrication; nanoprobe; ss.
XX
OS   Synthetic.
XX
PN   US2003049630-A1.
XX
PD   13-MAR-2003.
XX
PF   20-SEP-2001; 2001US-00957318.
XX
PR   29-JUL-1996;   96US-0031809P.
PR   21-JUL-1997;   97WO-US012783.
PR   29-JAN-1999;   99US-00240755.
PR   25-JUN-1999;   99US-00344667.
PR   26-APR-2000; 2000US-0200161P.
PR   26-JUN-2000; 2000US-00603830.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA;
XX
DR   WPI; 2003-615795/58.
XX
PT   Detecting nucleic acid having two portions, by providing nanoparticles
PT   having oligonucleotides attached to it, contacting nucleic acid and
PT   nanoparticles to allow hybridization, and observing detectable change.
XX
PS   Example 18; Page 40 ; 129pp; English.
XX
CC   This invention relates to a novel method for detecting nucleic acids. The
CC   method comprises providing nanoparticles with oligonucleotides attached
CC   to them, which have a sequence complementary to a sequence of two
CC   portions of nucleic acid, contacting the nucleic acid and nanoparticles
CC   to allow hybridisation of the oligonucleotides with two or more portions
CC   of the nucleic acid, and observing a detectable change brought about by
CC   the hybridisation. The nucleic acid to be detected must have at least two
CC   portions and the distances between these are chosen so that when the
CC   nanoparticle-oligonucleotide conjugate binds the target sequence a
CC   detectable change occurs. The method of the invention is useful for
CC   detecting two or more nucleic acids (from a biological source) having at
CC   least two portions, such as viral RNA, bacterial or fungal DNA, a gene
CC   associated with a disease, synthetic, or structurally- modified natural
CC   or synthetic RNA or DNA, or a product of a polymerase chain reaction
CC   amplification. Nanoparticle-oligonucleotide conjugates of the invention
CC   are useful for preparing a nanoprobe conjugate for detecting an analyte,
CC   and for detecting a nucleic acid bound to an electrode surface.
CC   Nanoparticles and nanoparticle conjugates of the invention are useful for
CC   nanofabrication and for separating a selected nucleic acid having two
CC   portions from other nucleic acids. Diagnostic assays employing
CC   nanoparticle-oligonucleotide conjugates improve the sensitivity of
CC   nucleic acid detection methods and can be used to detect nucleic acids
CC   that are present in only small amounts in a sample. The present sequence
CC   represents an oligonucleotide used to demonstrate the method of the
CC   invention
XX
SQ   Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match           0.7%;  Score 19;  DB 1;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 1143
ADE71592
ID   ADE71592 standard; DNA; 32 BP.
XX
AC   ADE71592;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Magneto-gold nanoparticle probe #2.
XX
KW   Magneto-gold nanoparticle; probe; ss; core nanoparticle;
KW   non-alloying gold shell; shell nanoparticle; gold salt.
XX
OS   Synthetic.
XX
PN   US2003129608-A1.
XX
PD   10-JUL-2003.
XX
PF   22-MAY-2002; 2002US-00153483.
XX
PR   25-MAY-2001; 2001US-0293861P.
PR   28-DEC-2001; 2001US-00034451.
PR   28-DEC-2001; 2001WO-US050825.
XX
PA   (MIRK/) MIRKIN C A.
PA   (CAOY/) CAO Y.
PA   (JINR/) JIN R.
XX
PI   Mirkin CA,  Cao Y,  Jin R;
XX
DR   WPI; 2004-031299/03.
XX
PT   Core/shell nanoparticle for detecting target molecules, e.g. nucleic
PT   acids, comprises inner metal-containing nanoparticle core, outer non-
PT   alloying gold shell, and oligonucleotides attached to gold shell.
XX
PS   Example 5; Page 8; 21pp; English.
XX
CC   The invention relates to a core/shell nanoparticle comprising an inner
CC   metal-containing nanoparticle core and an outer non-alloying gold shell
CC   surrounding the nanoparticle core. Oligonucleotides may be attached to
CC   the gold shell. The invention also relates to preparation of core/shell
CC   nanoparticles by treating inner metal-containing nanoparticle cores
CC   simultaneously with a solution containing gold salt and a solution
CC   containing a reducing agent to produce a non-alloying gold shell
CC   surrounding the nanoparticle cores, and isolating the core/shell
CC   nanoparticles. Detection of target analytes, e.g. a nucleic acid, bound
CC   to a surface comprises contacting the surface with a solution comprising
CC   a core/shell nanoparticle receptor conjugate under conditions effective
CC   to allow binding of nanoparticle conjugates with the bound nucleic acid,
CC   subjecting the nanoparticle conjugate to an external magnetic field to
CC   accelerate movement of the nanoparticle conjugate to the surface, to
CC   promote binding interaction between the nanoparticle conjugate and target
CC   analyte, removing any nanoparticle conjugates that have not bound with
CC   the target analyte and observing a detectable change brought about by a
CC   binding interaction of the target analyte with the nanoparticle
CC   conjugates. The invention is used for detecting target molecules such as
CC   nucleic acids, peptides and proteins. The optical properties of
CC   core/shell nanoparticles form a new calorimetric channel for nanoparticle
CC   -based DNA detection. This sequence represents a magneto-gold
CC   nanoparticle probe used in the scope of the invention.
XX
SQ   Sequence 32 BP; 24 A; 4 C; 0 G; 4 T; 0 U; 0 Other;
```

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  Query Match             0.7%;  Score 19;  DB 1;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 1144
ABQ80395
ID   ABQ80395 standard; DNA; 33 BP.
XX
AC   ABQ80395;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Probe APC 1-MUT.
XX
KW   Probe; target; nanoparticle; detection; DNA sequencing; pathogen;
KW   infection; screening; colour change; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /note= "Gold-S'-A"
XX
PN   WO2003048769-A1.
XX
PD   12-JUN-2003.
XX
PF   27-NOV-2002; 2002WO-US038069.
XX
PR   30-NOV-2001; 2001US-0334644P.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Storhoff JJ,  Fritz BM,  Herrmann M;
XX
DR   WPI; 2003-617993/58.
XX
PT   Detecting target polynucleotide in a sample, by amplifying target,
PT   hybridizing it to oligonucleotides bound to nanoparticles in nanoparticle
PT   detection system, and determining amount of signal generated due to
PT   binding.
XX
PS   Example 1; Page 35; 74pp; English.
XX
CC   The sequences given in ABQ80394-99 represent probes and targets which
CC   were used in the method of the invention for detecting a target
CC   polynucleotide in a sample. The method comprises amplifying the target,
CC   hybridizing the target to oligonucleotides bound to nanoparticles in a
CC   nanoparticle detection system, determining the amount of signal generated
CC   as a result of binding, optionally repeating the above steps, and
CC   detecting the presence of the target oligonucleotide by analysing for the
CC   amount of signal produced after at least one amplification cycle. The
CC   method is useful for detecting target polynucleotide in a sample, and for
CC   determining the quantity of target polynucleotide in a sample. The method
CC   is useful in research and analytical laboratories in DNA sequencing, in
CC   the field to detect the presence of specific pathogens, in the doctor's
CC   office for quick identification of an infection to assist in prescribing
CC   a drug for treatment, and in homes and health centres for inexpensive
CC   first-line screening. The method is based on observing colour change with
CC   the naked eye, hence the method is cheap, fast, simple, robust, do not
CC   require specialized or expensive equipment, and little or no
CC   instrumentation is required
XX
SQ   Sequence 33 BP; 29 A; 1 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 1145
ABQ80394
ID   ABQ80394 standard; DNA; 33 BP.
XX
AC   ABQ80394;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Probe APC 1-WT.
XX
KW   Probe; target; nanoparticle; detection; DNA sequencing; pathogen;
KW   infection; screening; colour change; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /note= "Gold-S'-A"
XX
PN   WO2003048769-A1.
XX
PD   12-JUN-2003.
XX
PF   27-NOV-2002; 2002WO-US038069.
XX
PR   30-NOV-2001; 2001US-0334644P.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Storhoff JJ,  Fritz BM,  Herrmann M;
XX
DR   WPI; 2003-617993/58.
XX
PT   Detecting target polynucleotide in a sample, by amplifying target,
PT   hybridizing it to oligonucleotides bound to nanoparticles in nanoparticle
PT   detection system, and determining amount of signal generated due to
PT   binding.
XX
PS   Example 1; Page 35; 74pp; English.
XX
CC   The sequences given in ABQ80394-99 represent probes and targets which
CC   were used in the method of the invention for detecting a target
CC   polynucleotide in a sample. The method comprises amplifying the target,
CC   hybridizing the target to oligonucleotides bound to nanoparticles in a
CC   nanoparticle detection system, determining the amount of signal generated
CC   as a result of binding, optionally repeating the above steps, and
CC   detecting the presence of the target oligonucleotide by analysing for the
CC   amount of signal produced after at least one amplification cycle. The
CC   method is useful for detecting target polynucleotide in a sample, and for
CC   determining the quantity of target polynucleotide in a sample. The method
CC   is useful in research and analytical laboratories in DNA sequencing, in
CC   the field to detect the presence of specific pathogens, in the doctor's
CC   office for quick identification of an infection to assist in prescribing
CC   a drug for treatment, and in homes and health centres for inexpensive
CC   first-line screening. The method is based on observing colour change with
CC   the naked eye, hence the method is cheap, fast, simple, robust, do not
CC   require specialized or expensive equipment, and little or no
CC   instrumentation is required
XX
SQ   Sequence 33 BP; 28 A; 1 C; 3 G; 1 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAA 19
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RESULT 1146
ADC60749/c
ID ADC60749 standard; DNA; 33 BP.
XX
AC ADC60749;
XX
DT 18-DEC-2003 (first entry)
XX
DE Termitomyces albuminosus acidic peroxidase-related RT-PCR primer.
XX
KW acidic peroxidase; TAP; organochlorine compound;
KW waste water purification; Western blotting; ss; PCR; RT-PCR; primer.
XX
OS Termitomyces albuminosus.
XX
PN JP2003070473-A.
XX
PD 11-MAR-2003.
XX
PF 03-SEP-2001; 2001JP-00266069.
XX
PR 03-SEP-2001; 2001JP-00266069.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
PA (RIKA) RIKAGAKU KENKYUSHO.
XX
DR WPI; 2003-590855/56.
XX
PT New protein with acidic peroxidase activity, derived from Termitomyces
PT albuminosus ATTC42010, useful in the analysis of organochlorine compounds
PT during waste water purification processes.
XX
PS Example 2; SEQ ID NO 3; 12pp; Japanese.
XX
CC The invention relates to a novel acidic peroxidase protein (TAP) obtained
CC from Termitomyces albuminosus ATTC42010. The polypeptide of the invention
CC may be useful in the analysis of organochlorine compounds during waste
CC water purification processes and in Western blotting techniques. The
CC polypeptide has enhanced activity under acidic pH relative to
CC conventional peroxidases. The current sequence is that of the
CC Termitomyces albuminosus acidic peroxidase-related RT-PCR primer of the
CC invention.
XX
SQ Sequence 33 BP; 2 A; 5 C; 1 G; 25 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              ||||||||||||||||||
Db         33 AAAAAAAAAAAAAAAAAA 15
```

RESULT 1147
ABK15694/c
ID ABK15694 standard; DNA; 33 BP.
XX
AC ABK15694;
XX
DT 21-MAY-2002 (first entry)
XX
DE Human activating GTPase negative regulator 11.66 PCR primer #1.
XX
KW Human; ss; activating GTPase negative regulator 11.66; PCR; primer;
KW malignant tumour; haemopathy; human immunodeficiency virus infection;
KW HIV; immunological disease; inflammation; cytostatic; haemostatic;
KW virucide; immunomodulatory; antiinflammatory.
XX
OS Homo sapiens.
XX
PN WO200211511-A1.
XX
PD 14-FEB-2002.
XX
PF 19-JUN-2001; 2001WO-CN001008.
XX
PR 21-JUN-2000; 2000CN-00116684.
XX
PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-172120/22.
XX
PT GTPase negative regulator 11.66 polypeptide and encoding polynucleotide,
PT used in diagnosis and treatment of malignant tumors, hemopathy, human
PT immunodeficiency virus infection, immunological diseases and
PT inflammation.
XX
PS Example 4; Page 13; 36pp; Chinese.
XX
CC The invention relates to an isolated polypeptide of activating GTPase
CC negative regulator 11.66, its fragment, analogue or derivative and the
CC nucleic acid encoding it. Also included are vectors expressing the
CC protein, a host cell comprising the vector, the isolation of modulators
CC of the protein and an antibody which recognises the protein. The protein
CC and nucleic acid are used in diagnosis and treatment of a malignant
CC tumour, haemopathy, human immunodeficiency virus (HIV) infection,
CC immunological diseases and various inflammations. The present sequence is
CC a PCR primer used to clone the cDNA encoding activating GTPase negative
CC regulator 11.66
XX
SQ Sequence 33 BP; 3 A; 5 C; 2 G; 23 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              ||||||||||||||||||
Db         33 AAAAAAAAAAAAAAAAAA 15
```

RESULT 1148
AAA75564/c
ID AAA75564 standard; DNA; 34 BP.
XX
AC AAA75564;
XX
DT 22-JAN-2001 (first entry)
XX
DE PCR primer for DNA encoding zeocin selective marker gene fragment.
XX
KW zalpha11 ligand; cytokine; haematopoietic cell proliferation; lymphoma;
KW tumourigenesis; leukaemia; hematopoiesis; B cell tumour; PCR primer; ss.
XX
OS Unidentified.
XX
PN WO200053761-A2.
XX
PD 14-SEP-2000.
XX
PF 09-MAR-2000; 2000WO-US006067.
XX
PR 09-MAR-1999; 99US-00264908.
PR 11-MAR-1999; 99US-00265992.
PR 01-JUL-1999; 99US-0142013P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX

PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
XX
DR WPI; 2000-565600/52.
XX
PT New human cytokine, designated zalpha11 ligand, useful for stimulating
PT the proliferation and/or development of hematopoietic cells in vitro and
PT in vivo, and for treating tumorigenesis.
XX
PS Example 6; Page 213; 256pp; English.
XX
CC The present PCR primer was used to amplify DNA encoding a fragment of
CC zeocin selective marker. The amplified fragment was used to construct a
CC vector for expression of zalpha11 ligand polypeptide. Zalpha11 ligand is
CC a cytokine. The zalpha11 ligand is useful for stimulating the
CC proliferation and development of haematopoietic cells in vitro and in
CC vivo. Zalpha11 ligand polynucleotides can be used as primers or probes
CC for cloning the zalpha11 gene. The zalpha11 ligand is useful for treating
CC tumourigenesis. A zalpha11 ligand-saporin fusion toxin may be used for
CC treating leukaemias and lymphomas. Antagonists against zalpha11 ligand
CC are useful as research reagents for characterizing ligand-receptor
CC interaction. Antagonists are also useful for inhibiting expansion,
CC proliferation, activation and differentiation of cells involved in
CC regulating hematopoiesis. The zalpha11 ligand may also be used to
CC stimulate an immune response against B cell tumour, a virus, a parasite
CC or a bacterium. The zalpha11 polypeptides, polynucleotides, antagonists,
CC agonists and antibodies are also useful for the detection, diagnosis,
CC prevention, and treatment of diseases associated with a zalpha11 ligand
CC genetic defect
XX
SQ Sequence 34 BP; 2 A; 3 C; 2 G; 27 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 34 AAAAAAAAAAAAAAAAAAA 16

RESULT 1149
AAD09727/c
ID AAD09727 standard; DNA; 34 BP.
XX
AC AAD09727;
XX
DT 10-SEP-2001 (first entry)
XX
DE ZC18698 primer, to synthesise human activated CD3+ selected cell cDNA.
XX
KW Human; cytostatic; cytokine; ZCYTO18 protein; genetic abnormality;
KW cancer; inflammation; gene therapy; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200146422-A1.
XX
PD 28-JUN-2001.
XX
PF 22-DEC-2000; 2000WO-US035308.
XX
PR 23-DEC-1999; 99US-00471767.
PR 01-DEC-2000; 2000US-0250841P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Presnell SR, Kindsvogel W;
XX
DR WPI; 2001-408648/43.
XX
PT Novel human cytokine polypeptide, ZCYTO18, useful for treating cancer.
XX
PS Example 4B; Page 145; 167pp; English.
XX
CC The patent discloses novel human cytokine, ZCYTO18 protein and its
CC corresponding DNA. ZCYTO18 protein induces proliferation of cells
CC expressing zcytor11, a receptor for ZCYTO18 or induces cytotoxicity in
CC K5626 cells. ZCYTO18 DNA is useful for detecting a genetic abnormality in
CC a patient. ZCYTO18 DNA and its antibodies are useful for detecting cancer
CC and inflammation. ZCYTO18 protein is useful for killing cancer cells. It
CC is useful for increasing platelets in a patient or injured tissue. It is
CC also used in gene therapy. The present sequence is a PCR primer, ZC18698
CC used to synthesise a cDNA strand from human activated CD3+ selected
CC cells. This primer is used for the identification of human ZCYTO18
CC message in activated T-cell library
XX
SQ Sequence 34 BP; 2 A; 3 C; 2 G; 27 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 34 AAAAAAAAAAAAAAAAAAA 16

RESULT 1150
AAS20662/c
ID AAS20662 standard; DNA; 34 BP.
XX
AC AAS20662;
XX
DT 09-APR-2002 (first entry)
XX
DE Primer ZC18698 ued to create XhoI site into human zalpha11 Ligand cDNA.
XX
KW Cytokine; zalpha11 Ligand; zalpha11 receptor; NK cell progenitor;
KW natural killer cell proliferation; T-cell proliferation;
KW B-cell proliferation; anti-tumour response; immune system;
KW immunostimulant; cytostatic; human; primer; ss.
XX
OS Synthetic.
XX
PN US6307024-B1.
XX
PD 23-OCT-2001.
XX
PF 09-MAR-2000; 2000US-00522217.
XX
PR 09-MAR-1999; 99US-0123547P.
PR 11-MAR-1999; 99US-0123904P.
PR 01-JUL-1999; 99US-0142013P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
XX
DR WPI; 2002-040208/05.
XX
PT New zalpha11 ligand polypeptides and polynucleotides, useful for
PT stimulating proliferation, activation, differentiation and/or induction
PT of inhibition of specialized cell function, or for stimulating an
PT antigenic response.
XX
PS Example 6; Col 135; 105pp; English.
XX
CC The present invention relates to the isolation of a novel cytokine,
CC zalpha11 Ligand and the polynucleotide encoding it. The invention also
CC gives the sequence for the zalpha11 receptor and the polynucleotide
CC encoding it. The zalpha11 Ligand polypeptide stimulates proliferation of
CC natural killer (NK) cells or NK cell progenitors, the activation of NK
CC cells, proliferation of T-cells, proliferation of B-cells stimulated with
CC anti-CD40 antibodies, stimulates an antigenic response in a mammal, and

```
CC   reduces proliferation of B-cells stimulated with anti-IgM antibodies. The
CC   zalpha11 Ligand polypeptide is also useful in preparing antibodies that
CC   bind to zalpha11 Ligand epitopes. The zalpha11 Ligand polynucleotides can
CC   be used as probes or primers to clone regions of a zalpha11 Ligand gene,
CC   and in gene therapy. Zalpha11 Ligand may also be used to identify
CC   inhibitors of its activity, to enhance the generation of anti-tumour
CC   responses with or without the infusion of donor lymphocytes, and to
CC   activate or stimulate the immune system. The present sequence represents
CC   a primer used in the methods of the present invention
XX
SQ   Sequence 34 BP; 2 A; 3 C; 2 G; 27 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         34 AAAAAAAAAAAAAAAAAAA 16


RESULT 1151
ADD68172/c
ID   ADD68172 standard; DNA; 34 BP.
XX
AC   ADD68172;
XX
DT   15-JAN-2004  (first entry)
XX
DE   PCR primer relating to the invention ZC18698 SEQ ID NO:30.
XX
KW   ss; PCR; primer; zcytor17; antiinflammatory; dermatological;
KW   immunosuppressive; antimicrobial; vaccine; inflammatory disease;
KW   inflammatory bowel disease; ulcerative colitis; Crohn's disease;
KW   atopic dermatitis; eczema; psoriasis; endotoxaemia; septicaemia;
KW   toxic shock syndrome; infectious disease.
XX
OS   Synthetic.
XX
PN   WO2003060090-A2.
XX
PD   24-JUL-2003.
XX
PF   21-JAN-2003; 2003WO-US001984.
XX
PR   18-JAN-2002; 2002US-0350325P.
PR   25-APR-2002; 2002US-0375323P.
PR   19-DEC-2002; 2002US-0435315P.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Sprecher CA,  Kuijper JL,  Dasovich MM,  Grant FJ,  Hammond AK;
PI   Novak JE,  Gross JA,  Dillon SR;
XX
DR   WPI; 2003-618179/58.
XX
PT   New zcytor17 ligand polypeptides, useful for treating inflammatory
PT   diseases, such as inflammatory bowel disease, ulcerative colitis, Crohn's
PT   disease, atopic dermatitis, eczema, psoriasis, endotoxemia, septicemia.
XX
PS   Example 6; SEQ ID NO 30; 372pp; English.
XX
CC   The invention relates to a novel isolated zcytor17 ligand polypeptide. A
CC   polypeptide of the invention has antiinflammatory, dermatological,
CC   immunosuppressive, and antimicrobial activity, and may have a use in a
CC   vaccine. The polypeptide is useful for treating inflammatory diseases,
CC   such as inflammatory bowel disease, ulcerative colitis, Crohn's disease,
CC   atopic dermatitis, eczema, psoriasis, endotoxaemia, septicaemia, toxic
CC   shock syndrome or infectious diseases. The present sequence is used in
CC   the exemplification of the invention.
XX
SQ   Sequence 34 BP; 2 A; 3 C; 2 G; 27 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         34 AAAAAAAAAAAAAAAAAAA 16


RESULT 1152
AAX14632/c
ID   AAX14632 standard; DNA; 35 BP.
XX
AC   AAX14632;
XX
DT   24-MAR-1999  (first entry)
XX
DE   Triple helix forming nucleotides 4791-4725 of the n-myc gene.
XX
KW   Triple-helix forming region; Triplex formation; DNA detection;
KW   identification; bacteria; oncogene; virus; ds.
XX
OS   Homo sapiens.
XX
PN   US5861244-A.
XX
PD   19-JAN-1999.
XX
PF   22-DEC-1993;  93US-00173489.
XX
PR   29-OCT-1992;  92US-00968436.
XX
PA   (PROF-) PROFILE DIAGNOSTIC SCI INC.
XX
PI   Hepburn AG,  Wang C;
XX
DR   WPI; 1999-130384/11.
XX
PT   Assay of genetic sequences based on triplex formation from double
PT   stranded analyte - and hybrid of anchor and reporter sequences, with
PT   reporter released if triplex formation occurs, used e.g. to identify
PT   bacteria.
XX
PS   Disclosure; Col 13-14; 168pp; English.
XX
CC   The present sequence represents a potential triple-helix forming region.
CC   It can be used to demonstrate the assay of the invention. The assay
CC   comprises adding a sample containing double-stranded DNA test sequences,
CC   e.g. containing the present sequence, to an aqueous medium containing at
CC   least one complex of anchor DNA, attached to a solid support, and
CC   reporter DNA, where either a part of the anchor DNA or reporter DNA is
CC   designed to form a triple-strand structure with part of the test
CC   sequence. Triplex formation results in displacement of the reporter DNA
CC   which is detected as an indication of the presence of the DNA test
CC   sequence. The method is used to detect DNA sequences, particularly for
CC   identification of bacteria (by detecting genes for ribosomal RNA) in
CC   clinical samples, but also detection of oncogenes and Hepatitis B virus
XX
SQ   Sequence 35 BP; 1 A; 4 C; 0 G; 30 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 35;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              |||||||||||||||||||
Db         35 GAAAAAAAAAAAAAAAAAA 17


RESULT 1153
ABZ46327/c
ID   ABZ46327 standard; DNA; 41 BP.
XX
```

```
AC   ABZ46327;
XX
DT   26-JUN-2003  (first entry)
XX
DE   Human aldehyde dehydrogenase ALDH1A2 gene polymorphic site, #3111.
XX
KW   Human; drug metabolising enzyme; gene; drug metabolism; chromosome 15;
KW   polymorphic site; drug evaluation; drug screening; genotyping;
KW   genetic profiling; therapeutic customisation; adverse reaction;
KW   clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace(21,G)
FT                   /*tag=  a
FT                   /standard_name= "Single nucleotide polymorphism (SNP)"
XX
PN   WO200252044-A2.
XX
PD   04-JUL-2002.
XX
PF   27-DEC-2001; 2001WO-JP011592.
XX
PR   27-DEC-2000; 2000JP-00399443.
PR   02-MAY-2001; 2001JP-00135256.
PR   27-AUG-2001; 2001JP-00256862.
XX
PA   (RIKE ) RIKEN KK.
XX
PI   Nakamura Y,  Sekine A,  Iida A,  Saito S;
XX
DR   WPI; 2002-583571/62.
XX
PT   Identifying individuals having a polymorphism, useful for determining the
PT   effectiveness or side effect of a drug or treatment protocol, comprises
PT   detecting at least one polymorphism in the drug metabolizing enzyme
PT   nucleic acid.
XX
PS   Claim 23; Page 116; 2785pp; English.
XX
CC   Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes
CC   encoding enzymes associated with drug metabolism. The invention relates
CC   to methods and compositions for identifying individuals who have at least
CC   one polymorphism in such drug metabolising enzyme-encoding genes. The
CC   polymorphisms may be identified in a nucleic acid sample using probes or
CC   primers specific for a sequence selected from ABZ43217-ABZ50887 using a
CC   variety of detection assays, including hybridisation assays, nucleic acid
CC   arrays and PCR-based methods. The invention also encompasses methods of
CC   evaluating and screening drugs using genetic polymorphism data. Genetic
CC   polymorphism data, particularly that relating to single nucleotide
CC   polymorphisms (SNPs), may be used in studying the relationship between
CC   DNA sequence variations and human diseases, conditions, and responses to
CC   drugs. SNPs are also useful as polymorphism markers for discovering genes
CC   that cause or exacerbate certain diseases. SNPs are particularly useful
CC   in the above respects as they are stable in populations, occur
CC   frequently, and have lower mutation rates than other genome variations
CC   such as repeating sequences. The detection and analysis of polymorphisms
CC   in genes encoding drug metabolising enzymes allows the customisation of
CC   drug therapies based upon the genetic profile of individual patients.
CC   This would not only take the guesswork out of selecting the drug with the
CC   greatest therapeutic effect for a particular patient, but would also
CC   reduce the likelihood of adverse reactions, thereby increasing safety.
CC   Methods of the invention are also useful in the drug discovery and
CC   approval processes. For example, individuals could be selected for
CC   clinical trials only if their genetic profiles indicate that they are
CC   capable of responding to a particular drug or drug class, and previously
CC   failed drug candidates could be revived if they were matched with more
CC   appropriate patient populations. The methods, data and compositions of
CC   the invention may therefore lead to a an increase in the range of
CC   possible drug targets and decreases in the number of adverse drug
CC   reactions, failed drug trials, the time taken for a drug to be approved,
CC   the length of time patients are on medication and the number of different
CC   medications a patient needs to take before finding an effective therapy
XX
SQ   Sequence 41 BP; 3 A; 2 C; 3 G; 33 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 41;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         40 AAAAAAAAAAAAAAAAAAA 22


RESULT 1154
ABZ48839/c
ID   ABZ48839 standard; DNA; 41 BP.
XX
AC   ABZ48839;
XX
DT   26-JUN-2003  (first entry)
XX
DE   Human aldehyde dehydrogenase ALDH1A2 gene polymorphic site, #5622.
XX
KW   Human; drug metabolising enzyme; gene; drug metabolism; polymorphic site;
KW   drug evaluation; drug screening; genotyping; genetic profiling;
KW   therapeutic customisation; adverse reaction; clinical trial;
KW   drug approval; single nucleotide polymorphism; SNP; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace(21,G)
FT                   /*tag=  a
FT                   /standard_name= "Single nucleotide polymorphism (SNP)"
XX
PN   WO200252044-A2.
XX
PD   04-JUL-2002.
XX
PF   27-DEC-2001; 2001WO-JP011592.
XX
PR   27-DEC-2000; 2000JP-00399443.
PR   02-MAY-2001; 2001JP-00135256.
PR   27-AUG-2001; 2001JP-00256862.
XX
PA   (RIKE ) RIKEN KK.
XX
PI   Nakamura Y,  Sekine A,  Iida A,  Saito S;
XX
DR   WPI; 2002-583571/62.
XX
PT   Identifying individuals having a polymorphism, useful for determining the
PT   effectiveness or side effect of a drug or treatment protocol, comprises
PT   detecting at least one polymorphism in the drug metabolizing enzyme
PT   nucleic acid.
XX
PS   Claim 23; Page 175; 2785pp; English.
XX
CC   Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes
CC   encoding enzymes associated with drug metabolism. The invention relates
CC   to methods and compositions for identifying individuals who have at least
CC   one polymorphism in such drug metabolising enzyme-encoding genes. The
CC   polymorphisms may be identified in a nucleic acid sample using probes or
CC   primers specific for a sequence selected from ABZ43217-ABZ50887 using a
CC   variety of detection assays, including hybridisation assays, nucleic acid
CC   arrays and PCR-based methods. The invention also encompasses methods of
CC   evaluating and screening drugs using genetic polymorphism data. Genetic
CC   polymorphism data, particularly that relating to single nucleotide
CC   polymorphisms (SNPs), may be used in studying the relationship between
CC   DNA sequence variations and human diseases, conditions, and responses to
CC   drugs. SNPs are also useful as polymorphism markers for discovering genes
CC   that cause or exacerbate certain diseases. SNPs are particularly useful
CC   in the above respects as they are stable in populations, occur
```

```
CC   frequently, and have lower mutation rates than other genome variations
CC   such as repeating sequences. The detection and analysis of polymorphisms
CC   in genes encoding drug metabolising enzymes allows the customisation of
CC   drug therapies based upon the genetic profile of individual patients.
CC   This would not only take the guesswork out of selecting the drug with the
CC   greatest therapeutic effect for a particular patient, but would also
CC   reduce the likelihood of adverse reactions, thereby increasing safety.
CC   Methods of the invention are also useful in the drug discovery and
CC   approval processes. For example, individuals could be selected for
CC   clinical trials only if their genetic profiles indicate that they are
CC   capable of responding to a particular drug or drug class, and previously
CC   failed drug candidates could be revived if they were matched with more
CC   appropriate patient populations. The methods, data and compositions of
CC   the invention may therefore lead to a an increase in the range of
CC   possible drug targets and decreases in the number of adverse drug
CC   reactions, failed drug trials, the time taken for a drug to be approved,
CC   the length of time patients are on medication and the number of different
CC   medications a patient needs to take before finding an effective therapy
XX
SQ   Sequence 41 BP; 3 A; 2 C; 3 G; 33 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19;  DB 1;  Length 41;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         40 AAAAAAAAAAAAAAAAAAA 22


RESULT 1155
ABA93238/c
ID   ABA93238 standard; DNA; 22 BP.
XX
AC   ABA93238;
XX
DT   18-APR-2002  (first entry)
XX
DE   PolyA adaptor oligonucleotide SEQ ID NO:1.
XX
KW   Detection; comparative detection; adaptor; ss.
XX
OS   Synthetic.
XX
PN   JP2001333800-A.
XX
PD   04-DEC-2001.
XX
PF   30-MAY-2000; 2000JP-00160324.
XX
PR   30-MAY-2000; 2000JP-00160324.
XX
PA   (UNIT-) UNITECH CO LTD.
XX
DR   WPI; 2002-135950/18.
XX
PT   Comparative detection of the amounts of RNA and DNA.
XX
PS   Disclosure; Page 9; 9pp; Japanese.
XX
CC   The present invention describes a method for the comparative detection of
CC   the amount of an RNA. The method comprises: (a) cDNAs obtained by
CC   transcribing respectively from at least two tissue RNAs are respectively
CC   fragmented by using a same restriction enzyme; (b) each different adaptor
CC   and a common adaptor are added to each of the cDNA fragments derived from
CC   the same or different tissues by the step (a); (c) the resultant adaptor-
CC   added cDNAs are mixed together; (d) an adaptor primer having the common
CC   sequence to said different adaptor and a gene-specific adaptor are used
CC   to amplify said adaptor-added cDNAs containing no region derived from
CC   polyadenylic acid of the mRNA before the addition of the adaptor among
CC   the adaptor-added cDNAs prepared by the step (b); (e) the ratios of the
CC   cDNA amounts are measured between the tissues; (f) the RNA is detected
CC   from the measured result; (g) each different adaptor and a common adaptor
CC   are added to each of the genomic DNA fragments derived from a same or
CC   different individuals; (h) the resultant adaptor-added genomic DNAs are
CC   mixed together; (i) the adaptor-added genomic DNAs are amplified by using
CC   an adaptor primer having the common sequence to the different adaptor and
CC   a sequence-specific adaptor; and (j) the ratios of the amplified amounts
CC   of the genomic DNAs are measured between the individuals. The method is
CC   used for the detection of the amounts of RNA and DNA. The present
CC   sequence represents an oligonucleotide which is used in the
CC   exemplification of the present invention
XX
SQ   Sequence 22 BP; 19 A; 1 C; 1 G; 1 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.8;  DB 1;  Length 22;
  Best Local Similarity   90.9%;  Pred. No. 8.7e+02;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTAAC 2189
              |||||||||||||||||||  | |
Db         22 TTTTTTTTTTTTTTTTTTGATC 1


RESULT 1156
ABV77669
ID   ABV77669 standard; DNA; 24 BP.
XX
AC   ABV77669;
XX
DT   03-FEB-2003  (first entry)
XX
DE   Human zinc finger protein 9.79 PCR primer #1.
XX
KW   Human; zinc finger protein 9.79; cancer; HIV infection; cytostatic;
KW   anti-HIV; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1343710-A.
XX
PD   10-APR-2002.
XX
PF   19-SEP-2000; 2000CN-00125246.
XX
PR   19-SEP-2000; 2000CN-00125246.
XX
PA   (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-548879/59.
XX
PT   A novel human zinc finger protein 9.79 polypeptide, useful for treating
PT   several diseases e.g. cancer and HIV infection.
XX
PS   Example 2; Page 16 (Disclosure); 31pp; Chinese.
XX
CC   The present invention relates to human zinc finger protein 9.79 (see
CC   ABP59011). The zinc finger protein is useful for treating several
CC   diseases e.g. cancer and HIV infection. The present sequence is a PCR
CC   primer, which was used in an example from the invention
XX
SQ   Sequence 24 BP; 1 A; 2 C; 1 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.8;  DB 1;  Length 24;
  Best Local Similarity   90.9%;  Pred. No. 1.1e+03;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||  ||
Db          3 CTTTTTTTTTTTTTTTTTCATT 24


RESULT 1157
AAH75510
```

ID AAH75510 standard; DNA; 24 BP.
XX
AC AAH75510;
XX
DT 18-OCT-2001 (first entry)
XX
DE Human CCR4 related protein 31 PCR primer 2.
XX
KW Human; CCR4; cancer; HIV; Human immunodeficiency virus; infection;
KW PCR primer; ss.
XX
OS Homo sapiens.
XX
PN CN1296960-A.
XX
PD 30-MAY-2001.
XX
PF 22-NOV-1999; 99CN-00124049.
XX
PR 22-NOV-1999; 99CN-00124049.
XX
PA (SHAN-) SHANGHAI BORONG GENE DEV CO LTD.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2001-489558/54.
XX
PT Polypeptide-human CCR4 related protein 31 and polynucleotide for coding
PT polypeptide, useful for treating e.g. cancer and HIV infection, is
PT prepared by DNA recombination.
XX
PS Example 3; Page 17 (Disclosure); 34pp; Chinese.
XX
CC The invention relates to human CCR4 related protein 31, the
CC polynucleotide encoding it and the use of the protein in treating e.g.
CC cancer and HIV infection. The present sequence is that of a human CCR4
CC PCR primer of the invention
XX
SQ Sequence 24 BP; 3 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.7%; Score 18.8; DB 1; Length 24;
Best Local Similarity 90.9%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2167 TTTTTTTTTTTTTTTTTTTTAA 2188
||||||||||| ||||| ||||
Db 2 TTTTTTTTTTTCTTTTTATTAA 23

RESULT 1158
AAH44623
ID AAH44623 standard; DNA; 24 BP.
XX
AC AAH44623;
XX
DT 16-NOV-2001 (first entry)
XX
DE Human FD 17 PCR primer 2 SEQ ID NO:4.
XX
KW Human; FD 17; cytostatic; virucidal; immunomodulatory; haemostatic;
KW antiinflammatory; gene therapy; malignant tumour; haemopathy;
KW human immunodeficiency virus infection; HIV infection;
KW immunological disease; inflammation; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200164729-A1.
XX
PD 07-SEP-2001.
XX
PF 26-FEB-2001; 2001WO-CN000221.
XX
PR 02-MAR-2000; 2000CN-00111868.
XX
PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2001-550164/61.
XX
PT New human polypeptide FD 17 for diagnosing and treating malignant tumor,
PT hemopathy, human immunodeficiency virus (HIV) infection, immunological
PT diseases and inflammations.
XX
PS Example 2; Page 11; 36pp; Chinese.
XX
CC The present invention describes the human FD 17 protein (I). (I) has
CC cytostatic, virucidal, immunomodulatory, antiinflammatory and haemostatic
CC activities. The polynucleotide encoding (I) can be used in gene therapy.
CC (I) and the polynucleotide encoding it are applicable in the diagnosis
CC and treatment of malignant tumour, haemopathy, human immunodeficiency
CC virus (HIV) infection, immunological diseases and various inflammations.
CC The present sequence represents a PCR primer for human FD 17, which is
CC used in an example from the present invention
XX
SQ Sequence 24 BP; 0 A; 2 C; 1 G; 21 T; 0 U; 0 Other;

Query Match 0.7%; Score 18.8; DB 1; Length 24;
Best Local Similarity 90.9%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2163 TCCTTTTTTTTTTTTTTTTTT 2184
| |||||| ||||||||||||||
Db 2 TTCTTTTTCTTTTTTTTTTTT 23

RESULT 1159
ABK13715
ID ABK13715 standard; DNA; 24 BP.
XX
AC ABK13715;
XX
DT 23-APR-2002 (first entry)
XX
DE RT-PCR primer #2 for human transcriptional activation subunit 14 cDNA.
XX
KW Human; transcriptional activation subunit 14; malignant neoplasm;
KW haematopathy; cytostatic; HIV infection; human immunodeficiency virus;
KW immunological disease; inflammation; virucide; immunomodulatory;
KW antiinflammatory; reverse transcriptase-PCR; RT-PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200194403-A1.
XX
PD 13-DEC-2001.
XX
PF 14-MAY-2001; 2001WO-CN000753.
XX
PR 16-MAY-2000; 2000CN-00115720.
XX
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-090139/12.
XX
PT Human transcriptional activation subunit 14 and encoding polynucleotide,
PT used in diagnosis and treatment of malignant tumors, hemopathy, human
PT immunodeficiency virus infection, immunological diseases and
PT inflammation.
XX
PS Example 2; Page 17; 36pp; Chinese.
XX
CC The present invention relates to the isolation of human transcriptional
CC activation subunit 14, and the polynucleotide encoding it. Also described

```
CC   is the process for preparing the protein by DNA recombination and the
CC   application of the polypeptide and polynucleotide in treating various
CC   diseases such as malignant neoplasms, haematopathy, human
CC   immunodeficiency virus (HIV) infection, immunological diseases, and
CC   various inflammations. Antagonists against the polypeptide can also be
CC   used in treating such diseases. The present sequence for reverse
CC   transcriptase (RT)-PCR primer #2 is used with RT-PCR primer #1 (ABK13714)
CC   for isolating cDNA encoding human transcriptional activation subunit 14
XX
SQ   Sequence 24 BP; 0 A; 2 C; 2 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.8;  DB 1;  Length 24;
  Best Local Similarity   90.9%;  Pred. No. 1.1e+03;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTTT 2184
              | ||||||| ||||||||||||||
Db          1 TTCTTTTTCTTTTTTTTTTTT 22


RESULT 1160
AAC96267
ID   AAC96267 standard; DNA; 25 BP.
XX
AC   AAC96267;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DPA1 gene PCR primer #24.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 48; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 4 A; 0 C; 3 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.8;  DB 1;  Length 25;
  Best Local Similarity   90.9%;  Pred. No. 1.2e+03;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTAACTTTGA 2194
              |||||||||||||| | |||||
Db          1 TTTTTTTTTTTTTTGAATTTGA 22


RESULT 1161
AAC96268
ID   AAC96268 standard; DNA; 25 BP.
XX
AC   AAC96268;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DPA1 gene PCR primer #25.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 48; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 3 A; 0 C; 4 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.8;  DB 1;  Length 25;
  Best Local Similarity   90.9%;  Pred. No. 1.2e+03;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTAACTTTGA 2194
              |||||||||||||| | |||||
Db          1 TTTTTTTTTTTTTTGAGTTTGA 22


RESULT 1162
ABA03917
ID   ABA03917 standard; DNA; 25 BP.
XX
AC   ABA03917;
XX
DT   18-FEB-2002  (first entry)
XX
DE   Human connexin 9 PCR primer 2 SEQ ID NO:4.
XX
KW   Human; connexin 9; cytostatic; virucidal; immunomodulatory;
KW   antiinflammatory; haemostatic; malignant tumour; haemopathy;
KW   HIV infection; immunological disease; inflammation; PCR primer; ss.
XX
```

OS Homo sapiens.
XX
PN WO200181538-A2.
XX
PD 01-NOV-2001.
XX
PF 23-APR-2001; 2001WO-CN000608.
XX
PR 27-APR-2000; 2000CN-00115456.
XX
PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-034440/04.
XX
PT Human connexin 9 and encoded polynucleotide, applicable in diagnosis and
PT treatment of malignant tumor, hemopathy, HIV infection, immunological
PT diseases and inflammation.
XX
PS Example 2; Page 12; 32pp; Chinese.
XX
CC The present invention describes human connexin 9 (I). (I) has cytostatic,
CC virucidal, immunomodulatory, antiinflammatory and haemostatic activities.
CC (I) and the polynucleotide encoding it (II) are applicable in the
CC diagnosis and treatment of malignant tumour, haemopathy, HIV infection,
CC immunological diseases and various inflammations. The present sequence
CC represents a PCR primer for human connexin 9, which is used in an example
CC from the present invention
XX
SQ Sequence 25 BP; 3 A; 0 C; 1 G; 21 T; 0 U; 0 Other;

Query Match 0.7%; Score 18.8; DB 1; Length 25;
Best Local Similarity 90.9%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTTA 2187
||||||| ||||| |||||||
Db 4 TTTTTTTATTTTTATTTTTTA 25

RESULT 1163
AAF74933/c
ID AAF74933 standard; DNA; 27 BP.
XX
AC AAF74933;
XX
DT 23-MAY-2001 (first entry)
XX
DE CD40L poly-A tract sequence SEQ ID NO:30.
XX
KW Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW diagnosis; antiarthritic; antirheumatic; immunosuppressive;
KW antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
OS Homo sapiens.
XX
PN WO200119844-A1.
XX
PD 22-MAR-2001.
XX
PF 13-SEP-2000; 2000WO-US024966.
XX
PR 13-SEP-1999; 99US-0153625P.
XX
PA (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
PI Crow MK, Li Y;
XX
DR WPI; 2001-244776/25.
XX
PT New altered CD40L promoter for use in the study, diagnosis and treatment
PT of a variety of inflammatory disorders and autoimmune diseases, such as
PT rheumatoid arthritis.
XX
PS Example 1; Fig 3; 90pp; English.
XX
CC The present invention describes an isolated, purified nucleic acid, which
CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC residues 331-455 of the sequence comprising 455 nucleotides given in
CC AAF74905 where A in the wild type sequence at position 331 (corresponding
CC to position -125) is replaced with C. (I) has antiarthritic,
CC antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC be used in gene therapy. (I) is useful in the study, diagnosis and
CC treatment of inflammatory and autoimmune diseases, as well as diseases in
CC which elevated expression of CD40L is a factor, e.g., rheumatoid
CC arthritis. The present sequence represents a CD40L poly-A tract sequence
CC which is used in an example from the present invention
XX
SQ Sequence 27 BP; 20 A; 3 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 18.8; DB 1; Length 27;
Best Local Similarity 90.9%; Pred. No. 1.4e+03;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2159 TTTCTCCTTTTTTTTTTTTTT 2180
||| || ||||||||||||||||
Db 22 TTTTTCGTTTTTTTTTTTTTT 1

RESULT 1164
AAC96079
ID AAC96079 standard; DNA; 25 BP.
XX
AC AAC96079;
XX
DT 26-FEB-2001 (first entry)
XX
DE 16s rRNA gene PCR primer #46.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 45; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 3 A; 2 C; 2 G; 18 T; 0 U; 0 Other;

```
  Query Match             0.7%;  Score 18.6;  DB 1;  Length 25;
  Best Local Similarity   84.0%;  Pred. No. 1.3e+03;
  Matches   21;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTAACTT 2191
              ||||||||||||   ||||||| |
Db          1 TTTTTTTTTTTTGAGTTTTAACCT 25


RESULT 1165
AAC95686
ID   AAC95686 standard; DNA; 25 BP.
XX
AC   AAC95686;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DPB1 gene PCR primer #21.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 38; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 2 A; 4 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.6;  DB 1;  Length 25;
  Best Local Similarity   84.0%;  Pred. No. 1.3e+03;
  Matches   21;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTAACTTTGAAAG 2197
              ||||||||||||||| ||||   ||
Db          1 TTTTTTTTTTTTTTACCTTTTCCAG 25


RESULT 1166
AAC96214/c
ID   AAC96214 standard; DNA; 25 BP.
XX
AC   AAC96214;
XX
DT   26-FEB-2001  (first entry)
XX
DE   16s rRNA gene PCR primer #181.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 47; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 4 A; 3 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.6;  DB 1;  Length 25;
  Best Local Similarity   84.0%;  Pred. No. 1.3e+03;
  Matches   21;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2775 TGTTAGAATTGAAAAAAAAAAAAAA 2799
              | | || | ||||||||||||||||
Db         25 TTTAAGCAGTGAAAAAAAAAAAAAA 1


RESULT 1167
AAC96367
ID   AAC96367 standard; DNA; 25 BP.
XX
AC   AAC96367;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DPB1 gene PCR primer #99.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
```

PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 50; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 2 A; 4 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.7%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2173 TTTTTTTTTTTTTTAACTTTGAAAG 2197
||||||||||||||| |||| ||
Db 1 TTTTTTTTTTTTTTACCTTTTCCAG 25

RESULT 1168
ACI00608/c
ID ACI00608 standard; DNA; 25 BP.
XX
AC ACI00608;
XX
DT 13-OCT-2003 (first entry)
XX
DE Human microarray DNA oligonucleotide SEQ ID NO 599.
XX
KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.
XX
OS Homo sapiens.
XX
PN US2003104410-A1.
XX
PD 05-JUN-2003.
XX
PF 15-MAR-2002; 2002US-00098263.
XX
PR 16-MAR-2001; 2001US-0276759P.
XX
PA (AFFY-) AFFYMETRIX INC.
XX
PI Mittmann MP;
XX
DR WPI; 2003-567953/53.
XX
PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
PS Claim 1; SEQ ID NO 599; 9pp; English.
XX
CC The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.goc/sequence.html
XX
SQ Sequence 25 BP; 2 A; 7 C; 7 G; 9 T; 0 U; 0 Other;

Query Match 0.7%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1269 AAGACCGGACACCCCATGGGACCAG 1293
||||| ||||||| || |||||| |
Db 25 AAGACAGGACACCTCAAGGGACCTG 1

RESULT 1169
ACI61005/c
ID ACI61005 standard; DNA; 25 BP.
XX
AC ACI61005;
XX
DT 13-OCT-2003 (first entry)
XX
DE Human microarray DNA oligonucleotide SEQ ID NO 60996.
XX
KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.
XX
OS Homo sapiens.
XX
PN US2003104410-A1.
XX
PD 05-JUN-2003.
XX
PF 15-MAR-2002; 2002US-00098263.
XX
PR 16-MAR-2001; 2001US-0276759P.
XX
PA (AFFY-) AFFYMETRIX INC.
XX
PI Mittmann MP;
XX
DR WPI; 2003-567953/53.
XX
PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
PS Claim 1; SEQ ID NO 60996; 9pp; English.
XX
CC The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis

```
CC   of at least one target sequence. The method of analysis comprises
CC   hybridising at least one or more nucleic acids to at least two or more
CC   nucleic acid probes and detecting the hybridisation. The nucleic acid
CC   probes are attached to a solid support. The analysis comprises monitoring
CC   gene expression levels, identifying biallelic markers or polymorphisms,
CC   or family members of a gene and a cross-species comparison. Each of the
CC   nucleic acids further comprises a tag sequence. The array of nucleic acid
CC   probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC   blot hybridisation to identify or detect the sequence or specific
CC   mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC   primer extensions or in screening cDNA or genomic libraries or subclones
CC   for additional subclones containing segments of DNA that have been
CC   isolated and previously sequenced. The sequence presented is one of the
CC   nucleic acid probes incorporated in the microarray. Note: The sequence
CC   data for this patent can also be obtained in electronic format directly
CC   from USPTO at seqdata.uspto.goc/sequence.html
XX
SQ   Sequence 25 BP; 4 A; 8 C; 9 G; 4 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.6;  DB 1;  Length 25;
  Best Local Similarity   84.0%;  Pred. No. 1.3e+03;
  Matches   21;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        572 GTGAGCGCCCGCAGGGATGCCTACC 596
              ||||||| |||||||| | ||| ||
Db         25 GTGAGCGACCGCAGGGCTACCTTCC 1


RESULT 1170
AAA88688
ID   AAA88688 standard; DNA; 26 BP.
XX
AC   AAA88688;
XX
DT   05-FEB-2001  (first entry)
XX
DE   Oligo-dT-XhoI primer.
XX
KW   Sweetgum; angiosperm; cytochrome P450-1; conifer; loblolly pine;
KW   transgenic plant; lignin; paper; pulping; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO200058489-A2.
XX
PD   05-OCT-2000.
XX
PF   24-MAR-2000; 2000WO-US008083.
XX
PR   26-MAR-1999;   99US-00277248.
XX
PA   (INTO ) INT PAPER CO.
XX
PI   Chiang VL,  Carraway DT;
XX
DR   WPI; 2000-647240/62.
XX
PT   Use of angiosperm coniferyl aldehyde 5-hydroxylase which catalyzes 5-
PT   hydroxylation of coniferyl aldehyde, for modifying lignin biosynthesis in
PT   gymnosperms, involves expressing the enzyme in a gymnosperm plant.
XX
PS   Example 3; Page 23; 123pp; English.
XX
CC   The present sequence is that of an oligo-dT primer including a 5' XboI
CC   site. The primer was used with a gene-specific primer to amplify sweetgum
CC   cytochrome P450-1 cDNA (see AAA88681). An aim of the invention is to
CC   identify, sequence and clone specific genes such as P450-1 from an
CC   angiosperm that are involved in production of syringyl lignin, and to
CC   then introduce such genes into the genome of a gymnosperm, such as
CC   loblolly pine, to induce production of syringyl lignin and thereby
CC   provide enhanced pulpability to the wood structure
XX
SQ   Sequence 26 BP; 2 A; 1 C; 3 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.6;  DB 1;  Length 26;
  Best Local Similarity   84.0%;  Pred. No. 1.4e+03;
  Matches   21;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTTTTTT 2185
              | | |  ||||||||||||||||||
Db          2 TGTGCAGTTTTTTTTTTTTTTTT 26


RESULT 1171
AAQ75596
ID   AAQ75596 standard; DNA; 20 BP.
XX
AC   AAQ75596;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 8.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTAA 2188
              |||||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTTTCAA 20


RESULT 1172
ABZ85312
ID   ABZ85312 standard; DNA; 20 BP.
XX
AC   ABZ85312;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
```

KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Claim 15; SEQ ID NO 554; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.7%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 8.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2168 TTTTTTTTTTTTTTTTTTA 2187
||||||||||||||||||
Db 1 TTTTTTTTTTTTTTTTTTCA 20

RESULT 1173
ABZ89546
ID ABZ89546 standard; DNA; 20 BP.
XX
AC ABZ89546;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;

KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4788; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 18 A; 0 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 0.7%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 8.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2783 TTGAAAAAAAAAAAAAAAAA 2802
|| ||||||||||||||||||
Db 1 TTAAAAAAAAAAAAAAAAAA 20

RESULT 1174
AAQ75598
ID AAQ75598 standard; DNA; 20 BP.
XX
AC AAQ75598;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;

```
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 1 A; 2 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 8.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAAC 2189
              |||||||||||||||||  ||
Db          1 TTTTTTTTTTTTTTTTTCAC 20


RESULT 1175
AAQ75581/c
ID   AAQ75581 standard; DNA; 20 BP.
XX
AC   AAQ75581;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 2 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 8.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAAA 2801
              ||| ||||||||||||||||
Db         20 ATTAAAAAAAAAAAAAAAAA 1


RESULT 1176
AAQ75580/c
ID   AAQ75580 standard; DNA; 20 BP.
XX
AC   AAQ75580;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 3 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 8.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAA 2802
              || |||||||||||||||||
Db         20 TTTAAAAAAAAAAAAAAAAA 1


RESULT 1177
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ABZ89085/c
ID ABZ89085 standard; DNA; 20 BP.
XX
AC ABZ89085;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4327; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 19 A; 0 C; 1 G; 0 T; 0 U; 0 Other;

 Query Match 0.7%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 8.1e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTT 2185
 ||||||||||||||||||| |
Db 20 TTTTTTTTTTTTTTTTTCT 1

RESULT 1178

ABZ88694
ID ABZ88694 standard; DNA; 20 BP.
XX
AC ABZ88694;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 3936; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 17 A; 0 C; 0 G; 3 T; 0 U; 0 Other;

 Query Match 0.7%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 8.1e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2783 TTGAAAAAAAAAAAAAAAAA 2802
 || |||||||||||||||||
Db 1 TTTAAAAAAAAAAAAAAAAA 20

RESULT 1179

```
AAQ49436
ID   AAQ49436 standard; cDNA; 20 BP.
XX
AC   AAQ49436;
XX
DT   25-MAR-2003  (revised)
DT   27-APR-1994  (first entry)
XX
DE   Cytochrome P450 sequence amplification PCR primer polyT.
XX
KW   Transgenic plants; altered petal colour; polymerase chain reaction; ss.
XX
OS   Synthetic.
XX
PN   WO9320206-A1.
XX
PD   14-OCT-1993.
XX
PF   25-MAR-1993;   93WO-AU000127.
XX
PR   27-MAR-1992;   92AU-00001538.
PR   07-JAN-1993;   93AU-00006698.
XX
PA   (ITFL-) INT FLOWER DEV PTY LTD.
XX
PI   Holton TA,  Cornish EC,  Tanaka Y;
XX
DR   WPI; 1993-336914/42.
XX
PT   Nucleic acid isolate encoding flavonoid-3'-hydroxylase - is used to
PT   create transgenic plants with altered petal colour.
XX
PS   Disclosure; Page 25; 86pp; English.
XX
CC   The sequence is that of a PCR primer which was used in polymerase chain
CC   reactions for the amplification of cloned cytochrome P450 sequences.
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 8.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAAC 2189
                ||||||||||||||||||  |
Db          1 TTTTTTTTTTTTTTTTTAGC 20


RESULT 1180
AAQ75566
ID   AAQ75566 standard; DNA; 20 BP.
XX
AC   AAQ75566;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 8.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAAC 2189
                ||||||||||||||||||  ||
Db          1 TTTTTTTTTTTTTTTTTGAC 20


RESULT 1181
AAQ75569
ID   AAQ75569 standard; DNA; 20 BP.
XX
AC   AAQ75569;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 0 A; 0 C; 1 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 8.1e+02;
```

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  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              |||||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTTTGTT 20


RESULT 1182
AAQ75584
ID   AAQ75584 standard; DNA; 20 BP.
XX
AC   AAQ75584;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 2 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 8.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTTTTATA 20


RESULT 1183
AAQ75585
ID   AAQ75585 standard; DNA; 20 BP.
XX
AC   AAQ75585;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 1 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 8.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              |||||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTTTATT 20


RESULT 1184
AAQ75568
ID   AAQ75568 standard; DNA; 20 BP.
XX
AC   AAQ75568;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
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CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 8.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTTTGTA 20


RESULT 1185
AAQ75570/c
ID   AAQ75570 standard; DNA; 20 BP.
XX
AC   AAQ75570;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 8.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2804
              || |||||||||||||||||
Db         20 GACAAAAAAAAAAAAAAAAA 1


RESULT 1186
AAQ75572/c
ID   AAQ75572 standard; DNA; 20 BP.
XX
AC   AAQ75572;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 8.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAA 2803
              || |||||||||||||||||
Db         20 TGCAAAAAAAAAAAAAAAAA 1


RESULT 1187
AAQ75586
ID   AAQ75586 standard; DNA; 20 BP.
XX
AC   AAQ75586;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
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DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 8.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTAAC 2189
              ||||||||||||||||||  |
Db          1 TTTTTTTTTTTTTTTTATC 20


RESULT 1188
AAQ75586/c
ID   AAQ75586 standard; DNA; 20 BP.
XX
AC   AAQ75586;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 8.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2804
              || |||||||||||||||||
Db         20 GATAAAAAAAAAAAAAAAA 1


RESULT 1189
AAQ75589
ID   AAQ75589 standard; DNA; 20 BP.
XX
AC   AAQ75589;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 8.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTTAACT 2190
              ||||||||||||||||| |||
Db          1 TTTTTTTTTTTTTTTTTACT 20


RESULT 1190
AAQ75604/c
ID   AAQ75604 standard; DNA; 20 BP.
XX
AC   AAQ75604;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
```

PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 1 A; 2 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 0.7%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 8.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2783 TTGAAAAAAAAAAAAAAAAA 2802
| ||||||||||||||||||
Db 20 TGGAAAAAAAAAAAAAAAAA 1

RESULT 1191
AAQ75588/c
ID AAQ75588 standard; DNA; 20 BP.
XX
AC AAQ75588;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 0.7%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 8.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2784 TGAAAAAAAAAAAAAAAAAA 2803
|| ||||||||||||||||||
Db 20 TGTAAAAAAAAAAAAAAAAA 1

RESULT 1192
AAQ75601
ID AAQ75601 standard; DNA; 20 BP.
XX
AC AAQ75601;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 0 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 0.7%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 8.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTT 2185
|||||||||||||||||| ||
Db 1 TTTTTTTTTTTTTTTTTCTT 20

RESULT 1193
AAQ75564
ID AAQ75564 standard; DNA; 20 BP.
XX
AC AAQ75564;

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XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 2 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 8.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTAA 2188
              |||||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTTTGAA 20


RESULT 1194
AAQ75564/c
ID   AAQ75564 standard; DNA; 20 BP.
XX
AC   AAQ75564;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 2 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 8.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAA 2802
              || ||||||||||||||||||
Db         20 TTCAAAAAAAAAAAAAAAA 1


RESULT 1195
AAQ75600
ID   AAQ75600 standard; DNA; 20 BP.
XX
AC   AAQ75600;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 8.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy       2168 TTTTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTTTCTA 20
```

RESULT 1196
AAQ75600/c
ID AAQ75600 standard; DNA; 20 BP.
XX
AC AAQ75600;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

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  Query Match              0.7%;  Score 18.4;  DB 1;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 8.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAA 2802
              | ||||||||||||||||||
Db         20 TAGAAAAAAAAAAAAAAAAA 1
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RESULT 1197
AAQ75578
ID AAQ75578 standard; DNA; 20 BP.
XX
AC AAQ75578;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

```
  Query Match              0.7%;  Score 18.4;  DB 1;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 8.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTAAC 2189
              |||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTAGC 20
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RESULT 1198
AAQ75590
ID AAQ75590 standard; DNA; 20 BP.
XX
AC AAQ75590;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of

```
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 1 A; 2 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 8.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAAC 2189
                ||||||||||||||||||  |
Db          1 TTTTTTTTTTTTTTTTTACC 20


RESULT 1199
AAQ75602/c
ID   AAQ75602 standard; DNA; 20 BP.
XX
AC   AAQ75602;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 0 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 8.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2804
                || ||||||||||||||||
Db         20 GAGAAAAAAAAAAAAAAAA 1


RESULT 1200
AAQ75592/c
ID   AAQ75592 standard; DNA; 20 BP.
XX
AC   AAQ75592;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 8.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAA 2802
                |  ||||||||||||||||||
Db         20 TCGAAAAAAAAAAAAAAAAA 1


RESULT 1201
ABZ88266/c
ID   ABZ88266 standard; DNA; 20 BP.
XX
AC   ABZ88266;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135
XX
PR   24-APR-2001; 2001US-0286137P.
XX
```

PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 3508; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 17 A; 1 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 0.7%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 8.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2170 TTTTTTTTTTTTTTTTTAAC 2189
||||||||||||||||||| |
Db 20 TTTTTTTTTTTTTTTTTAGC 1

RESULT 1202
ABZ85534/c
ID ABZ85534 standard; DNA; 20 BP.
XX
AC ABZ85534;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX

PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Claim 15; SEQ ID NO 776; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 18 A; 0 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 8.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2165 CTTTTTTTTTTTTTTTTTTT 2184
||||| |||||||||||||||
Db 20 CTTTTCTTTTTTTTTTTTTT 1

RESULT 1203
ABZ92865/c
ID ABZ92865 standard; DNA; 20 BP.
XX
AC ABZ92865;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX

PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 8107; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 18 A; 0 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 0.7%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 8.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2172 TTTTTTTTTTTTTTTAACTT 2191
||||||||||||||| ||||
Db 20 TTTTTTTTTTTTTTTACTT 1

RESULT 1204
ABZ88938/c
ID ABZ88938 standard; DNA; 20 BP.
XX
AC ABZ88938;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX

PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4180; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 17 A; 1 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 0.7%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 8.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2170 TTTTTTTTTTTTTTTTAAC 2189
||||||||||||||||| ||
Db 20 TTTTTTTTTTTTTTTTGAC 1

RESULT 1205
ABZ88813
ID ABZ88813 standard; DNA; 20 BP.
XX
AC ABZ88813;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX

```
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 4055; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 16 A; 0 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 8.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAA 2799
              ||||| ||||||||||||||
Db          1 GAATTTAAAAAAAAAAAAA 20


RESULT 1206
AAQ75757
ID   AAQ75757 standard; DNA; 21 BP.
XX
AC   AAQ75757;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTAA 2188
              ||||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTTCAA 20


RESULT 1207
AAQ75756
ID   AAQ75756 standard; DNA; 21 BP.
XX
AC   AAQ75756;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 3 A; 1 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTAA 2188
```

```
                  |||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTTCAA 20


RESULT 1208
AAQ75755
ID   AAQ75755 standard; DNA; 21 BP.
XX
AC   AAQ75755;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTAA 2188
                  |||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTTTCAA 20


RESULT 1209
AAQ75630/c
ID   AAQ75630 standard; DNA; 21 BP.
XX
AC   AAQ75630;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAA 2802
                  || ||||||||||||||||
Db         20 TTCAAAAAAAAAAAAAAAA 1


RESULT 1210
AAQ75629
ID   AAQ75629 standard; DNA; 21 BP.
XX
AC   AAQ75629;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
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```
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTAA 2188
              |||||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTTTGAA 20


RESULT 1211
AAQ75773
ID   AAQ75773 standard; DNA; 21 BP.
XX
AC   AAQ75773;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTTTTCTA 20


RESULT 1212
AAQ75684
ID   AAQ75684 standard; DNA; 21 BP.
XX
AC   AAQ75684;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAAC 2189
              |||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTTATC 20


RESULT 1213
AAQ75726/c
ID   AAQ75726 standard; DNA; 21 BP.
XX
AC   AAQ75726;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
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```
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 3 A; 1 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAA 2802
              || |||||||||||||||||
Db         20 TTTAAAAAAAAAAAAAAAA 1


RESULT 1214
AAQ75685/c
ID   AAQ75685 standard; DNA; 21 BP.
XX
AC   AAQ75685;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2804
              || |||||||||||||||||
Db         20 GATAAAAAAAAAAAAAAAA 1


RESULT 1215
AAQ75772/c
ID   AAQ75772 standard; DNA; 21 BP.
XX
AC   AAQ75772;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAA 2802
              | |||||||||||||||||
Db         20 TAGAAAAAAAAAAAAAAAA 1


RESULT 1216
AAQ75724/c
ID   AAQ75724 standard; DNA; 21 BP.
XX
AC   AAQ75724;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
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XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 4 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAA 2802
              || ||||||||||||||||||
Db         20 TTTAAAAAAAAAAAAAAAAA 1


RESULT 1217
AAQ75730/c
ID   AAQ75730 standard; DNA; 21 BP.
XX
AC   AAQ75730;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAAA 2801
              ||| ||||||||||||||||
Db         20 ATTAAAAAAAAAAAAAAAAA 1


RESULT 1218
AAQ75763
ID   AAQ75763 standard; DNA; 21 BP.
XX
AC   AAQ75763;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAAC 2189
              |||||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTTTCAC 20


RESULT 1219
AAQ75728/c
ID   AAQ75728 standard; DNA; 21 BP.
XX
AC   AAQ75728;
XX
DT   04-AUG-1995  (first entry)
XX
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```
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 3 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAA 2801
              ||| ||||||||||||||||
Db         20 ATTAAAAAAAAAAAAAAAA 1


RESULT 1220
AAQ75727/c
ID   AAQ75727 standard; DNA; 21 BP.
XX
AC   AAQ75727;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAA 2801
              ||| ||||||||||||||||
Db         20 ATTAAAAAAAAAAAAAAAA 1


RESULT 1221
AAQ75764
ID   AAQ75764 standard; DNA; 21 BP.
XX
AC   AAQ75764;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTAAC 2189
              |||||||||||||||||  ||
Db          1 TTTTTTTTTTTTTTTTCAC 20
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```
RESULT 1222
AAQ75723/c
ID   AAQ75723 standard; DNA; 21 BP.
XX
AC   AAQ75723;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 3 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAA 2802
              || |||||||||||||||||
Db         20 TTTAAAAAAAAAAAAAAAA 1


RESULT 1223
AAQ75766
ID   AAQ75766 standard; DNA; 21 BP.
XX
AC   AAQ75766;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 3 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAAC 2189
              |||||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTTTCAC 20


RESULT 1224
AAQ75651/c
ID   AAQ75651 standard; DNA; 21 BP.
XX
AC   AAQ75651;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
```

```
XX
SQ   Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2804
              || |||||||||||||||||
Db         20 GACAAAAAAAAAAAAAAAAA 1


RESULT 1225
AAQ75702
ID   AAQ75702 standard; DNA; 21 BP.
XX
AC   AAQ75702;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 3 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAAC 2189
              |||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTTACC 20


RESULT 1226
AAQ75661/c
ID   AAQ75661 standard; DNA; 21 BP.
XX
AC   AAQ75661;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAA 2803
              || |||||||||||||||||
Db         20 TGCAAAAAAAAAAAAAAAAA 1


RESULT 1227
AAQ75675
ID   AAQ75675 standard; DNA; 21 BP.
XX
AC   AAQ75675;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
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PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTTTATA 20


RESULT 1228
AAQ75771
ID   AAQ75771 standard; DNA; 21 BP.
XX
AC   AAQ75771;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTTTCTA 20


RESULT 1229
AAQ75771/c
ID   AAQ75771 standard; DNA; 21 BP.
XX
AC   AAQ75771;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAA 2802
              | ||||||||||||||||||
Db         20 TAGAAAAAAAAAAAAAAAAA 1


RESULT 1230
AAQ75627
ID   AAQ75627 standard; DNA; 21 BP.
XX
AC   AAQ75627;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
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XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTAA 2188
              ||||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTTTGAA 20


RESULT 1231
AAQ75627/c
ID   AAQ75627 standard; DNA; 21 BP.
XX
AC   AAQ75627;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAA 2802
              || ||||||||||||||||||
Db         20 TTCAAAAAAAAAAAAAAAA 1


RESULT 1232
AAQ75693/c
ID   AAQ75693 standard; DNA; 21 BP.
XX
AC   AAQ75693;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAA 2803
              || ||||||||||||||||||
Db         20 TGTAAAAAAAAAAAAAAAAA 1


RESULT 1233
AAQ75739/c
ID   AAQ75739 standard; DNA; 21 BP.
XX
AC   AAQ75739;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
```

KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 0.7%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 9.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2783 TTGAAAAAAAAAAAAAAAA 2802
| ||||||||||||||||||
Db 20 TCGAAAAAAAAAAAAAAAAA 1

RESULT 1234
AAQ75778
ID AAQ75778 standard; DNA; 21 BP.
XX
AC AAQ75778;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 9; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 2 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 0.7%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 9.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTT 2185
|||||||||||||||||| ||
Db 1 TTTTTTTTTTTTTTTTTCTT 20

RESULT 1235
AAQ75778/c
ID AAQ75778 standard; DNA; 21 BP.
XX
AC AAQ75778;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 9; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 2 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 0.7%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 9.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAAAAAAAAA 2804
||| ||||||||||||||||
Db 21 GAAGAAAAAAAAAAAAAAAA 2

```
RESULT 1236
AAQ75787/c
ID   AAQ75787 standard; DNA; 21 BP.
XX
AC   AAQ75787;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAA 2802
                | ||||||||||||||||||
Db         20 TGGAAAAAAAAAAAAAAAAA 1


RESULT 1237
AAQ75643
ID   AAQ75643 standard; DNA; 21 BP.
XX
AC   AAQ75643;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTA 2187
                ||||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTTTGTA 20


RESULT 1238
AAQ75781/c
ID   AAQ75781 standard; DNA; 21 BP.
XX
AC   AAQ75781;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 2 C; 0 G; 19 T; 0 U; 0 Other;
```

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  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2804
              || |||||||||||||||||
Db         20 GAGAAAAAAAAAAAAAAAA 1


RESULT 1239
AAQ75695
ID   AAQ75695 standard; DNA; 21 BP.
XX
AC   AAQ75695;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTTAACT 2190
              |||||||||||||||||  |||
Db          1 TTTTTTTTTTTTTTTTTACT 20


RESULT 1240
AAQ75718
ID   AAQ75718 standard; DNA; 21 BP.
XX
AC   AAQ75718;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTAAC 2189
              |||||||||||||||||  |
Db          1 TTTTTTTTTTTTTTTTAGC 20


RESULT 1241
AAQ75646
ID   AAQ75646 standard; DNA; 21 BP.
XX
AC   AAQ75646;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
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CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTTTGTA 20


RESULT 1242
AAQ75650
ID   AAQ75650 standard; DNA; 21 BP.
XX
AC   AAQ75650;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              |||||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTTTGTT 20


RESULT 1243
AAQ75650/c
ID   AAQ75650 standard; DNA; 21 BP.
XX
AC   AAQ75650;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2804
              ||| ||||||||||||||||
Db         21 GAACAAAAAAAAAAAAAAA 2


RESULT 1244
AAQ75682
ID   AAQ75682 standard; DNA; 21 BP.
XX
AC   AAQ75682;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
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XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTTTATT 20


RESULT 1245
AAQ75682/c
ID   AAQ75682 standard; DNA; 21 BP.
XX
AC   AAQ75682;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2804
              ||| |||||||||||||||
Db         21 GAATAAAAAAAAAAAAAAA 2


RESULT 1246
AAQ75678
ID   AAQ75678 standard; DNA; 21 BP.
XX
AC   AAQ75678;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTTTATA 20


RESULT 1247
AAQ75694/c
ID   AAQ75694 standard; DNA; 21 BP.
XX
AC   AAQ75694;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
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```
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAA 2803
              || |||||||||||||||||
Db         20 TGTAAAAAAAAAAAAAAAAA 1


RESULT 1248
AAQ75700
ID   AAQ75700 standard; DNA; 21 BP.
XX
AC   AAQ75700;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTAAC 2189
              |||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTACC 20


RESULT 1249
AAQ75742/c
ID   AAQ75742 standard; DNA; 21 BP.
XX
AC   AAQ75742;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAA 2802
              | ||||||||||||||||||
Db         20 TCGAAAAAAAAAAAAAAAA 1


RESULT 1250
AAQ75659/c
```

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ID   AAQ75659 standard; DNA; 21 BP.
XX
AC   AAQ75659;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAA 2803
              || ||||||||||||||||||
Db         20 TGCAAAAAAAAAAAAAAAAA 1


RESULT 1251
AAQ75715
ID   AAQ75715 standard; DNA; 21 BP.
XX
AC   AAQ75715;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAAC 2189
              |||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTTAGC 20


RESULT 1252
AAQ75716
ID   AAQ75716 standard; DNA; 21 BP.
XX
AC   AAQ75716;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
```

```
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTAAC 2189
              ||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTAGC 20


RESULT 1253
AAQ75740/c
ID   AAQ75740 standard; DNA; 21 BP.
XX
AC   AAQ75740;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAA 2802
              | ||||||||||||||||||
Db         20 TCGAAAAAAAAAAAAAAAA 1


RESULT 1254
AAQ75779/c
ID   AAQ75779 standard; DNA; 21 BP.
XX
AC   AAQ75779;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2804
              || |||||||||||||||||
Db         20 GAGAAAAAAAAAAAAAAAA 1


RESULT 1255
AAQ75628
ID   AAQ75628 standard; DNA; 21 BP.
XX
AC   AAQ75628;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
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CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 3 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTAA 2188
              ||||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTTGAA 20


RESULT 1256
AAQ75628/c
ID   AAQ75628 standard; DNA; 21 BP.
XX
AC   AAQ75628;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 3 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAA 2802
              || ||||||||||||||||||
Db         20 TTCAAAAAAAAAAAAAAAA 1


RESULT 1257
AAQ75636
ID   AAQ75636 standard; DNA; 21 BP.
XX
AC   AAQ75636;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAAC 2189
              ||||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTTTGAC 20


RESULT 1258
AAQ75686
ID   AAQ75686 standard; DNA; 21 BP.
XX
AC   AAQ75686;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
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XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTAAC 2189
                ||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTATC 20


RESULT 1259
AAQ75686/c
ID   AAQ75686 standard; DNA; 21 BP.
XX
AC   AAQ75686;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2804
                || |||||||||||||||||
Db         20 GATAAAAAAAAAAAAAAAAA 1


RESULT 1260
AAQ75775
ID   AAQ75775 standard; DNA; 21 BP.
XX
AC   AAQ75775;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
                ||||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTTCTT 20


RESULT 1261
AAQ75790/c
ID   AAQ75790 standard; DNA; 21 BP.
XX
AC   AAQ75790;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
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```
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 3 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match              0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAA 2802
              | ||||||||||||||||||
Db         20 TGGAAAAAAAAAAAAAAAAA 1


RESULT 1262
AAQ75698
ID   AAQ75698 standard; DNA; 21 BP.
XX
AC   AAQ75698;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match              0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTTAACT 2190
              |||||||||||||||| |||
Db          1 TTTTTTTTTTTTTTTTTACT 20


RESULT 1263
AAQ75699
ID   AAQ75699 standard; DNA; 21 BP.
XX
AC   AAQ75699;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match              0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTAAC 2189
              ||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTACC 20


RESULT 1264
AAQ75635
ID   AAQ75635 standard; DNA; 21 BP.
XX
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AC   AAQ75635;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAAC 2189
              ||||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTTTGAC 20


RESULT 1265
AAQ75645
ID   AAQ75645 standard; DNA; 21 BP.
XX
AC   AAQ75645;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTTTGTA 20


RESULT 1266
AAQ75691/c
ID   AAQ75691 standard; DNA; 21 BP.
XX
AC   AAQ75691;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy       2784 TGAAAAAAAAAAAAAAAAAA 2803
              || |||||||||||||||||
Db         20 TGTAAAAAAAAAAAAAAAAA 1
```

RESULT 1267
AAQ75782/c
ID AAQ75782 standard; DNA; 21 BP.
XX
AC AAQ75782;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 9; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 3 C; 0 G; 18 T; 0 U; 0 Other;

 Query Match 0.7%; Score 18.4; DB 1; Length 21;
 Best Local Similarity 95.0%; Pred. No. 9.1e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2785 GAAAAAAAAAAAAAAAAAA 2804
              || |||||||||||||||||
Db         20 GAGAAAAAAAAAAAAAAAA 1
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RESULT 1268
AAQ75662/c
ID AAQ75662 standard; DNA; 21 BP.
XX
AC AAQ75662;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 6; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

 Query Match 0.7%; Score 18.4; DB 1; Length 21;
 Best Local Similarity 95.0%; Pred. No. 9.1e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2784 TGAAAAAAAAAAAAAAAAAA 2803
              || |||||||||||||||||
Db         20 TGCAAAAAAAAAAAAAAAAA 1
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RESULT 1269
AAQ75679
ID AAQ75679 standard; DNA; 21 BP.
XX
AC AAQ75679;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse

```
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||  ||
Db          1 TTTTTTTTTTTTTTTTTATT 20


RESULT 1270
AAQ75774
ID   AAQ75774 standard; DNA; 21 BP.
XX
AC   AAQ75774;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||  ||
Db          1 TTTTTTTTTTTTTTTTTCTA 20


RESULT 1271
AAQ75774/c
ID   AAQ75774 standard; DNA; 21 BP.
XX
AC   AAQ75774;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAA 2802
              | ||||||||||||||||||
Db         20 TAGAAAAAAAAAAAAAAAA 1


RESULT 1272
AAQ75638
ID   AAQ75638 standard; DNA; 21 BP.
XX
AC   AAQ75638;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
```

```
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTAAC 2189
              ||||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTTGAC 20


RESULT 1273
AAQ75653/c
ID   AAQ75653 standard; DNA; 21 BP.
XX
AC   AAQ75653;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2804
              || |||||||||||||||||
Db         20 GACAAAAAAAAAAAAAAAAA 1


RESULT 1274
AAQ75677
ID   AAQ75677 standard; DNA; 21 BP.
XX
AC   AAQ75677;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTTTATA 20


RESULT 1275
AAQ75683
ID   AAQ75683 standard; DNA; 21 BP.
XX
AC   AAQ75683;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
```

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XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTAAC 2189
                ||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTATC 20


RESULT 1276
AAQ75683/c
ID   AAQ75683 standard; DNA; 21 BP.
XX
AC   AAQ75683;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2804
                || |||||||||||||||||
Db         20 GATAAAAAAAAAAAAAAAAA 1


RESULT 1277
AAQ75696
ID   AAQ75696 standard; DNA; 21 BP.
XX
AC   AAQ75696;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTTAACT 2190
                ||||||||||||||||| |||
Db          1 TTTTTTTTTTTTTTTTTACT 20


RESULT 1278
AAQ75647
ID   AAQ75647 standard; DNA; 21 BP.
XX
AC   AAQ75647;
XX
```

```
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 0 C; 2 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
                ||||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTTTGTT 20


RESULT 1279
AAQ75654/c
ID   AAQ75654 standard; DNA; 21 BP.
XX
AC   AAQ75654;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 9.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2804
                || |||||||||||||||||
Db         20 GACAAAAAAAAAAAAAAAAA 1


RESULT 1280
ABA93238
ID   ABA93238 standard; DNA; 22 BP.
XX
AC   ABA93238;
XX
DT   18-APR-2002  (first entry)
XX
DE   PolyA adaptor oligonucleotide SEQ ID NO:1.
XX
KW   Detection; comparative detection; adaptor; ss.
XX
OS   Synthetic.
XX
PN   JP2001333800-A.
XX
PD   04-DEC-2001.
XX
PF   30-MAY-2000; 2000JP-00160324.
XX
PR   30-MAY-2000; 2000JP-00160324.
XX
PA   (UNIT-) UNITECH CO LTD.
XX
DR   WPI; 2002-135950/18.
XX
PT   Comparative detection of the amounts of RNA and DNA.
XX
PS   Disclosure; Page 9; 9pp; Japanese.
XX
CC   The present invention describes a method for the comparative detection of
CC   the amount of an RNA. The method comprises: (a) cDNAs obtained by
CC   transcribing respectively from at least two tissue RNAs are respectively
CC   fragmented by using a same restriction enzyme; (b) each different adaptor
CC   and a common adaptor are added to each of the cDNA fragments derived from
CC   the same or different tissues by the step (a); (c) the resultant adaptor-
CC   added cDNAs are mixed together; (d) an adaptor primer having the common
CC   sequence to said different adaptor and a gene-specific adaptor are used
CC   to amplify said adaptor-added cDNAs containing no region derived from
CC   polyadenylic acid of the mRNA before the addition of the adaptor among
CC   the adaptor-added cDNAs prepared by the step (b); (e) the ratios of the
CC   cDNA amounts are measured between the tissues; (f) the RNA is detected
CC   from the measured result; (g) each different adaptor and a common adaptor
CC   are added to each of the genomic DNA fragments derived from a same or
CC   different individuals; (h) the resultant adaptor-added genomic DNAs are
CC   mixed together; (i) the adaptor-added genomic DNAs are amplified by using
CC   an adaptor primer having the common sequence to the different adaptor and
CC   a sequence-specific adaptor; and (j) the ratios of the amplified amounts
```

```
CC   of the genomic DNAs are measured between the individuals. The method is
CC   used for the detection of the amounts of RNA and DNA. The present
CC   sequence represents an oligonucleotide which is used in the
CC   exemplification of the present invention
XX
SQ   Sequence 22 BP; 19 A; 1 C; 1 G; 1 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 22;
  Best Local Similarity   95.0%;  Pred. No. 1e+03;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAA 2803
              | ||||||||||||||||||
Db          3 TCAAAAAAAAAAAAAAAAAA 22


RESULT 1281
ABK12409
ID   ABK12409 standard; DNA; 24 BP.
XX
AC   ABK12409;
XX
DT   18-JUN-2002  (first entry)
XX
DE   RT-PCR primer #1 for cDNA encoding polypeptide-laminin B210.67.
XX
KW   Polypeptide-laminin B210.67; embryo development teratogenesis;
KW   cytostatic; reverse transcriptase-PCR; RT-PCR; primer; ss.
XX
OS   Unidentified.
XX
PN   CN1328013-A.
XX
PD   26-DEC-2001.
XX
PF   14-JUN-2000; 2000CN-00116514.
XX
PR   14-JUN-2000; 2000CN-00116514.
XX
PA   (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-270054/32.
XX
PT   Polypeptide-laminin B210.67, useful for treating diseases such as embryo
PT   development teratogenesis.
XX
PS   Example 2; Page 18 (disclosure); 33pp; Chinese.
XX
CC   The present invention relates to the isolation of polypeptide-laminin
CC   B210.67, and the polynucleotide encoding it. Also described is the
CC   process for preparing the protein by DNA recombination. The polypeptide
CC   is useful for treating diseases such as embryo development teratogenesis.
CC   The present sequence for reverse transcriptase (RT)-PCR primer #1 is used
CC   with RT-PCR primer #2 (ABK12410) for isolating cDNA encoding polypeptide-
CC   laminin B210.67
XX
SQ   Sequence 24 BP; 19 A; 2 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 24;
  Best Local Similarity   95.0%;  Pred. No. 1.3e+03;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAA 2802
              || ||||||||||||||||||
Db          5 TTAAAAAAAAAAAAAAAAAA 24


RESULT 1282
AAL47515
ID   AAL47515 standard; DNA; 24 BP.
XX
AC   AAL47515;
XX
DT   13-SEP-2002  (first entry)
XX
DE   Human cyclophilin-40-12-54 coding sequence PCR primer #2.
XX
KW   Human; cyclophilin-40-12.54; immunopathy; cancer; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1331162-A.
XX
PD   16-JAN-2002.
XX
PF   28-JUN-2000; 2000CN-00116823.
XX
PR   28-JUN-2000; 2000CN-00116823.
XX
PA   (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-305482/35.
XX
PT   Polypeptide-human cyclophilin-40-12.54 and polynucleotide for coding it.
XX
PS   Example 2; Page 17 (Disclosure); 33pp; Chinese.
XX
CC   The present invention provides the protein and coding sequences of human
CC   cyclophilin-40-12.54. The sequences can be used in the treatment of
CC   immunopathy and cancer. The present sequence is a PCR primer for the
CC   coding sequence of the invention
XX
SQ   Sequence 24 BP; 2 A; 1 C; 2 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 24;
  Best Local Similarity   95.0%;  Pred. No. 1.3e+03;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTTA 2187
              ||||||| ||||||||||||
Db          1 TTTTTTCTTTTTTTTTTTA 20


RESULT 1283
AAF74925/c
ID   AAF74925 standard; DNA; 25 BP.
XX
AC   AAF74925;
XX
DT   23-MAY-2001  (first entry)
XX
DE   CD40L poly-A tract sequence SEQ ID NO:22.
XX
KW   Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW   diagnosis; antiarthritic; antirheumatic; immunosuppressive;
KW   antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200119844-A1.
XX
PD   22-MAR-2001.
XX
PF   13-SEP-2000; 2000WO-US024966.
XX
PR   13-SEP-1999;   99US-0153625P.
XX
PA   (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
PI   Crow MK,  Li Y;
XX
DR   WPI; 2001-244776/25.
```

```
XX
PT   New altered CD40L promoter for use in the study, diagnosis and treatment
PT   of a variety of inflammatory disorders and autoimmune diseases, such as
PT   rheumatoid arthritis.
XX
PS   Example 1; Fig 3; 90pp; English.
XX
CC   The present invention describes an isolated, purified nucleic acid, which
CC   is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC   residues 331-455 of the sequence comprising 455 nucleotides given in
CC   AAF74905 where A in the wild type sequence at position 331 (corresponding
CC   to position -125) is replaced with C. (I) has antiarthritic,
CC   antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC   be used in gene therapy. (I) is useful in the study, diagnosis and
CC   treatment of inflammatory and autoimmune diseases, as well as diseases in
CC   which elevated expression of CD40L is a factor, e.g., rheumatoid
CC   arthritis. The present sequence represents a CD40L poly-A tract sequence
CC   which is used in an example from the present invention
XX
SQ   Sequence 25 BP; 19 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 25;
  Best Local Similarity   95.0%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              ||||| |||||||||||||
Db         20 TTTTTGTTTTTTTTTTTTT 1


RESULT 1284
AAF74930/c
ID   AAF74930 standard; DNA; 25 BP.
XX
AC   AAF74930;
XX
DT   23-MAY-2001  (first entry)
XX
DE   CD40L poly-A tract sequence SEQ ID NO:27.
XX
KW   Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW   diagnosis; antiarthritic; antirheumatic; immunosuppressive;
KW   antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200119844-A1.
XX
PD   22-MAR-2001.
XX
PF   13-SEP-2000; 2000WO-US024966.
XX
PR   13-SEP-1999;   99US-0153625P.
XX
PA   (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
PI   Crow MK,  Li Y;
XX
DR   WPI; 2001-244776/25.
XX
PT   New altered CD40L promoter for use in the study, diagnosis and treatment
PT   of a variety of inflammatory disorders and autoimmune diseases, such as
PT   rheumatoid arthritis.
XX
PS   Example 1; Fig 3; 90pp; English.
XX
CC   The present invention describes an isolated, purified nucleic acid, which
CC   is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC   residues 331-455 of the sequence comprising 455 nucleotides given in
CC   AAF74905 where A in the wild type sequence at position 331 (corresponding
CC   to position -125) is replaced with C. (I) has antiarthritic,
CC   antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC   be used in gene therapy. (I) is useful in the study, diagnosis and
CC   treatment of inflammatory and autoimmune diseases, as well as diseases in
CC   which elevated expression of CD40L is a factor, e.g., rheumatoid
CC   arthritis. The present sequence represents a CD40L poly-A tract sequence
CC   which is used in an example from the present invention
XX
SQ   Sequence 25 BP; 19 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 25;
  Best Local Similarity   95.0%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              ||||| |||||||||||||
Db         20 TTTTTGTTTTTTTTTTTTT 1


RESULT 1285
AAA62140
ID   AAA62140 standard; DNA; 26 BP.
XX
AC   AAA62140;
XX
DT   06-AUG-2003  (revised)
DT   10-NOV-2000  (first entry)
XX
DE   A. auricaliformis (RT-) PCR primer.
XX
KW   PCR primer; RT-PCR primer; plant genetic marker; plant breeding; ss.
XX
OS   Acacia auriculiformis.
XX
PN   AU9960643-A.
XX
PD   01-JUN-2000.
XX
PF   24-NOV-1999;   99AU-00060643.
XX
PR   25-NOV-1998;   98JP-00333469.
XX
PA   (REAS-) RES ASSOC REFORESTATION TROPICAL FOREST.
XX
PI   Hibino T,  Koshiyama J;
XX
DR   WPI; 2000-412598/36.
XX
PT   Method for obtaining plant DNA fragments useful as novel genetic markers,
PT   comprising digesting plant DNA, subjecting fragments to genome
PT   subtraction and screening the polymorphic fragments.
XX
PS   Example 1; Page 13; 21pp; English.
XX
CC   The present sequence is a primer for Acacia auricaliformis. This sequence
CC   was used in RT-PCR reactions to produce cDNA from A. auricaliformis RNA.
CC   The resulting cDNA was amplified via PCR using the present sequence and
CC   another PCR primer (see AAA62141). The PCR product was used as an
CC   expression probe. The expression probe was used to obtain desired DNA
CC   fragments. The plant genetic fragments obtained by this method may be
CC   useful as markers in plant breeding. In addition, genes encoding the DNA
CC   fragments or their promoter regions may be used to modify expression.
CC   (Updated on 06-AUG-2003 to correct OS field.)
XX
SQ   Sequence 26 BP; 1 A; 4 C; 5 G; 16 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 26;
  Best Local Similarity   95.0%;  Pred. No. 1.5e+03;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTTTTT 2181
              | ||||||||||||||||||
Db          7 CCCCTTTTTTTTTTTTTTTT 26


RESULT 1286
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```
AAC93128
ID   AAC93128 standard; DNA; 26 BP.
XX
AC   AAC93128;
XX
DT   21-MAR-2001  (first entry)
XX
DE   Stephania tetrandra S. moore RNA reverse transcriptase primer NotI-dT.
XX
KW   Stephania tetrandra S. Moore; IL-6; interleukin-6; hepatotropic;
KW   antiinflammatory; hepatocirrhosis; hepatitis; alcoholism; primer; ss.
XX
OS   Unidentified.
XX
PN   US6162437-A.
XX
PD   19-DEC-2000.
XX
PF   25-NOV-1997;   97US-00978321.
XX
PR   05-JUN-1995;   95WO-KR000073.
PR   06-DEC-1996;   96US-00750462.
XX
PA   (KOAD ) KOREA ADV INST SCI & TECHNOLOGY.
XX
PI   Lee J,  Kim Y,  Kang H,  Pyun K,  Choi I;
XX
DR   WPI; 2001-146043/15.
XX
PT   Treatment of hepatocirrhosis comprises administering an extract of the
PT   root of Stephania tetrandra in an amount effective to inhibit production
PT   of interleukin-6.
XX
PS   Example 4; Col 9; 27pp; English.
XX
CC   The present sequence was used in an example to illustrate a method for
CC   treating hepatocirrhosis. The method comprises administering an extract
CC   of the root of Stephania tetrandra in an amount effective to inhibit
CC   production of interleukin-6 (IL-6). Hepatocirrhosis is often associated
CC   with chronic hepatitis or chronic alcoholism
XX
SQ   Sequence 26 BP; 0 A; 4 C; 4 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 26;
  Best Local Similarity   95.0%;  Pred. No. 1.5e+03;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTTTTTT 2183
              | ||||||||||||||||||
Db          7 CGTTTTTTTTTTTTTTTTTT 26


RESULT 1287
AAQ36362
ID   AAQ36362 standard; DNA; 28 BP.
XX
AC   AAQ36362;
XX
DT   25-MAR-2003  (revised)
DT   07-JUN-1993  (first entry)
XX
DE   GL6anti, targetted to human beta globin sequence.
XX
KW   Heamoglobin; beta thalassemia; sickle cell anaemia; delta protein;
KW   triplex; target; duplex; promoter; coding domain; ss.
XX
OS   Synthetic.
XX
PN   US5176996-A.
XX
PD   05-JAN-1993.
XX
PF   22-DEC-1989;   89US-00453532.
XX
PR   20-DEC-1988;   88US-00287359.
XX
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PI   Hogan ME,  Kessler DJ;
XX
DR   WPI; 1993-035718/04.
XX
PT   Synthetic oligo-nucleotide(s), prodn. useful e.g. for HIV-1 inhibition -
PT   which bind to target sequence in duplex DNA forming colinear triplex by
PT   binding to major groove.
XX
PS   Example 13; Col 36; 29pp; English.
XX
CC   The beta globin gene encodes on of the proteins comprising human adult
CC   haemoglobin. . Mutation in this gene is responsible for beta thalassemia
CC   and sickle cell anaemia. Expression of the gene may be prevented by the
CC   formation of a triplex between the duplex target DNA sequence and an anti
CC   parallel or parallel synthetic oligonucleotide. The triplex
CC   oligonucleotides are designed to inhibit the beta globin gene in
CC   thallassemics and in patients with sickle cell anaemia, to be replaced by
CC   the naturally occurring delta protein. Two classes of triplex
CC   oligonucleotides may be used, targetted against the 5' enhancer or the
CC   promoter/coding domain, in this case from base 874 to 900 (numbering is
CC   relative to the principal mRNA start site). A suitable antiparallel
CC   oligonucleotide is GL6anti. See also AAQ36219-361. (Updated on 25-MAR-
CC   2003 to correct PF field.)
XX
SQ   Sequence 28 BP; 0 A; 0 C; 6 G; 22 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 28;
  Best Local Similarity   95.0%;  Pred. No. 1.8e+03;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              ||||||||  ||||||||||
Db          9 TTTTTTTTGTTTTTTTTTT 28


RESULT 1288
AAD33514/c
ID   AAD33514 standard; DNA; 28 BP.
XX
AC   AAD33514;
XX
DT   01-JUL-2002  (first entry)
XX
DE   T7T18Apad_PS19-28-0003 probe for calibration of molecular array data.
XX
KW   Molecular array; probe; ss.
XX
OS   Unidentified.
XX
PN   EP1186673-A2.
XX
PD   13-MAR-2002.
XX
PF   10-SEP-2001; 2001EP-00307665.
XX
PR   11-SEP-2000; 2000US-00659173.
XX
PA   (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI   Wobler PK,  Delenstarr GC;
XX
DR   WPI; 2002-282886/33.
XX
PT   Calibration of molecular array data by employing calibration probes that
PT   generate signals proportional to total concentrations of labeled target
PT   molecules, and molecular arrays incorporating sets of calibration probes.
XX
PS   Disclosure; Page 14; 32pp; English.
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XX
CC   The invention relates to a method for calibrating data scanned from a
CC   molecular array. The method involves employing calibration probes that
CC   generate signals proportional to the total concentrations of labelled
CC   target molecules to which the molecular array probes are directed over an
CC   entire range of sample solutions and molecular arrays incorporating sets
CC   of calibration probes. Method is useful for calibrating different types
CC   of signals scanned from a molecular array, or calibrating signals scanned
CC   from different molecular arrays. The present sequence is poly (A)
CC   normalisation probe used in calibration of molecular array data
XX
SQ   Sequence 28 BP; 22 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 28;
  Best Local Similarity   78.6%;  Pred. No. 1.8e+03;
  Matches   22;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTT 2182
              ||||||      ||||||||||||||||
Db         28 TTTTTTGGGAGATTTTTTTTTTTTTT 1


RESULT 1289
AAD33512/c
ID   AAD33512 standard; DNA; 28 BP.
XX
AC   AAD33512;
XX
DT   01-JUL-2002  (first entry)
XX
DE   T7T18Apad_PS8-28-0001 probe for calibration of molecular array data.
XX
KW   Molecular array; probe; ss.
XX
OS   Unidentified.
XX
PN   EP1186673-A2.
XX
PD   13-MAR-2002.
XX
PF   10-SEP-2001; 2001EP-00307665.
XX
PR   11-SEP-2000; 2000US-00659173.
XX
PA   (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI   Wobler PK,  Delenstarr GC;
XX
DR   WPI; 2002-282886/33.
XX
PT   Calibration of molecular array data by employing calibration probes that
PT   generate signals proportional to total concentrations of labeled target
PT   molecules, and molecular arrays incorporating sets of calibration probes.
XX
PS   Disclosure; Page 14; 32pp; English.
XX
CC   The invention relates to a method for calibrating data scanned from a
CC   molecular array. The method involves employing calibration probes that
CC   generate signals proportional to the total concentrations of labelled
CC   target molecules to which the molecular array probes are directed over an
CC   entire range of sample solutions and molecular arrays incorporating sets
CC   of calibration probes. Method is useful for calibrating different types
CC   of signals scanned from a molecular array, or calibrating signals scanned
CC   from different molecular arrays. The present sequence is poly (A)
CC   normalisation probe used in calibration of molecular array data
XX
SQ   Sequence 28 BP; 22 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 28;
  Best Local Similarity   78.6%;  Pred. No. 1.8e+03;
  Matches   22;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTTTTTTTTTTTT 2183
              ||||      ||||||||||||||||||
Db         28 TTTTGGGAGATTTTTTTTTTTTTTTT 1


RESULT 1290
AAX06572
ID   AAX06572 standard; DNA; 19 BP.
XX
AC   AAX06572;
XX
DT   06-APR-1999  (first entry)
XX
DE   (-)-limonene-6-hydroxylase primer 3.B.
XX
KW   (-)-limonene-6-hydroxylase; (-)-limonene-3-hydroxylase; L3H; L6H;
KW   spear mint; peppermint; enzyme; limonene hydroxylase; trans-carveol;
KW   trans-isopiperitenol; pathogen defense mechanism; attractant;
KW   environmental signal; monoterpene hydroxylase; PCR primer; ss.
XX
OS   Synthetic.
OS   Mentha spicata.
XX
PN   WO9859042-A1.
XX
PD   30-DEC-1998.
XX
PF   15-JUN-1998;   98WO-US012581.
XX
PR   24-JUN-1997;   97US-00881784.
XX
PA   (UNIW ) UNIV WASHINGTON STATE RES FOUND.
XX
PI   Croteau RB,  Lupien SL,  Karp F;
XX
DR   WPI; 1999-105618/09.
XX
PT   New isolated limonene hydroxylase nucleic acids - which encode limonene-6
PT   -hydroxylase and limonene-3-hydroxylase, which can be used to produce
PT   trans-carveol and trans-isopiperitenol.
XX
PS   Example 4; Page 27; 80pp; English.
XX
CC   The invention relates to nucleotide sequences encoding spearmint (-)-
CC   limonene-6-hydroxylase (L6H) and peppermint (-)-limonene-3- hydroxylase
CC   (L3H). Host cells containing a vector comprising the nucleotide sequences
CC   can be used for the recombinant production of limonene hydroxylases or of
CC   primary enzyme products. The primary enzyme products are trans-carveol in
CC   the case of (-)-L6H or trans-isopiperitenol in the case of (-)-L3H, which
CC   are of subsequent use, to obtain enhanced expression of limonene
CC   hydroxylase in plants to attain enhanced trans- carveol or trans-
CC   isopiperitenol production as a predator or pathogen defense mechanism,
CC   attractant or environmental signal. The limonene hydroxylase cDNAs also
CC   provide a useful tool for isolating other monoterpene hydroxylase genes
CC   and for examining the developmental regulation of monoterpene
CC   biosynthesis. Sequences AAX06564-73 represent primers for the PCR
CC   amplification of (-)-limonene-6-hydroxylase cDNA
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 7.7e+02;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2184
              ||||||||||||||||||:
Db          1 TTTTTTTTTTTTTTTTTTH 19


RESULT 1291
AAX06572/c
ID   AAX06572 standard; DNA; 19 BP.
XX
AC   AAX06572;
```

```
XX
DT   06-APR-1999  (first entry)
XX
DE   (-)-limonene-6-hydroxylase primer 3.B.
XX
KW   (-)-limonene-6-hydroxylase; (-)-limonene-3-hydroxylase; L3H; L6H;
KW   spear mint; peppermint; enzyme; limonene hydroxylase; trans-carveol;
KW   trans-isopiperitenol; pathogen defense mechanism; attractant;
KW   environmental signal; monoterpene hydroxylase; PCR primer; ss.
XX
OS   Synthetic.
OS   Mentha spicata.
XX
PN   WO9859042-A1.
XX
PD   30-DEC-1998.
XX
PF   15-JUN-1998;   98WO-US012581.
XX
PR   24-JUN-1997;   97US-00881784.
XX
PA   (UNIW ) UNIV WASHINGTON STATE RES FOUND.
XX
PI   Croteau RB,  Lupien SL,  Karp F;
XX
DR   WPI; 1999-105618/09.
XX
PT   New isolated limonene hydroxylase nucleic acids - which encode limonene-6
PT   -hydroxylase and limonene-3-hydroxylase, which can be used to produce
PT   trans-carveol and trans-isopiperitenol.
XX
PS   Example 4; Page 27; 80pp; English.
XX
CC   The invention relates to nucleotide sequences encoding spearmint (-)-
CC   limonene-6-hydroxylase (L6H) and peppermint (-)-limonene-3- hydroxylase
CC   (L3H). Host cells containing a vector comprising the nucleotide sequences
CC   can be used for the recombinant production of limonene hydroxylases or of
CC   primary enzyme products. The primary enzyme products are trans-carveol in
CC   the case of (-)-L6H or trans-isopiperitenol in the case of (-)-L3H, which
CC   are of subsequent use, to obtain enhanced expression of limonene
CC   hydroxylase in plants to attain enhanced trans- carveol or trans-
CC   isopiperitenol production as a predator or pathogen defense mechanism,
CC   attractant or environmental signal. The limonene hydroxylase cDNAs also
CC   provide a useful tool for isolating other monoterpene hydroxylase genes
CC   and for examining the developmental regulation of monoterpene
CC   biosynthesis. Sequences AAX06564-73 represent primers for the PCR
CC   amplification of (-)-limonene-6-hydroxylase cDNA
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 7.7e+02;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              :||||||||||||||||||
Db         19 DAAAAAAAAAAAAAAAAAA 1


RESULT 1292
AAZ99489
ID   AAZ99489 standard; DNA; 19 BP.
XX
AC   AAZ99489;
XX
DT   03-JUL-2000  (first entry)
XX
DE   Primer HOOK for cDNA encoding a C-20 oxidase polypeptide.
XX
KW   Gibberellic acid; copalyl diphosphate synthase; 3beta-hydroxylase;
KW   2-oxidase; phytoene synthase; C-20 oxidase; 2beta,3beta-hydroxylase;
KW   seed germination; seedling growth; gibberellin biosynthetic pathway;
KW   transgenic plant; hypocotyl; epicotyl; PCR primer; ss.
XX
OS   Cucurbita maxima.
XX
PN   WO200009722-A2.
XX
PD   24-FEB-2000.
XX
PF   10-AUG-1999;   99WO-US018066.
XX
PR   10-AUG-1998;   98US-0096111P.
PR   07-JUN-1999;   99US-0137977P.
XX
PA   (MONS ) MONSANTO CO.
XX
PI   Brown SM,  Elich TD,  Heck GR,  Kishore GM,  Logusch EW,  Logusch SJ;
PI   Piller KJ,  Rao S,  Ream JE;
XX
DR   WPI; 2000-224351/19.
XX
PT   Obtaining transgenic plant useful for controlling seed germination and
PT   seedling growth comprises transgene comprising a sequence expressing
PT   altered levels of an essential hormone.
XX
PS   Example 17; Page 262; 267pp; English.
XX
CC   The present primer was used to reverse transcribe cDNA encoding a C-20
CC   oxidase. The amplifie fragment is used in the method of the invention.
CC   The specification describes methods for the inhibition and control of
CC   gibberellic acid levels. Gibberellic acid levels may be inhibited or
CC   controlled by use of a chimeric expression construct expressing a RNA or
CC   protein which suppresses the gibberellin biosynthetic pathway sequence,
CC   diverts substrate from the pathway, or degrades pathway substrates or
CC   products. The methods uses copalyl diphosphate synthase, 3beta-
CC   hydroxylase, 2-oxidase, phytoene synthase, C-20 oxidase, and a
CC   2beta,3beta-hydroxylase polynucleotides to achieve this. The method is
CC   used to control seed germination and seedling growth especially to
CC   regulate gene products of gibberellin biosynthetic pathway and
CC   restoration of normal seed germination, in transgenic plants. The plants
CC   produced are gibberellin deficient, and have shortened hypocotyl and/or
CC   epicotyl phenotypes compared to normal plants
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 7.7e+02;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||:
Db          1 TTTTTTTTTTTTTTTTTV 19


RESULT 1293
AAZ99489/c
ID   AAZ99489 standard; DNA; 19 BP.
XX
AC   AAZ99489;
XX
DT   03-JUL-2000  (first entry)
XX
DE   Primer HOOK for cDNA encoding a C-20 oxidase polypeptide.
XX
KW   Gibberellic acid; copalyl diphosphate synthase; 3beta-hydroxylase;
KW   2-oxidase; phytoene synthase; C-20 oxidase; 2beta,3beta-hydroxylase;
KW   seed germination; seedling growth; gibberellin biosynthetic pathway;
KW   transgenic plant; hypocotyl; epicotyl; PCR primer; ss.
XX
OS   Cucurbita maxima.
XX
PN   WO200009722-A2.
XX
PD   24-FEB-2000.
XX
```

```
PF   10-AUG-1999;   99WO-US018066.
XX
PR   10-AUG-1998;   98US-0096111P.
PR   07-JUN-1999;   99US-0137977P.
XX
PA   (MONS ) MONSANTO CO.
XX
PI   Brown SM,  Elich TD,  Heck GR,  Kishore GM,  Logusch EW,  Logusch SJ;
PI   Piller KJ,  Rao S,  Ream JE;
XX
DR   WPI; 2000-224351/19.
XX
PT   Obtaining transgenic plant useful for controlling seed germination and
PT   seedling growth comprises transgene comprising a sequence expressing
PT   altered levels of an essential hormone.
XX
PS   Example 17; Page 262; 267pp; English.
XX
CC   The present primer was used to reverse transcribe cDNA encoding a C-20
CC   oxidase. The amplifie fragment is used in the method of the invention.
CC   The specification describes methods for the inhibition and control of
CC   gibberellic acid levels. Gibberellic acid levels may be inhibited or
CC   controlled by use of a chimeric expression construct expressing a RNA or
CC   protein which suppresses the gibberellin biosynthetic pathway sequence,
CC   diverts substrate from the pathway, or degrades pathway substrates or
CC   products. The methods uses copalyl diphosphate synthase, 3beta-
CC   hydroxylase, 2-oxidase, phytoene synthase, C-20 oxidase, and a
CC   2beta,3beta-hydroxylase polynucleotides to achieve this. The method is
CC   used to control seed germination and seedling growth especially to
CC   regulate gene products of gibberellin biosynthetic pathway and
CC   restoration of normal seed germination, in transgenic plants. The plants
CC   produced are gibberellin deficient, and have shortened hypocotyl and/or
CC   epicotyl phenotypes compared to normal plants
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 7.7e+02;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              :||||||||||||||||||
Db         19 BAAAAAAAAAAAAAAAAAA 1


RESULT 1294
AAD15201
ID   AAD15201 standard; DNA; 19 BP.
XX
AC   AAD15201;
XX
DT   01-NOV-2001  (first entry)
XX
DE   3' sequencing primer #1 to identify and characterise polynucleotides.
XX
KW   Fatty lesion development; atherosclerosis; Alzheimer's disease;
KW   nervous system disorder; Parkinson's disease; immune system disorder;
KW   ischaemia; lymphopaenia; leukocyte adhesion deficiency syndrome;
KW   haemoglobinuria; anaemia; hyperproliferative disorder; Gaucher's disease;
KW   coagulation disorder; blood platelet disorder; autoimmune disorder;
KW   dermatitis; herpes simplex; Addison's disease; rheumatoid arthritis;
KW   Grave's disease; gene therapy; antiarteriosclerotic; immunostimulant;
KW   cardiovascular; antiviral; primer; ss.
XX
OS   Unidentified.
XX
PN   WO200154651-A2.
XX
PD   02-AUG-2001.
XX
PF   25-JAN-2001; 2001WO-US002439.
XX
PR   25-JAN-2000; 2000US-0177963P.
XX
PA   (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX
PI   Leonardi A,  Sartani A,  Glass JR,  Sutcliffe JG,  Hasel KW;
XX
DR   WPI; 2001-514526/56.
XX
PT   New polynucleotides regulated by fatty lesion development and their
PT   encoded polypeptides, useful for preventing, treating or ameliorating
PT   atherosclerosis, as well as for immune or hyperproliferative disorders.
XX
PS   Example 1; Page 79; 188pp; English.
XX
CC   The present invention relates to an isolated nucleic acid regulated by
CC   fatty lesion development, which comprises any of 55 polynucleotide
CC   sequences from Oryctolagus cuniculus. The polynucleotide, polypeptide or
CC   antibody is useful for preventing, treating, modulating or ameliorating a
CC   medical condition, particularly atherosclerosis. The invention is used as
CC   a marker or detector of nervous system disorder or disease (e.g.
CC   Parkinson's disease, Alzheimer's disease, ischaemia, dementia). The
CC   invention may also be useful for treating deficiencies or disorders of
CC   the immune system (e.g. lymphopaenia, leukocyte adhesion deficiency
CC   syndrome or haemoglobinuria, anaemia), hyperproliferative disorders
CC   (e.g.Gaucher's disease), infectious disease (e.g. herpes simplex),
CC   coagulation disorders, blood platelet disorders and autoimmune disorders
CC   (Addison's disease, rheumatoid arthritis, dermatitis, Grave's disease).
CC   The polynucleotide sequence is also used in gene therapy. The present
CC   sequence is a 3' sequencing primer used in the identification and
CC   characterisation of polynucleotides up-regulated by fatty lesion
CC   development
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 7.7e+02;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||:
Db          1 TTTTTTTTTTTTTTTTTTV 19


RESULT 1295
AAD15201/c
ID   AAD15201 standard; DNA; 19 BP.
XX
AC   AAD15201;
XX
DT   01-NOV-2001  (first entry)
XX
DE   3' sequencing primer #1 to identify and characterise polynucleotides.
XX
KW   Fatty lesion development; atherosclerosis; Alzheimer's disease;
KW   nervous system disorder; Parkinson's disease; immune system disorder;
KW   ischaemia; lymphopaenia; leukocyte adhesion deficiency syndrome;
KW   haemoglobinuria; anaemia; hyperproliferative disorder; Gaucher's disease;
KW   coagulation disorder; blood platelet disorder; autoimmune disorder;
KW   dermatitis; herpes simplex; Addison's disease; rheumatoid arthritis;
KW   Grave's disease; gene therapy; antiarteriosclerotic; immunostimulant;
KW   cardiovascular; antiviral; primer; ss.
XX
OS   Unidentified.
XX
PN   WO200154651-A2.
XX
PD   02-AUG-2001.
XX
PF   25-JAN-2001; 2001WO-US002439.
XX
PR   25-JAN-2000; 2000US-0177963P.
XX
PA   (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX
```

PI Leonardi A, Sartani A, Glass JR, Sutcliffe JG, Hasel KW;
XX
DR WPI; 2001-514526/56.
XX
PT New polynucleotides regulated by fatty lesion development and their
PT encoded polypeptides, useful for preventing, treating or ameliorating
PT atherosclerosis, as well as for immune or hyperproliferative disorders.
XX
PS Example 1; Page 79; 188pp; English.
XX
CC The present invention relates to an isolated nucleic acid regulated by
CC fatty lesion development, which comprises any of 55 polynucleotide
CC sequences from Oryctolagus cuniculus. The polynucleotide, polypeptide or
CC antibody is useful for preventing, treating, modulating or ameliorating a
CC medical condition, particularly atherosclerosis. The invention is used as
CC a marker or detector of nervous system disorder or disease (e.g.
CC Parkinson's disease, Alzheimer's disease, ischaemia, dementia). The
CC invention may also be useful for treating deficiencies or disorders of
CC the immune system (e.g. lymphopaenia, leukocyte adhesion deficiency
CC syndrome or haemoglobinuria, anaemia), hyperproliferative disorders
CC (e.g.Gaucher's disease), infectious disease (e.g. herpes simplex),
CC coagulation disorders, blood platelet disorders and autoimmune disorders
CC (Addison's disease, rheumatoid arthritis, dermatitis, Grave's disease).
CC The polynucleotide sequence is also used in gene therapy. The present
CC sequence is a 3' sequencing primer used in the identification and
CC characterisation of polynucleotides up-regulated by fatty lesion
CC development
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match 0.6%; Score 18.2; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 7.7e+02;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAAAAAAAA 2803
:||||||||||||||||||
Db 19 BAAAAAAAAAAAAAAAAA 1

RESULT 1296
AAH21968
ID AAH21968 standard; DNA; 19 BP.
XX
AC AAH21968;
XX
DT 16-AUG-2001 (first entry)
XX
DE Mouse total gene expression analysis (TOGA) 3' sequencing primer SEQ:92.
XX
KW Mouse; human; total gene expression analysis; TOGA; DST; EST;
KW digital sequence tag; expressed sequence tag; neuroleptic; antimanic;
KW central nervous system; antidepressant; gene therapy; diagnosis;
KW neuropsychiatric disorder; schizophrenia; bipolar disorder;
KW addiction-related behaviour; chromosome identification; immune response;
KW PCR primer; probe; ss.
XX
OS Mus musculus.
XX
PN WO200130972-A2.
XX
PD 03-MAY-2001.
XX
PF 26-OCT-2000; 2000WO-US029690.
XX
PR 26-OCT-1999; 99US-0161379P.
XX
PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX
PI Thomas EA, Sutcliffe JG, Pribyl TM, Hilbush B, Hasel KW;
XX
DR WPI; 2001-300499/31.
XX
PT New neuroleptic-regulated polynucleotides expressed in the central
PT nervous system for diagnosing and treating neuropsychiatric disorders
PT such as schizophrenia, bipolar disorder and addiction-related behavior.
XX
PS Example 1; Page 87; 210pp; English.
XX
CC The present invention describes isolated neuroleptic-regulated nucleic
CC acid molecules. (I) have neuroleptic, antimanic and antidepressant
CC activities, and can be used in gene therapy. (I), polypeptides (II)
CC encoded by (I), or a host cell (III) comprising (I), are useful for
CC preventing, treating, modulating or ameliorating a medical condition such
CC as a neuropsychiatric disorder. (I) are useful as diagnostic agents for
CC diagnosing a pathological condition or susceptibility to a pathological
CC condition such as neuropsychiatric disorder e.g. schizophrenia, a bipolar
CC disorder or addiction-related behaviour. (I) are useful for detecting the
CC presence of a nucleic acid encoding a protein in a mammalian tissue
CC sample. (I) can be used as probes and primers, for chromosome
CC identification, to control gene expression through triple helix formation
CC or antisense DNA or RNA, in gene therapy to treat the above mentioned
CC disorders, identifying individuals from minute biological samples, as an
CC alternative to restriction fragment length polymorphism (RFLP) and as
CC polymorphic markers for forensic purposes. (I) is also useful as
CC molecular weight markers on Southern gels, diagnostic probes for the
CC presence of specific mRNA in a particular cell type, as a probe to
CC subtract-out known sequences in the process of discovering novel
CC polynucleotides, for selecting and making oligomers for attachment to a
CC gene chip or other support, to raise anti-DNA antibodies using DNA
CC immunisation technique, and as an antigen to elicit an immune response.
CC AAH21877 to AAH21984, AAB98083 and AAB98084 represent sequences used in
CC the exemplification of the present invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match 0.6%; Score 18.2; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 7.7e+02;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2169 TTTTTTTTTTTTTTTTTA 2187
||||||||||||||||||:
Db 1 TTTTTTTTTTTTTTTTTV 19

RESULT 1297
AAH21968/c
ID AAH21968 standard; DNA; 19 BP.
XX
AC AAH21968;
XX
DT 16-AUG-2001 (first entry)
XX
DE Mouse total gene expression analysis (TOGA) 3' sequencing primer SEQ:92.
XX
KW Mouse; human; total gene expression analysis; TOGA; DST; EST;
KW digital sequence tag; expressed sequence tag; neuroleptic; antimanic;
KW central nervous system; antidepressant; gene therapy; diagnosis;
KW neuropsychiatric disorder; schizophrenia; bipolar disorder;
KW addiction-related behaviour; chromosome identification; immune response;
KW PCR primer; probe; ss.
XX
OS Mus musculus.
XX
PN WO200130972-A2.
XX
PD 03-MAY-2001.
XX
PF 26-OCT-2000; 2000WO-US029690.
XX
PR 26-OCT-1999; 99US-0161379P.
XX
PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX
PI Thomas EA, Sutcliffe JG, Pribyl TM, Hilbush B, Hasel KW;
XX
DR WPI; 2001-300499/31.

```
XX
PT   New neuroleptic-regulated polynucleotides expressed in the central
PT   nervous system for diagnosing and treating neuropsychiatric disorders
PT   such as schizophrenia, bipolar disorder and addiction-related behavior.
XX
PS   Example 1; Page 87; 210pp; English.
XX
CC   The present invention describes isolated neuroleptic-regulated nucleic
CC   acid molecules. (I) have neuroleptic, antimanic and antidepressant
CC   activities, and can be used in gene therapy. (I), polypeptides (II)
CC   encoded by (I), or a host cell (III) comprising (I), are useful for
CC   preventing, treating, modulating or ameliorating a medical condition such
CC   as a neuropsychiatric disorder. (I) are useful as diagnostic agents for
CC   diagnosing a pathological condition or susceptibility to a pathological
CC   condition such as neuropsychiatric disorder e.g. schizophrenia, a bipolar
CC   disorder or addiction-related behaviour. (I) are useful for detecting the
CC   presence of a nucleic acid encoding a protein in a mammalian tissue
CC   sample. (I) can be used as probes and primers, for chromosome
CC   identification, to control gene expression through triple helix formation
CC   or antisense DNA or RNA, in gene therapy to treat the above mentioned
CC   disorders, identifying individuals from minute biological samples, as an
CC   alternative to restriction fragment length polymorphism (RFLP) and as
CC   polymorphic markers for forensic purposes. (I) is also useful as
CC   molecular weight markers on Southern gels, diagnostic probes for the
CC   presence of specific mRNA in a particular cell type, as a probe to
CC   subtract-out known sequences in the process of discovering novel
CC   polynucleotides, for selecting and making oligomers for attachment to a
CC   gene chip or other support, to raise anti-DNA antibodies using DNA
CC   immunisation technique, and as an antigen to elicit an immune response.
CC   AAH21877 to AAH21984, AAB98083 and AAB98084 represent sequences used in
CC   the exemplification of the present invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 7.7e+02;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2803
              :||||||||||||||||||
Db         19 BAAAAAAAAAAAAAAAAA 1


RESULT 1298
AAF76617
ID   AAF76617 standard; DNA; 19 BP.
XX
AC   AAF76617;
XX
DT   15-MAY-2001  (first entry)
XX
DE   Spearmint (-)-limonene-6-hydroxylase PCR primer SEQ ID NO: 18.
XX
KW   Spearmint; peppermint; (-)-limonene-6-hydroxylase;
KW   (-)-limonene-3-hydroxylase; flavour; aroma; probe; PCR primer; ss.
XX
OS   Mentha spicata.
XX
PN   US6194185-B1.
XX
PD   27-FEB-2001.
XX
PF   14-APR-1999;   99US-00292768.
XX
PR   24-JUN-1997;   97US-00881784.
XX
PA   (UNIW ) UNIV WASHINGTON STATE RES FOUND.
XX
PI   Croteau RB,  Lupien SL,  Karp F;
XX
DR   WPI; 2001-243405/25.
XX
PT   Novel isolated limonene hydroxylase encoding nucleic acid molecule,
PT   useful for altering production of limonene-6-hydroxylase or limonene-3-
PT   hydroxylase in suitable host cell.
XX
PS   Example 4; Col 55; 57pp; English.
XX
CC   The present invention provides the protein and coding sequences of the
CC   peppermint and spearmint (-)-limonene-3-hydroxylase and the spearmint (-)
CC   -limonene-6-hydroxylase. Also provided are a number of probes and PCR
CC   primers which were used to isolate the sequences. These are useful in the
CC   production of transgenic plants with altered flavour and aroma
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 7.7e+02;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2184
              ||||||||||||||||||:
Db          1 TTTTTTTTTTTTTTTTTH 19


RESULT 1299
AAF76617/c
ID   AAF76617 standard; DNA; 19 BP.
XX
AC   AAF76617;
XX
DT   15-MAY-2001  (first entry)
XX
DE   Spearmint (-)-limonene-6-hydroxylase PCR primer SEQ ID NO: 18.
XX
KW   Spearmint; peppermint; (-)-limonene-6-hydroxylase;
KW   (-)-limonene-3-hydroxylase; flavour; aroma; probe; PCR primer; ss.
XX
OS   Mentha spicata.
XX
PN   US6194185-B1.
XX
PD   27-FEB-2001.
XX
PF   14-APR-1999;   99US-00292768.
XX
PR   24-JUN-1997;   97US-00881784.
XX
PA   (UNIW ) UNIV WASHINGTON STATE RES FOUND.
XX
PI   Croteau RB,  Lupien SL,  Karp F;
XX
DR   WPI; 2001-243405/25.
XX
PT   Novel isolated limonene hydroxylase encoding nucleic acid molecule,
PT   useful for altering production of limonene-6-hydroxylase or limonene-3-
PT   hydroxylase in suitable host cell.
XX
PS   Example 4; Col 55; 57pp; English.
XX
CC   The present invention provides the protein and coding sequences of the
CC   peppermint and spearmint (-)-limonene-3-hydroxylase and the spearmint (-)
CC   -limonene-6-hydroxylase. Also provided are a number of probes and PCR
CC   primers which were used to isolate the sequences. These are useful in the
CC   production of transgenic plants with altered flavour and aroma
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 7.7e+02;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2803
              :||||||||||||||||||
Db         19 DAAAAAAAAAAAAAAAAA 1
```

```
RESULT 1300
AAS06525
ID   AAS06525 standard; DNA; 19 BP.
XX
AC   AAS06525;
XX
DT   07-SEP-2001  (first entry)
XX
DE   Mouse microglia and macrophage regulatory gene primer #60.
XX
KW   Mouse; microglia; macrophage; regulatory gene; digital sequence tag; DST;
KW   PCR-based total gene expression analysis; TOGA; infectious disorder;
KW   neuroinflammatory pathology; neurodegenerative disease; gene therapy;
KW   hyperproliferative disorder; autoimmune; inflammatory disorder; primer;
KW   ss.
XX
OS   Mus musculus.
XX
PN   WO200134770-A2.
XX
PD   17-MAY-2001.
XX
PF   06-NOV-2000; 2000WO-US030585.
XX
PR   12-NOV-1999;   99WO-US026824.
PR   03-MAR-2000; 2000US-0186770P.
PR   19-JUN-2000; 2000US-0212465P.
XX
PA   (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX
PI   Carson MJ,  Sutcliffe JG,  Almazan MT,  Tobal GM;
XX
DR   WPI; 2001-308782/32.
XX
PT   New regulated genes of microglia and macrophages, useful for diagnosing,
PT   preventing or treating neuroinflammatory pathology and neurodegenerative
PT   disease.
XX
PS   Example 1; Page 88; 244pp; English.
XX
CC   The present sequence represents a primer used to isolate novel mouse
CC   microglia and macrophage regulatory gene DST (digital sequence tag)
CC   sequences. AAS06401-AAS06590 represent these novel sequences and the
CC   primer sequences used to isolate them. The PCR-based total gene
CC   expression analysis (TOGA) system is used to examine the expression
CC   pattern of molecules corresponding to genes that are regulated in
CC   unstimulated microglia, activated microglia, unstimulated macrophage and
CC   activated macrophage. The polynucleotides of the invention, the
CC   polypeptides encoded by them and antibodies that bind to these
CC   polypeptides are useful for the diagnosis, prevention,
CC   treatment or amelioration of a medical condition, preferably a
CC   neuroinflammatory pathology or a neurodegenerative disease such as
CC   Alzheimer's disease, senile dementia, Parkinson's disease, obsessive
CC   compulsive disorders, epilepsy, schizophrenia, multiple sclerosis,
CC   depression and bipolar manic-depressive disorder. The sequences and
CC   methods of the invention can also be used for detecting or treating
CC   infectious disorders (e.g. AIDS), hyperproliferative disorders (e.g.
CC   cancer), immune disorders (e.g. severe combined immunodeficiency, SCID)
CC   autoimmune diseases (e.g. insulin dependent diabetes mellitus),
CC   inflammatory disorders (e.g. arthritis). The polynucleotides can be used
CC   for gene therapy
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 7.7e+02;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||:
Db          1 TTTTTTTTTTTTTTTTTV 19
```

```
RESULT 1301
AAS06525/c
ID   AAS06525 standard; DNA; 19 BP.
XX
AC   AAS06525;
XX
DT   07-SEP-2001  (first entry)
XX
DE   Mouse microglia and macrophage regulatory gene primer #60.
XX
KW   Mouse; microglia; macrophage; regulatory gene; digital sequence tag; DST;
KW   PCR-based total gene expression analysis; TOGA; infectious disorder;
KW   neuroinflammatory pathology; neurodegenerative disease; gene therapy;
KW   hyperproliferative disorder; autoimmune; inflammatory disorder; primer;
KW   ss.
XX
OS   Mus musculus.
XX
PN   WO200134770-A2.
XX
PD   17-MAY-2001.
XX
PF   06-NOV-2000; 2000WO-US030585.
XX
PR   12-NOV-1999;   99WO-US026824.
PR   03-MAR-2000; 2000US-0186770P.
PR   19-JUN-2000; 2000US-0212465P.
XX
PA   (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX
PI   Carson MJ,  Sutcliffe JG,  Almazan MT,  Tobal GM;
XX
DR   WPI; 2001-308782/32.
XX
PT   New regulated genes of microglia and macrophages, useful for diagnosing,
PT   preventing or treating neuroinflammatory pathology and neurodegenerative
PT   disease.
XX
PS   Example 1; Page 88; 244pp; English.
XX
CC   The present sequence represents a primer used to isolate novel mouse
CC   microglia and macrophage regulatory gene DST (digital sequence tag)
CC   sequences. AAS06401-AAS06590 represent these novel sequences and the
CC   primer sequences used to isolate them. The PCR-based total gene
CC   expression analysis (TOGA) system is used to examine the expression
CC   pattern of molecules corresponding to genes that are regulated in
CC   unstimulated microglia, activated microglia, unstimulated macrophage and
CC   activated macrophage. The polynucleotides of the invention, the
CC   polypeptides encoded by them and antibodies that bind to these
CC   polypeptides are useful are useful for the diagnosis, prevention,
CC   treatment or amelioration of a medical condition, preferably a
CC   neuroinflammatory pathology or a neurodegenerative disease such as
CC   Alzheimer's disease, senile dementia, Parkinson's disease, obsessive
CC   compulsive disorders, epilepsy, schizophrenia, multiple sclerosis,
CC   depression and bipolar manic-depressive disorder. The sequences and
CC   methods of the invention can also be used for detecting or treating
CC   infectious disorders (e.g. AIDS), hyperproliferative disorders (e.g.
CC   cancer), immune disorders (e.g. severe combined immunodeficiency, SCID)
CC   autoimmune diseases (e.g. insulin dependent diabetes mellitus),
CC   inflammatory disorders (e.g. arthritis). The polynucleotides can be used
CC   for gene therapy
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 7.7e+02;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2803
              :||||||||||||||||||
Db         19 BAAAAAAAAAAAAAAAAA 1
```

```
RESULT 1302
ABK71509
ID   ABK71509 standard; DNA; 19 BP.
XX
AC   ABK71509;
XX
DT   30-JUL-2002  (first entry)
XX
DE   CNS related 3' sequencing primer.
XX
KW   Central nervous system; CNS; neuroleptic; mouse; human; psychoses;
KW   neuropsychiatric disorder; psychiatric disorder; Alzheimer's disease;
KW   Pick's disease; Binswanger's disease; senile dementia; encephalopathy;
KW   Parkinson's disease; obsessive compulsive disorder; epilepsy; ischaemia;
KW   addiction; multiple sclerosis; depression; manic-depressive disorder;
KW   primer; ss.
XX
OS   Synthetic.
XX
PN   WO200226936-A2.
XX
PD   04-APR-2002.
XX
PF   01-OCT-2001; 2001WO-US030695.
XX
PR   29-SEP-2000; 2000US-0236790P.
PR   18-JAN-2001; 2001US-0263084P.
XX
PA   (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX
PI   Thomas EA,  Sutcliffe JG,  Pribyl TM,  Hilbush BS,  Hasel KW;
XX
DR   WPI; 2002-383271/41.
XX
PT   New polynucleotide useful in gene therapy for preventing, treating
PT   modulating or ameliorating a medical condition such as psychoses or a
PT   neuro psychiatric disorder e.g. schizophrenia, or a bipolar disorder in a
PT   mammal.
XX
PS   Example 1; Page 40; 254pp; English.
XX
CC   This invention relates to the cDNA sequences of novel isolated
CC   polynucleotides associated with psychoses or other neuropsychiatric
CC   disorders. The sequences of the invention may act as blockers of D_2
CC   receptors in the meso-limbic dopamine system. The nucleotide sequences of
CC   the invention and the polypeptides encoded by them are useful in the
CC   manufacture of a medicament useful for preventing, treating, modulating
CC   or ameliorating a medical condition e.g. a neuropsychiatric disorder. An
CC   antibody that binds the proteins of the invention is useful for
CC   preventing, treating, modulating or ameliorating neurological disorders
CC   such as psychoses or other neuropsychiatric disorders in a subject. The
CC   sequences are also useful for diagnosing neurological disorders or a
CC   susceptibility to a neurological disorder such as psychoses and other
CC   neuro psychiatric disorders in a subject by determining the presence or
CC   absence of mutation in the nucleotide sequence of apolipoprotein D or by
CC   determining the alteration (increase or decrease) in the expression of
CC   apolipoprotein D. The sequences of the invention are useful in treating
CC   deficiencies or disorders of the central nervous system or peripheral
CC   nervous system by activating or inhibiting the proliferation,
CC   differentiation or mobilisation (chemotaxis) of neuroblasts, stem cells
CC   or glial cells. The sequences are useful as a marker or detector of a
CC   particular nervous system disease or disorder such as Alzheimer's
CC   disease, Pick's disease, Binswanger's disease, other senile dementia,
CC   Parkinson's disease, obsessive compulsive disorders, epilepsy,
CC   encephalopathy, ischaemia, addiction, multiple sclerosis, depression and
CC   manic-depressive disorder. The present sequence represents an
CC   oligonucleotide primer used in the identification of the cDNA sequences
CC   of the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

  Query Match           0.6%;  Score 18.2;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 7.7e+02;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||:
Db          1 TTTTTTTTTTTTTTTTTTV 19


RESULT 1303
ABK71509/c
ID   ABK71509 standard; DNA; 19 BP.
XX
AC   ABK71509;
XX
DT   30-JUL-2002  (first entry)
XX
DE   CNS related 3' sequencing primer.
XX
KW   Central nervous system; CNS; neuroleptic; mouse; human; psychoses;
KW   neuropsychiatric disorder; psychiatric disorder; Alzheimer's disease;
KW   Pick's disease; Binswanger's disease; senile dementia; encephalopathy;
KW   Parkinson's disease; obsessive compulsive disorder; epilepsy; ischaemia;
KW   addiction; multiple sclerosis; depression; manic-depressive disorder;
KW   primer; ss.
XX
OS   Synthetic.
XX
PN   WO200226936-A2.
XX
PD   04-APR-2002.
XX
PF   01-OCT-2001; 2001WO-US030695.
XX
PR   29-SEP-2000; 2000US-0236790P.
PR   18-JAN-2001; 2001US-0263084P.
XX
PA   (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX
PI   Thomas EA,  Sutcliffe JG,  Pribyl TM,  Hilbush BS,  Hasel KW;
XX
DR   WPI; 2002-383271/41.
XX
PT   New polynucleotide useful in gene therapy for preventing, treating
PT   modulating or ameliorating a medical condition such as psychoses or a
PT   neuro psychiatric disorder e.g. schizophrenia, or a bipolar disorder in a
PT   mammal.
XX
PS   Example 1; Page 40; 254pp; English.
XX
CC   This invention relates to the cDNA sequences of novel isolated
CC   polynucleotides associated with psychoses or other neuropsychiatric
CC   disorders. The sequences of the invention may act as blockers of D_2
CC   receptors in the meso-limbic dopamine system. The nucleotide sequences of
CC   the invention and the polypeptides encoded by them are useful in the
CC   manufacture of a medicament useful for preventing, treating, modulating
CC   or ameliorating a medical condition e.g. a neuropsychiatric disorder. An
CC   antibody that binds the proteins of the invention is useful for
CC   preventing, treating, modulating or ameliorating neurological disorders
CC   such as psychoses or other neuropsychiatric disorders in a subject. The
CC   sequences are also useful for diagnosing neurological disorders or a
CC   susceptibility to a neurological disorder such as psychoses and other
CC   neuro psychiatric disorders in a subject by determining the presence or
CC   absence of mutation in the nucleotide sequence of apolipoprotein D or by
CC   determining the alteration (increase or decrease) in the expression of
CC   apolipoprotein D. The sequences of the invention are useful in treating
CC   deficiencies or disorders of the central nervous system or peripheral
CC   nervous system by activating or inhibiting the proliferation,
CC   differentiation or mobilisation (chemotaxis) of neuroblasts, stem cells
CC   or glial cells. The sequences are useful as a marker or detector of a
CC   particular nervous system disease or disorder such as Alzheimer's
CC   disease, Pick's disease, Binswanger's disease, other senile dementia,
CC   Parkinson's disease, obsessive compulsive disorders, epilepsy,
CC   encephalopathy, ischaemia, addiction, multiple sclerosis, depression and
```

```
CC   manic-depressive disorder. The present sequence represents an
CC   oligonucleotide primer used in the identification of the cDNA sequences
CC   of the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 7.7e+02;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2803
              :||||||||||||||||||
Db         19 BAAAAAAAAAAAAAAAAA 1


RESULT 1304
ABQ73231
ID   ABQ73231 standard; DNA; 19 BP.
XX
AC   ABQ73231;
XX
DT   27-SEP-2002  (first entry)
XX
DE   Rabbit atherosclerosis related TOGA primer SEQ ID NO:26.
XX
KW   Rabbit; Oryctolagus cuniculus; atherosclerosis; intimal hyperplasia;
KW   TOGA primer; ss.
XX
OS   Oryctolagus cuniculus.
OS   Synthetic.
XX
PN   WO200242420-A2.
XX
PD   30-MAY-2002.
XX
PF   21-NOV-2001; 2001WO-US044072.
XX
PR   21-NOV-2000; 2000US-0252216P.
XX
PA   (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX
PI   Leonardi A,  Sartani A,  Glass JR,  Hasel KW;
XX
DR   WPI; 2002-575233/61.
XX
PT   New polynucleotides related to regulated genes characteristic of
PT   atherosclerosis, useful for diagnosing, preventing, treating, modulating
PT   or ameliorating atherosclerosis in a mammalian subject.
XX
PS   Disclosure; Page 28; 130pp; English.
XX
CC   The present invention describes an isolated polynucleotide (I) and its
CC   complements, and degenerate variants, comprising a sequence selected from
CC   those given in ABQ73206 to ABQ73222 (NS), which is a digital sequence tag
CC   (DST) corresponding to mRNAs whose expression is regulated by
CC   proliferative lesion development caused by mechanically induced intimal
CC   hyperplasia, or by lercanidipine treatment, or by proliferative lesions
CC   and reversed by lercanidipine treatment. (I) has antiatherosclerotic
CC   activity and can be used in gene therapy. (I) can be used for diagnosing
CC   a medical condition (e.g. atherosclerosis) in a subject which involves
CC   determining the presence or absence of a mutation in (I) and diagnosing
CC   the medical condition based on the presence or absence of the mutation.
CC   (I) is also useful for diagnosing atherosclerosis, or the susceptibility
CC   to atherosclerosis in a subject which involves detecting an alteration
CC   (an increase or decrease) in amount of expression of (I). (I) is also
CC   useful for diagnosing or monitoring the effects of treating a subject
CC   with dihydropyridine calcium antagonist e.g., lercanidipine. (I) can also
CC   be used for preventing, treating, modulating, or ameliorating a medical
CC   condition such as atherosclerosis in a mammalian subject. The present
CC   sequence represents a TOGA primer which is used in the exemplification of
CC   the present invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 7.7e+02;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||:
Db          1 TTTTTTTTTTTTTTTTTV 19


RESULT 1305
ABQ73231/c
ID   ABQ73231 standard; DNA; 19 BP.
XX
AC   ABQ73231;
XX
DT   27-SEP-2002  (first entry)
XX
DE   Rabbit atherosclerosis related TOGA primer SEQ ID NO:26.
XX
KW   Rabbit; Oryctolagus cuniculus; atherosclerosis; intimal hyperplasia;
KW   TOGA primer; ss.
XX
OS   Oryctolagus cuniculus.
OS   Synthetic.
XX
PN   WO200242420-A2.
XX
PD   30-MAY-2002.
XX
PF   21-NOV-2001; 2001WO-US044072.
XX
PR   21-NOV-2000; 2000US-0252216P.
XX
PA   (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX
PI   Leonardi A,  Sartani A,  Glass JR,  Hasel KW;
XX
DR   WPI; 2002-575233/61.
XX
PT   New polynucleotides related to regulated genes characteristic of
PT   atherosclerosis, useful for diagnosing, preventing, treating, modulating
PT   or ameliorating atherosclerosis in a mammalian subject.
XX
PS   Disclosure; Page 28; 130pp; English.
XX
CC   The present invention describes an isolated polynucleotide (I) and its
CC   complements, and degenerate variants, comprising a sequence selected from
CC   those given in ABQ73206 to ABQ73222 (NS), which is a digital sequence tag
CC   (DST) corresponding to mRNAs whose expression is regulated by
CC   proliferative lesion development caused by mechanically induced intimal
CC   hyperplasia, or by lercanidipine treatment, or by proliferative lesions
CC   and reversed by lercanidipine treatment. (I) has antiatherosclerotic
CC   activity and can be used in gene therapy. (I) can be used for diagnosing
CC   a medical condition (e.g. atherosclerosis) in a subject which involves
CC   determining the presence or absence of a mutation in (I) and diagnosing
CC   the medical condition based on the presence or absence of the mutation.
CC   (I) is also useful for diagnosing atherosclerosis, or the susceptibility
CC   to atherosclerosis in a subject which involves detecting an alteration
CC   (an increase or decrease) in amount of expression of (I). (I) is also
CC   useful for diagnosing or monitoring the effects of treating a subject
CC   with dihydropyridine calcium antagonist e.g., lercanidipine. (I) can also
CC   be used for preventing, treating, modulating, or ameliorating a medical
CC   condition such as atherosclerosis in a mammalian subject. The present
CC   sequence represents a TOGA primer which is used in the exemplification of
CC   the present invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 7.7e+02;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;
```

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Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              :||||||||||||||||||
Db         19 BAAAAAAAAAAAAAAAAAA 1


RESULT 1306
AAD34663
ID   AAD34663 standard; DNA; 19 BP.
XX
AC   AAD34663;
XX
DT   16-JUL-2002  (first entry)
XX
DE   PCR primer #4 used for direct sequencing of TOGA generated PCR products.
XX
KW   Hepatitis B virus; HBV infection; chronic hepatitis; toxicity; virucide;
KW   acute hepatitis; therapeutic; gene therapy; vaccine; infectious disease;
KW   TOGA; TOtal Gene expression Analysis; PCR; primer; ss.
XX
OS   Unidentified.
XX
PN   WO200222783-A2.
XX
PD   21-MAR-2002.
XX
PF   17-SEP-2001; 2001WO-US029123.
XX
PR   15-SEP-2000; 2000US-0233176P.
XX
PA   (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX
PI   Chisari FV,  Wieland SF,  Guidotti LGDVM,  Mueller R,  Hilbush BS;
XX
DR   WPI; 2002-339865/37.
XX
PT   Preventing and treating hepatitis viral infection in a mammal, comprises
PT   administering nucleic acid molecules that up- or down-regulate in
PT   hepatitis B virus infection or polypeptides encoded by the nucleic acid
PT   molecules.
XX
PS   Disclosure; Page 28; 125pp; English.
XX
CC   The present invention relates to a method for preventing, treating,
CC   modulating or ameliorating a medical condition. The method involves
CC   administering one or more nucleic acid molecules up- or down-regulated in
CC   hepatitis B virus (HBV) infection or polypeptides encoded by the nucleic
CC   acid molecules or antibodies that bind to the polypeptide. The method is
CC   useful for preventing, treating, modulating or ameliorating a medical
CC   condition. It is also useful for determining the presence or absence of a
CC   mutation in the nucleic acid molecules or detecting an alteration in
CC   expression of the polypeptide which is useful for the diagnosis of
CC   hepatitis viral infection. The method is useful for assessing the stage
CC   of hepatitis viral infection (e.g., acute hepatitis versus chronic
CC   hepatitis) or assessing the efficacy or toxicity of therapeutic treatment
CC   for hepatitis viral infection and a gene expression profile is useful for
CC   identifying polypeptides and polynucleotides which are associated with
CC   hepatitis viral infection. Sequences of the invention are used in gene
CC   therapy and as vaccines. Nucleic acid sequences are useful as a
CC   diagnostic markers for HBV infection and for treating infectious
CC   diseases. The present DNA sequence is a PCR primer which is used for
CC   direct sequencing of TOGA (TOtal Gene expression Analysis) generated PCR
CC   products
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 7.7e+02;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||:
Db          1 TTTTTTTTTTTTTTTTTV 19


RESULT 1307
AAD34663/c
ID   AAD34663 standard; DNA; 19 BP.
XX
AC   AAD34663;
XX
DT   16-JUL-2002  (first entry)
XX
DE   PCR primer #4 used for direct sequencing of TOGA generated PCR products.
XX
KW   Hepatitis B virus; HBV infection; chronic hepatitis; toxicity; virucide;
KW   acute hepatitis; therapeutic; gene therapy; vaccine; infectious disease;
KW   TOGA; TOtal Gene expression Analysis; PCR; primer; ss.
XX
OS   Unidentified.
XX
PN   WO200222783-A2.
XX
PD   21-MAR-2002.
XX
PF   17-SEP-2001; 2001WO-US029123.
XX
PR   15-SEP-2000; 2000US-0233176P.
XX
PA   (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX
PI   Chisari FV,  Wieland SF,  Guidotti LGDVM,  Mueller R,  Hilbush BS;
XX
DR   WPI; 2002-339865/37.
XX
PT   Preventing and treating hepatitis viral infection in a mammal, comprises
PT   administering nucleic acid molecules that up- or down-regulate in
PT   hepatitis B virus infection or polypeptides encoded by the nucleic acid
PT   molecules.
XX
PS   Disclosure; Page 28; 125pp; English.
XX
CC   The present invention relates to a method for preventing, treating,
CC   modulating or ameliorating a medical condition. The method involves
CC   administering one or more nucleic acid molecules up- or down-regulated in
CC   hepatitis B virus (HBV) infection or polypeptides encoded by the nucleic
CC   acid molecules or antibodies that bind to the polypeptide. The method is
CC   useful for preventing, treating, modulating or ameliorating a medical
CC   condition. It is also useful for determining the presence or absence of a
CC   mutation in the nucleic acid molecules or detecting an alteration in
CC   expression of the polypeptide which is useful for the diagnosis of
CC   hepatitis viral infection. The method is useful for assessing the stage
CC   of hepatitis viral infection (e.g., acute hepatitis versus chronic
CC   hepatitis) or assessing the efficacy or toxicity of therapeutic treatment
CC   for hepatitis viral infection and a gene expression profile is useful for
CC   identifying polypeptides and polynucleotides which are associated with
CC   hepatitis viral infection. Sequences of the invention are used in gene
CC   therapy and as vaccines. Nucleic acid sequences are useful as a
CC   diagnostic markers for HBV infection and for treating infectious
CC   diseases. The present DNA sequence is a PCR primer which is used for
CC   direct sequencing of TOGA (TOtal Gene expression Analysis) generated PCR
CC   products
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 7.7e+02;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              :||||||||||||||||||
Db         19 BAAAAAAAAAAAAAAAAAA 1


RESULT 1308
AAD40279
ID   AAD40279 standard; DNA; 19 BP.
```

```
XX
AC   AAD40279;
XX
DT   22-OCT-2002  (first entry)
XX
DE   HOOK PCR primer used to isolate pumpkin 2beta-3beta hydroxylase cDNA.
XX
KW   Gibberellin; transgenic plant; seed germination; seedling growth; GA;
KW   transgenic; 2beta-3beta hydroxylase; enzyme; pumpkin; PCR; primer; ss.
XX
OS   Cucurbita pepo.
XX
PN   US2002053095-A1.
XX
PD   02-MAY-2002.
XX
PF   10-AUG-1999;   99US-00371307.
XX
PR   10-AUG-1999;   99US-00371307.
XX
PA   (BROW/) BROWN S M.
XX
PI   Brown SM,  Elich TD,  Heck GR,  Kishore GM,  Logusch EW,  Logusch SJ;
PI   Piller KJ,  Rao S,  Ream JE;
XX
DR   WPI; 2002-489107/52.
XX
PT   Control of gibberellin levels in plants useful to avoid unfavorable
PT   conditions in crops to increase yields, using transgenic plants having
PT   reduced seed germination and early seedling growth then treatment to
PT   restore these properties.
XX
PS   Example 19; Page 104; 155pp; English.
XX
CC   The invention relates to control of gibberellin (GA) levels in plants.
CC   The method involves producing transgenic plants having a phenotype of
CC   reduced seed germination and reduced early seedling growth, then
CC   restoring seed germination and early seedling growth by treating plants
CC   with an appropriate compound when conditions are favourable. The method
CC   is useful to control seed germination and/or early seedling growth in
CC   agricultural production so that unfavorable environmental conditions
CC   normally reducing agronomic output can be avoided and yields increased.
CC   Plants also demonstrate increased uniformity of germination, emergence
CC   and seedling vigor, so increasing yields at harvest. The method is
CC   especially useful in crop plants such as e.g. canola, soybean, cotton,
CC   etc., and is also useful in storage and transport of seeds to reduce
CC   premature germination which may affect agronomic or food quality of the
CC   seeds. The present sequence is a PCR primer used to isolate pumpkin 2beta
CC   -3beta hydroxylase cDNA. This primer is used in the exemplification of
CC   the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 7.7e+02;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||:
Db          1 TTTTTTTTTTTTTTTTTV 19


RESULT 1309
AAD40279/c
ID   AAD40279 standard; DNA; 19 BP.
XX
AC   AAD40279;
XX
DT   22-OCT-2002  (first entry)
XX
DE   HOOK PCR primer used to isolate pumpkin 2beta-3beta hydroxylase cDNA.
XX
KW   Gibberellin; transgenic plant; seed germination; seedling growth; GA;
KW   transgenic; 2beta-3beta hydroxylase; enzyme; pumpkin; PCR; primer; ss.
XX
OS   Cucurbita pepo.
XX
PN   US2002053095-A1.
XX
PD   02-MAY-2002.
XX
PF   10-AUG-1999;   99US-00371307.
XX
PR   10-AUG-1999;   99US-00371307.
XX
PA   (BROW/) BROWN S M.
XX
PI   Brown SM,  Elich TD,  Heck GR,  Kishore GM,  Logusch EW,  Logusch SJ;
PI   Piller KJ,  Rao S,  Ream JE;
XX
DR   WPI; 2002-489107/52.
XX
PT   Control of gibberellin levels in plants useful to avoid unfavorable
PT   conditions in crops to increase yields, using transgenic plants having
PT   reduced seed germination and early seedling growth then treatment to
PT   restore these properties.
XX
PS   Example 19; Page 104; 155pp; English.
XX
CC   The invention relates to control of gibberellin (GA) levels in plants.
CC   The method involves producing transgenic plants having a phenotype of
CC   reduced seed germination and reduced early seedling growth, then
CC   restoring seed germination and early seedling growth by treating plants
CC   with an appropriate compound when conditions are favourable. The method
CC   is useful to control seed germination and/or early seedling growth in
CC   agricultural production so that unfavorable environmental conditions
CC   normally reducing agronomic output can be avoided and yields increased.
CC   Plants also demonstrate increased uniformity of germination, emergence
CC   and seedling vigor, so increasing yields at harvest. The method is
CC   especially useful in crop plants such as e.g. canola, soybean, cotton,
CC   etc., and is also useful in storage and transport of seeds to reduce
CC   premature germination which may affect agronomic or food quality of the
CC   seeds. The present sequence is a PCR primer used to isolate pumpkin 2beta
CC   -3beta hydroxylase cDNA. This primer is used in the exemplification of
CC   the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 7.7e+02;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2803
              :||||||||||||||||||
Db         19 BAAAAAAAAAAAAAAAAAA 1


RESULT 1310
ABZ68389
ID   ABZ68389 standard; DNA; 19 BP.
XX
AC   ABZ68389;
XX
DT   22-APR-2003  (first entry)
XX
DE   Reverse transcription primer used to produce yeast cDNA.
XX
KW   Histone acetyltransferase; histone deacetylase; gene expression profile;
KW   chromatin-associated protein; gene expression; primer; ss.
XX
OS   Synthetic.
XX
PN   WO2003000715-A1.
XX
PD   03-JAN-2003.
XX
```

PF 21-JUN-2002; 2002WO-US019750.
XX
PR 22-JUN-2001; 2001US-0300135P.
XX
PA (CERE-) CERES INC.
XX
PI Dang V, Okamuro J;
XX
DR WPI; 2003-175280/17.
XX
PT New chimeric polypeptide comprising a histone acetyltransferase
PT polypeptide segment and a segment comprising a histone deacetylase
PT chromatin-associated protein complex subunit, useful for modulating gene
PT expression in cells.
XX
PS Example 10; Page 54; 85pp; English.
XX
CC The specification describes chimeric histone acetyltransferase
CC polypeptides. The chimeric polypeptides comprise a polypeptide segment
CC that exhibits histone acetyltransferase activity, and a polypeptide
CC segment having 40% or greater sequence identity to a subunit of a histone
CC deacetylase chromatin-associated protein complex. The chimeric
CC polypeptides are useful for determining gene expression profiles in
CC specific cells, for modulating gene expression in specific cells, and for
CC making genetically modified eukaryotes. The present sequence represents a
CC reverse transcription primer used in the method of the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match 0.6%; Score 18.2; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 7.7e+02;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2169 TTTTTTTTTTTTTTTTTA 2187
:||||||||||||||||||
Db 1 TTTTTTTTTTTTTTTTTV 19

RESULT 1311
ABZ68389/c
ID ABZ68389 standard; DNA; 19 BP.
XX
AC ABZ68389;
XX
DT 22-APR-2003 (first entry)
XX
DE Reverse transcription primer used to produce yeast cDNA.
XX
KW Histone acetyltransferase; histone deacetylase; gene expression profile;
KW chromatin-associated protein; gene expression; primer; ss.
XX
OS Synthetic.
XX
PN WO2003000715-A1.
XX
PD 03-JAN-2003.
XX
PF 21-JUN-2002; 2002WO-US019750.
XX
PR 22-JUN-2001; 2001US-0300135P.
XX
PA (CERE-) CERES INC.
XX
PI Dang V, Okamuro J;
XX
DR WPI; 2003-175280/17.
XX
PT New chimeric polypeptide comprising a histone acetyltransferase
PT polypeptide segment and a segment comprising a histone deacetylase
PT chromatin-associated protein complex subunit, useful for modulating gene
PT expression in cells.
XX
PS Example 10; Page 54; 85pp; English.
XX
CC The specification describes chimeric histone acetyltransferase
CC polypeptides. The chimeric polypeptides comprise a polypeptide segment
CC that exhibits histone acetyltransferase activity, and a polypeptide
CC segment having 40% or greater sequence identity to a subunit of a histone
CC deacetylase chromatin-associated protein complex. The chimeric
CC polypeptides are useful for determining gene expression profiles in
CC specific cells, for modulating gene expression in specific cells, and for
CC making genetically modified eukaryotes. The present sequence represents a
CC reverse transcription primer used in the method of the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match 0.6%; Score 18.2; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 7.7e+02;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAAAAAAAA 2803
:||||||||||||||||||
Db 19 BAAAAAAAAAAAAAAAAA 1

RESULT 1312
ACC79402
ID ACC79402 standard; DNA; 19 BP.
XX
AC ACC79402;
XX
DT 04-AUG-2003 (first entry)
XX
DE M13 sequencing primer 3' primer SEQ ID NO:84.
XX
KW Pathological condition; ataxia telangiectasia; AT; tumour; cancer;
KW cytostatic; vaccine; gene therapy; PCR primer; ss.
XX
OS Enterobacteria phage M13.
OS Synthetic.
XX
PN WO2003033668-A2.
XX
PD 24-APR-2003.
XX
PF 17-OCT-2002; 2002WO-US033311.
XX
PR 17-OCT-2001; 2001US-0330206P.
XX
PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX
PI Barlow C, Winrow CJ, Callahan MLA, Pankratz DG, Vibat CRT;
PI Warren AJ;
XX
DR WPI; 2003-393520/37.
XX
PT Preventing or treating a pathological condition e.g., ataxia
PT telangiectasia (AT), AT tumors or other cancers comprises administering
PT polynucleotides.
XX
PS Example 1; Page 76; 184pp; English.
XX
CC The present invention describes a method for preventing or treating a
CC pathological condition (comprising ataxia telangiectasia (AT), AT tumours
CC or other cancers), which comprises administering to a mammalian subject
CC at least one of: (a) a first polynucleotide comprising a sequence having
CC 38-889 bp (consisting of the sequences in ACC79319 to ACC79392 (I)) or a
CC second polynucleotide at least 95% identical to the first polynucleotide;
CC (b) a third polynucleotide comprising at least 10-bp sequence that is
CC hybridisable to the first polynucleotide under stringent conditions; or
CC (c) a gene corresponding to any of (1)-(2) or another gene at least 95%
CC identical to the gene. (I) have cytostatic activities, and can be used in
CC vaccines and in gene therapy. The method is useful for preventing or
CC treating e.g., ataxia telangiectasia (AT), AT tumours or other cancers.
CC ACC79393 to ACC79423 represent primers used in the exemplification of the
CC present invention

```
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 7.7e+02;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||:
Db          1 TTTTTTTTTTTTTTTTTV 19


RESULT 1313
ACC79402/c
ID   ACC79402 standard; DNA; 19 BP.
XX
AC   ACC79402;
XX
DT   04-AUG-2003  (first entry)
XX
DE   M13 sequencing primer 3' primer SEQ ID NO:84.
XX
KW   Pathological condition; ataxia telangiectasia; AT; tumour; cancer;
KW   cytostatic; vaccine; gene therapy; PCR primer; ss.
XX
OS   Enterobacteria phage M13.
OS   Synthetic.
XX
PN   WO2003033668-A2.
XX
PD   24-APR-2003.
XX
PF   17-OCT-2002; 2002WO-US033311.
XX
PR   17-OCT-2001; 2001US-0330206P.
XX
PA   (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX
PI   Barlow C,  Winrow CJ,  Callahan MLA,  Pankratz DG,  Vibat CRT;
PI   Warren AJ;
XX
DR   WPI; 2003-393520/37.
XX
PT   Preventing or treating a pathological condition e.g., ataxia
PT   telangiectasia (AT), AT tumors or other cancers comprises administering
PT   polynucleotides.
XX
PS   Example 1; Page 76; 184pp; English.
XX
CC   The present invention describes a method for preventing or treating a
CC   pathological condition (comprising ataxia telangiectasia (AT), AT tumours
CC   or other cancers), which comprises administering to a mammalian subject
CC   at least one of: (a) a first polynucleotide comprising a sequence having
CC   38-889 bp (consisting of the sequences in ACC79319 to ACC79392 (I)) or a
CC   second polynucleotide at least 95% identical to the first polynucleotide;
CC   (b) a third polynucleotide comprising at least 10-bp sequence that is
CC   hybridisable to the first polynucleotide under stringent conditions; or
CC   (c) a gene corresponding to any of (1)-(2) or another gene at least 95%
CC   identical to the gene. (I) have cytostatic activities, and can be used in
CC   vaccines and in gene therapy. The method is useful for preventing or
CC   treating e.g., ataxia telangiectasia (AT), AT tumours or other cancers.
CC   ACC79393 to ACC79423 represent primers used in the exemplification of the
CC   present invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 7.7e+02;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2803
              :||||||||||||||||||
Db         19 BAAAAAAAAAAAAAAAAA 1


RESULT 1314
AAD49149
ID   AAD49149 standard; DNA; 19 BP.
XX
AC   AAD49149;
XX
DT   07-MAR-2003  (first entry)
XX
DE   3' sequencing primer #1 used in the invention.
XX
KW   Atherosclerosis; vaccine; nervous system disorder; Alzheimer's disease;
KW   Parkinson's disease; multiple sclerosis; immune disorder; gene therapy;
KW   autoimmune disorder; rheumatoid arthritis; hyperproliferative disorder;
KW   haemolytic anaemia; graft-versus-host disease; inflammation; infection;
KW   epilepsy; Addison's disease; neoplasm; tissue regeneration; chemotaxis;
KW   food additive; food preservative; primer; ss.
XX
OS   Unidentified.
XX
PN   WO200281726-A2.
XX
PD   17-OCT-2002.
XX
PF   15-NOV-2001; 2001WO-US043741.
XX
PR   15-NOV-2000; 2000US-0248892P.
PR   28-NOV-2000; 2000US-0253623P.
XX
PA   (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX
PI   Leonardi A,  Sartani A,  Glass J,  Sutcliffe JG,  Hasel KW;
XX
DR   WPI; 2003-058561/05.
XX
PT   New polypeptide associated with atherosclerosis, useful for treating
PT   atherosclerosis, nervous system disorders, immune disorders,
PT   hyperproliferative disorders and infectious diseases.
XX
PS   Disclosure; Page 139; 146pp; English.
XX
CC   The invention relates to polynucleotides and polypeptides associated with
CC   atherosclerosis. Polynucleotides of the invention are useful for delivery
CC   of genes, DNA vaccines, diagnostic reagents, peptides, proteins or
CC   macromolecules. Sequences of the invention are useful for treating
CC   nervous system disorders (e.g., Alzheimer's disease, Parkinson's disease,
CC   multiple sclerosis, epilepsy), immune disorders (e.g., autoimmune
CC   disorders such as rheumatoid arthritis, Addison's disease, haemolytic
CC   anaemia, graft-versus-host disease, inflammation), hyperproliferative
CC   disorders (e.g., neoplasms) and infectious diseases (e.g., viral,
CC   bacterial, fungal or parasite infection). They are used for regeneration
CC   of tissues, to repair, replace or protect damage tissues, for increasing
CC   chemotaxis activity of cells, for increasing or decreasing the
CC   differentiation or proliferation of embryonic stem cells from a lineage,
CC   for modulating mammalian characteristics, (such as body weight or
CC   height), for modulating mammalian metabolism affecting catabolism,
CC   anabolism, processing utilisation and storage of energy, to change a
CC   mammal's mental or physical state, or as a food additive or preservative.
CC   The invention is useful in gene therapy. The present sequence is a
CC   sequencing primer used in the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 7.7e+02;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||:
Db          1 TTTTTTTTTTTTTTTTTV 19
```

```
RESULT 1315
AAD49149/c
ID   AAD49149 standard; DNA; 19 BP.
XX
AC   AAD49149;
XX
DT   07-MAR-2003  (first entry)
XX
DE   3' sequencing primer #1 used in the invention.
XX
KW   Atherosclerosis; vaccine; nervous system disorder; Alzheimer's disease;
KW   Parkinson's disease; multiple sclerosis; immune disorder; gene therapy;
KW   autoimmune disorder; rheumatoid arthritis; hyperproliferative disorder;
KW   haemolytic anaemia; graft-versus-host disease; inflammation; infection;
KW   epilepsy; Addison's disease; neoplasm; tissue regeneration; chemotaxis;
KW   food additive; food preservative; primer; ss.
XX
OS   Unidentified.
XX
PN   WO200281726-A2.
XX
PD   17-OCT-2002.
XX
PF   15-NOV-2001; 2001WO-US043741.
XX
PR   15-NOV-2000; 2000US-0248892P.
PR   28-NOV-2000; 2000US-0253623P.
XX
PA   (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX
PI   Leonardi A,  Sartani A,  Glass J,  Sutcliffe JG,  Hasel KW;
XX
DR   WPI; 2003-058561/05.
XX
PT   New polypeptide associated with atherosclerosis, useful for treating
PT   atherosclerosis, nervous system disorders, immune disorders,
PT   hyperproliferative disorders and infectious diseases.
XX
PS   Disclosure; Page 139; 146pp; English.
XX
CC   The invention relates to polynucleotides and polypeptides associated with
CC   atherosclerosis. Polynucleotides of the invention are useful for delivery
CC   of genes, DNA vaccines, diagnostic reagents, peptides, proteins or
CC   macromolecules. Sequences of the invention are useful for treating
CC   nervous system disorders (e.g., Alzheimer's disease, Parkinson's disease,
CC   multiple sclerosis, epilepsy), immune disorders (e.g., autoimmune
CC   disorders such as rheumatoid arthritis, Addison's disease, haemolytic
CC   anaemia, graft-versus-host disease, inflammation), hyperproliferative
CC   disorders (e.g., neoplasms) and infectious diseases (e.g., viral,
CC   bacterial, fungal or parasite infection). They are used for regeneration
CC   of tissues, to repair, replace or protect damage tissues, for increasing
CC   chemotaxis activity of cells, for increasing or decreasing the
CC   differentiation or proliferation of embryonic stem cells from a lineage,
CC   for modulating mammalian characteristics, (such as body weight or
CC   height), for modulating mammalian metabolism affecting catabolism,
CC   anabolism, processing utilisation and storage of energy, to change a
CC   mammal's mental or physical state, or as a food additive or preservative.
CC   The invention is useful in gene therapy. The present sequence is a
CC   sequencing primer used in the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 7.7e+02;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              :||||||||||||||||||
Db         19 BAAAAAAAAAAAAAAAAAA 1


RESULT 1316
AAD50267
ID   AAD50267 standard; DNA; 19 BP.
XX
AC   AAD50267;
XX
DT   24-MAR-2003  (first entry)
XX
DE   3' sequencing primer #1 used to illustrate the method of the invention.
XX
KW   Gene expression; drug interaction mechanism; drug screening; primer;
KW   genomic mapping; ss.
XX
OS   Unidentified.
XX
PN   WO200261045-A2.
XX
PD   08-AUG-2002.
XX
PF   01-FEB-2002; 2002WO-US002666.
XX
PR   01-FEB-2001; 2001US-00775217.
XX
PA   (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
PA   (QUAN/) QUAN J.
XX
PI   Quan J,  Hilbush BS,  Hasel KWPD,  Sutcliffe GJ,  Chang HW;
PI   Callahan MA;
XX
DR   WPI; 2003-092784/08.
XX
PT   Simplified TOGA method for simultaneous sequence-specific identification
PT   of multiple mRNA molecules in mRNA population, useful for determining
PT   tissue-specific patterns of gene expression or mechanisms of drug
PT   interaction.
XX
PS   Disclosure; Page 39; 93pp; English.
XX
CC   The present invention relates to a novel simplified TOGA (RTM) method for
CC   simultaneous sequence-specific identification of multiple mRNA molecules
CC   in a RNA population. The method involves characterising each of the
CC   sequence-specific polymerase chain reaction (PCR) products by partial
CC   sequence and length. The method is useful for determining tissue-specific
CC   patterns of gene expression or mechanisms of drug interaction. It is also
CC   useful for drug screening, studying physiological processes, genomic
CC   mapping or manufacture of diagnostic, prognostic or therapeutic reagents.
CC   The present sequence is a primer used to illustrate the method of the
CC   invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 7.7e+02;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||:
Db          1 TTTTTTTTTTTTTTTTTTV 19


RESULT 1317
AAD50267/c
ID   AAD50267 standard; DNA; 19 BP.
XX
AC   AAD50267;
XX
DT   24-MAR-2003  (first entry)
XX
DE   3' sequencing primer #1 used to illustrate the method of the invention.
XX
KW   Gene expression; drug interaction mechanism; drug screening; primer;
KW   genomic mapping; ss.
XX
OS   Unidentified.
XX
```

```
PN   WO200261045-A2.
XX
PD   08-AUG-2002.
XX
PF   01-FEB-2002; 2002WO-US002666.
XX
PR   01-FEB-2001; 2001US-00775217.
XX
PA   (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
PA   (QUAN/) QUAN J.
XX
PI   Quan J,  Hilbush BS,  Hasel KWPD,  Sutcliffe GJ,  Chang HW;
PI   Callahan MA;
XX
DR   WPI; 2003-092784/08.
XX
PT   Simplified TOGA method for simultaneous sequence-specific identification
PT   of multiple mRNA molecules in mRNA population, useful for determining
PT   tissue-specific patterns of gene expression or mechanisms of drug
PT   interaction.
XX
PS   Disclosure; Page 39; 93pp; English.
XX
CC   The present invention relates to a novel simplified TOGA (RTM) method for
CC   simultaneous sequence-specific identification of multiple mRNA molecules
CC   in a RNA population. The method involves characterising each of the
CC   sequence-specific polymerase chain reaction (PCR) products by partial
CC   sequence and length. The method is useful for determining tissue-specific
CC   patterns of gene expression or mechanisms of drug interaction. It is also
CC   useful for drug screening, studying physiological processes, genomic
CC   mapping or manufacture of diagnostic, prognostic or therapeutic reagents.
CC   The present sequence is a primer used to illustrate the method of the
CC   invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 7.7e+02;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2803
              :||||||||||||||||||
Db         19 BAAAAAAAAAAAAAAAAAA 1


RESULT 1318
ADC21495
ID   ADC21495 standard; DNA; 19 BP.
XX
AC   ADC21495;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human PRDI-BF1 RT-PCR primer.
XX
KW   tumor; antigen; CD8+ cytotoxic T lymphocyte; CTL; CTL-induced lysis;
KW   multiple myeloma cell; human; PRDI-BF1;
KW   positive regulatory domain I-binding factor-1; MHC;
KW   major histocompatibility complex Class I; cytostatic; vaccine; ss;
KW   primer; PCR.
XX
OS   Homo sapiens.
XX
PN   WO2003029282-A2.
XX
PD   10-APR-2003.
XX
PF   24-SEP-2002; 2002WO-EP010701.
XX
PR   29-SEP-2001; 2001DE-01048236.
XX
PA   (IMMU-) IMMUGENICS AG.
XX
PI   Theobald M,  Lotz C;
XX
DR   WPI; 2003-354724/33.
XX
PT   New tumor-associated oligopeptide, useful particularly for treating
PT   multiple myeloma, is recognized by CD8 cytotoxic T cells, also
PT   derivatives and related nucleic acid.
XX
PS   Disclosure; Page 22; 64pp; German.
XX
CC   This invention describes a novel tumor-associated oligopeptide that is
CC   recognized as an antigen by CD8+ cytotoxic T lymphocytes (CTL) and causes
CC   CTL-induced lysis and/or apoptosis of tumor cells, especially multiple
CC   myeloma cells. The oligopeptide is derived from human PRDI-BF1 (positive
CC   regulatory domain I-binding factor-1) which is able to induce an MHC
CC   (major histocompatibility complex) Class I allele variant A2-restricted
CC   immune response of CD8+ CTL against tumor cells. The products of the
CC   invention have cytostatic activity and can be used in a vaccine. The
CC   peptide of the invention, also related retro-inverse and pseudopeptides,
CC   fusion proteins (FP), polynucleotides, vectors, host cells and antibodies
CC   and T cell receptors specific for PRDI-BFI peptides are useful for
CC   treating diseases associated with PRDI-BF1, particularly tumors. The
CC   products of the invention are also useful as diagnostic, therapeutic and
CC   prophylactic agents for detecting, modifying, generating, expanding
CC   and/or regulating activation and functional status of T cells, and for
CC   preparation of poly- or mono-clonal or recombinant A2-restricted T cell
CC   receptors and their functional equivalents. This sequence represents an
CC   RT-PCR primer used to amplify the human PRDI-BF1 gene described in the
CC   invention.
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 7.7e+02;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||:
Db          1 TTTTTTTTTTTTTTTTTV 19


RESULT 1319
ADC21495/c
ID   ADC21495 standard; DNA; 19 BP.
XX
AC   ADC21495;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human PRDI-BF1 RT-PCR primer.
XX
KW   tumor; antigen; CD8+ cytotoxic T lymphocyte; CTL; CTL-induced lysis;
KW   multiple myeloma cell; human; PRDI-BF1;
KW   positive regulatory domain I-binding factor-1; MHC;
KW   major histocompatibility complex Class I; cytostatic; vaccine; ss;
KW   primer; PCR.
XX
OS   Homo sapiens.
XX
PN   WO2003029282-A2.
XX
PD   10-APR-2003.
XX
PF   24-SEP-2002; 2002WO-EP010701.
XX
PR   29-SEP-2001; 2001DE-01048236.
XX
PA   (IMMU-) IMMUGENICS AG.
XX
PI   Theobald M,  Lotz C;
XX
DR   WPI; 2003-354724/33.
XX
```

```
PT   New tumor-associated oligopeptide, useful particularly for treating
PT   multiple myeloma, is recognized by CD8 cytotoxic T cells, also
PT   derivatives and related nucleic acid.
XX
PS   Disclosure; Page 22; 64pp; German.
XX
CC   This invention describes a novel tumor-associated oligopeptide that is
CC   recognized as an antigen by CD8+ cytotoxic T lymphocytes (CTL) and causes
CC   CTL-induced lysis and/or apoptosis of tumor cells, especially multiple
CC   myeloma cells. The oligopeptide is derived from human PRDI-BF1 (positive
CC   regulatory domain I-binding factor-1) which is able to induce an MHC
CC   (major histocompatibility complex) Class I allele variant A2-restricted
CC   immune response of CD8+ CTL against tumor cells. The products of the
CC   invention have cytostatic activity and can be used in a vaccine. The
CC   peptide of the invention, also related retro-inverse and pseudopeptides,
CC   fusion proteins (FP), polynucleotides, vectors, host cells and antibodies
CC   and T cell receptors specific for PRDI-BFI peptides are useful for
CC   treating diseases associated with PRDI-BF1, particularly tumors. The
CC   products of the invention are also useful as diagnostic, therapeutic and
CC   prophylactic agents for detecting, modifying, generating, expanding
CC   and/or regulating activation and functional status of T cells, and for
CC   preparation of poly- or mono-clonal or recombinant A2-restricted T cell
CC   receptors and their functional equivalents. This sequence represents an
CC   RT-PCR primer used to amplify the human PRDI-BF1 gene described in the
CC   invention.
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 7.7e+02;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              :||||||||||||||||||
Db         19 BAAAAAAAAAAAAAAAAAA 1


RESULT 1320
AAZ09197
ID   AAZ09197 standard; DNA; 20 BP.
XX
AC   AAZ09197;
XX
DT   19-OCT-1999  (first entry)
XX
DE   Oligonucleotide 9 for DNA analysis.
XX
KW   Primer; DNA analysis; amplification; hybridisation; ss.
XX
OS   Synthetic.
XX
PN   JP11196874-A.
XX
PD   27-JUL-1999.
XX
PF   14-JAN-1998;   98JP-00005399.
XX
PR   14-JAN-1998;   98JP-00005399.
XX
PA   (HITA ) HITACHI LTD.
XX
DR   WPI; 1999-496652/42.
XX
PT   Analysis of DNA fragment - comprises addition of known common
PT   oligonucleotide, amplification of resultant DNA fragment and analysis and
PT   labelling of amplified DNA.
XX
PS   Example 5; Page 12; 17pp; Japanese.
XX
CC   This invention descibes a novel method for the analysis of a DNA fragment
CC   which comprises: (i) addition of a known common oligonucleotide sequence
CC   to at least one terminal of each DNA fragment, (ii) amplification of the
CC   resultant DNA fragment as a primer using a first common primer containing
CC   a complementary nucleotide sequence to the above mentioned known common
CC   oligonucleotide sequence, a second common primer containing a
CC   complementary nucleotide sequence to the prepared known common
CC   oligonucleotide sequence optionally having been introduced with
CC   complementary nucleotide sequence at a terminal, and a specific primer
CC   capable of hybridisation with a DNA fragment containing whole or part of
CC   the gene having known sequence, to give amplified DNA, (iii) analysis of
CC   the amplified DNA to find the information of the DNA fragment, in which
CC   the specific primer is designed to prepare fragments of the common first
CC   and second primers and to give short fragment of amplified DNA and (iv)
CC   labelling them to make their differentiation. Differentiation of
CC   informations of known and unknown genes readily provides information of
CC   unknown gene and simultaneous monitoring of signals derived from minor
CC   genes. Furthermore, labelling of DNAs according to functions of known
CC   genes can be performed. AAZ09189-Z09201 represent oligonucleotide primers
CC   used to illustrate the method of the invention
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 2 Other;

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 8.7e+02;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||:
Db          1 TTTTTTTTTTTTTTTTTV 19


RESULT 1321
AAZ09197/c
ID   AAZ09197 standard; DNA; 20 BP.
XX
AC   AAZ09197;
XX
DT   19-OCT-1999  (first entry)
XX
DE   Oligonucleotide 9 for DNA analysis.
XX
KW   Primer; DNA analysis; amplification; hybridisation; ss.
XX
OS   Synthetic.
XX
PN   JP11196874-A.
XX
PD   27-JUL-1999.
XX
PF   14-JAN-1998;   98JP-00005399.
XX
PR   14-JAN-1998;   98JP-00005399.
XX
PA   (HITA ) HITACHI LTD.
XX
DR   WPI; 1999-496652/42.
XX
PT   Analysis of DNA fragment - comprises addition of known common
PT   oligonucleotide, amplification of resultant DNA fragment and analysis and
PT   labelling of amplified DNA.
XX
PS   Example 5; Page 12; 17pp; Japanese.
XX
CC   This invention descibes a novel method for the analysis of a DNA fragment
CC   which comprises: (i) addition of a known common oligonucleotide sequence
CC   to at least one terminal of each DNA fragment, (ii) amplification of the
CC   resultant DNA fragment as a primer using a first common primer containing
CC   a complementary nucleotide sequence to the above mentioned known common
CC   oligonucleotide sequence, a second common primer containing a
CC   complementary nucleotide sequence to the prepared known common
CC   oligonucleotide sequence optionally having been introduced with
CC   complementary nucleotide sequence at a terminal, and a specific primer
CC   capable of hybridisation with a DNA fragment containing whole or part of
CC   the gene having known sequence, to give amplified DNA, (iii) analysis of
CC   the amplified DNA to find the information of the DNA fragment, in which
CC   the specific primer is designed to prepare fragments of the common first
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CC   and second primers and to give short fragment of amplified DNA and (iv)
CC   labelling them to make their differentiation. Differentiation of
CC   informations of known and unknown genes readily provides information of
CC   unknown gene and simultaneous monitoring of signals derived from minor
CC   genes. Furthermore, labelling of DNAs according to functions of known
CC   genes can be performed. AAZ09189-Z09201 represent oligonucleotide primers
CC   used to illustrate the method of the invention
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 2 Other;

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 8.7e+02;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              :||||||||||||||||||
Db         19 BAAAAAAAAAAAAAAAAAA 1


RESULT 1322
AAQ45360
ID   AAQ45360 standard; DNA; 23 BP.
XX
AC   AAQ45360;
XX
DT   25-MAR-2003  (revised)
DT   09-OCT-1994  (first entry)
XX
DE   Human protein-tyrosine-phosphatase-1D cDNA primer.
XX
KW   Protein-tyrosine-phosphatase; enzyme; disease diagnosis; DNA primer; ss.
XX
OS   Synthetic.
XX
PN   WO9408017-A1.
XX
PD   14-APR-1994.
XX
PF   06-OCT-1993;   93WO-EP002728.
XX
PR   06-OCT-1992;   92US-00956315.
PR   16-FEB-1993;   93US-00018129.
XX
PA   (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI   Ullrich A,  Vogel W;
XX
DR   WPI; 1994-135583/16.
XX
PT   New protein tyrosine phosphatase (PTP) protein, PTP-ID - are useful for
PT   diagnosis and treatment of diseases associated with abnormal PTP-ID
PT   levels.
XX
PS   Disclosure; Page 48; 99pp; English.
XX
CC   This DNA primer is used in the PCR-based amplification of protein-
CC   tyrosine-phosphatase-1B cDNA. (Updated on 25-MAR-2003 to correct PN
CC   field.)
XX
SQ   Sequence 23 BP; 1 A; 2 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 23;
  Best Local Similarity   87.0%;  Pred. No. 1.2e+03;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTTTTTTT 2184
              |||   ||||||||||||||||||
Db          1 CTCGAGTTTTTTTTTTTTTTTT 23


RESULT 1323
AAT37316
ID   AAT37316 standard; DNA; 23 BP.
XX
AC   AAT37316;
XX
DT   06-FEB-1997  (first entry)
XX
DE   RT-PCR Primer for aromatic acyl transferase sequence.
XX
KW   Aromatic acyl transferase; transformation; anthocyanin pigment; plants;
KW   acylation; colour; tone; colouration; colour change; Gentiana triflora;
KW   Petunia hybrida; Perilla ocimoides; Scenecio cruentus;
KW   Lavandula angustifolia; ss.
XX
OS   Synthetic.
XX
PN   WO9625500-A1.
XX
PD   22-AUG-1996.
XX
PF   16-FEB-1996;   96WO-JP000348.
XX
PR   17-FEB-1995;   95JP-00067159.
PR   29-JUN-1995;   95JP-00196915.
PR   30-JAN-1996;   96JP-00046534.
XX
PA   (SUNR ) SUNTORY LTD.
XX
PI   Ashikari T,  Tanaka Y,  Fujiwara H,  Nakao M,  Fukui Y,  Yonekura K;
PI   Mizutani M,  Kusumi T;
XX
DR   WPI; 1996-393401/39.
XX
PT   DNA coding for aromatic acyl transferase - for transforming plants which
PT   produce anthocyanin pigments and thus altering colour tone, e.g. of
PT   flowers.
XX
PS   Example 2; Page 21; 94pp; Japanese.
XX
CC   Vectors containing DNA fragments encoding proteins of plant origin with
CC   aromatic acyl transferase activity may be used to transform plants which
CC   produce anthocyanin pigments. The aromatic acyl transferase acylates the
CC   pigments in the flower resulting in colour tone changes and allowing new
CC   colourations to be produced. Six specific DNA sequences encoding aromatic
CC   acyl transferase from different plants are described in AAT37308-T37313.
CC   This primer was used to reverse transcribe aromatic acyl transferase RNA
CC   to produce a cDNA ready for cloning into expression vectors
XX
SQ   Sequence 23 BP; 1 A; 2 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 23;
  Best Local Similarity   87.0%;  Pred. No. 1.2e+03;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTTTTTTT 2184
              |||   ||||||||||||||||||
Db          1 CTCGAGTTTTTTTTTTTTTTTT 23


RESULT 1324
AAZ28229
ID   AAZ28229 standard; DNA; 23 BP.
XX
AC   AAZ28229;
XX
DT   20-DEC-1999  (first entry)
XX
DE   Second round PCR primer #5 for amplifying gene trapped cDNA.
XX
KW   Gene trapping; splicing; integration; mutation; genome; intron; exon;
KW   splice acceptor; identification; reverse transcription; ss.
XX
OS   Synthetic.
XX
PN   WO9950426-A1.
```

XX
PD 07-OCT-1999.
XX
PF 26-MAR-1999; 99WO-US006474.
XX
PR 27-MAR-1998; 98US-0079729P.
PR 08-APR-1998; 98US-00057328.
PR 14-APR-1998; 98US-0081727P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Zambrowicz B, Friedrich GA, Sands AT;
XX
DR WPI; 1999-591324/50.
XX
PT New gene trapping vectors, useful for identifying, activating or mutating
PT genes in eukaryotic cells.
XX
PS Example 2; Page 53; 74pp; English.
XX
CC This sequence represents a PCR primer, #5, used in a second round of PCR
CC amplification of a cDNA. The cDNA had previously been amplified by a
CC first round of PCR from cDNA produced by reverse transcription of RNA
CC which had been generated after 3' gene trapping. The amplified cDNA was
CC then sequenced to obtain the gene trapped sequence. Such gene trapping
CC can be used to acquire novel sequence information from the trapped exons,
CC useful to identify new genes and in screening e.g., to identify the
CC genetic basis of diseases (such as cancer) or phenotypes, especially in
CC the analysis of single nucleotide polymorphisms. The vector can also be
CC introduced into a cell to activate expression of a naturally occurring
CC cellular gene, useful to study gene function. They can be used to produce
CC mutated cells or animals, and are useful in screening, for example, to
CC identify mutations associated with tumorigenic phenotypes. They can also
CC be used to create cDNA libraries of cells, useful for large scale genetic
CC analysis of the genome and to identify novel and mutated genes. The
CC vectors are more efficient (e.g., their use identified 13-fold more
CC genes) than conventional 3' gene trap vectors that rely on gene trapping
CC as detected by antibiotic selection. Use of vectors incorporating 5' gene
CC trap cassettes increase the probability of identifying the 5' ends of
CC gene open reading frames, important because these are difficult to obtain
CC by conventional methods, and often code for the signal sequence in
CC secreted and transmembrane proteins, an important group for potential
CC drug targets
XX
SQ Sequence 23 BP; 7 A; 6 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 0.6%; Score 18.2; DB 1; Length 23;
Best Local Similarity 87.0%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1999 CTAGCTTCTTCAGAGATCAAGTC 2021
| || ||||||||||||||||||
Db 1 CCAGAGTCTTCAGAGATCAAGTC 23

RESULT 1325
AAA29299
ID AAA29299 standard; DNA; 23 BP.
XX
AC AAA29299;
XX
DT 12-SEP-2000 (first entry)
XX
DE Second round primer Btk-i for 3' gene trapped cDNA from ES cells.
XX
KW Splice acceptor; vector; gene trap; gene discovery; cloning; analysis;
KW shuttling; gene activation; over-expression; primer; 3' gene trap;
KW embryonic stem cell; ES; ss.
XX
OS Synthetic.
XX
PN WO200031236-A2.
XX
PD 02-JUN-2000.
XX
PF 19-NOV-1999; 99WO-US027366.
XX
PR 20-NOV-1998; 98US-0109302P.
PR 25-MAR-1999; 99US-00276533.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Zambrowicz B, Friedrich GA, Lilleberg S, Sands AT;
XX
DR WPI; 2000-400053/34.
XX
PT Recombinant vectors for use in, for example, gene discovery, gene cloning
PT and gene mutation.
XX
PS Example 2; Page 62; 78pp; English.
XX
CC A 3' gene trapping vector was constructed containing the murine
CC phosphoglycerate kinase (PGK) gene promoter, the first exon of the murine
CC btk gene (nucleotides 40043-40250) and a splice donor (SD) sequence. The
CC PGKbtkSD vector lacks a 3' polyadenylation signal. Any transcript
CC produced by the cassette cannot be properly processed, and therefore
CC identified by 3' RACE, unless it is spliced to a 3' exon that can be
CC polyadenylated. The btk vector was introduced into embryonic stem cells
CC and G418 resistant cells were subsequently isolated and subjected to RNA
CC isolation, reverse transcription, PCR and sequencing to obtain the gene
CC trapped sequences. The claimed genetically engineered vectors comprise 5'
CC and 3' gene trap cassettes. The vectors incorporate structural elements
CC which, after integration into the host cell genome, enhance the number of
CC cellular genes that can be identified and mutated. A 5' gene trap
CC cassette comprises a splice acceptor (SA), an exon sequence (Ex1) located
CC 3' to the SA, which encodes a marker enabling the identification of a
CC cell expressing the exon and a polyadenylation sequence defining the 3'
CC end of Ex1. The vectors may be used for gene discovery, gene cloning,
CC gene mutation, gene regulation, shuttling nucleic acid sequences
CC throughout the genome and gene activation and over expression. The
CC vectors can be used to trap genes with a high level of efficiency
CC regardless of whether the genes are normally expressed in the cell type
CC into which the vector is incorporated. Cells harboring the vectors can be
CC screened using automated gene identification assays such as 3' RACE.
CC Using these vectors, it is possible to produce large numbers of mutations
CC and rapidly identify the mutated or trapped genes
XX
SQ Sequence 23 BP; 7 A; 6 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 0.6%; Score 18.2; DB 1; Length 23;
Best Local Similarity 87.0%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1999 CTAGCTTCTTCAGAGATCAAGTC 2021
| || ||||||||||||||||||
Db 1 CCAGAGTCTTCAGAGATCAAGTC 23

RESULT 1326
ABA97431
ID ABA97431 standard; DNA; 23 BP.
XX
AC ABA97431;
XX
DT 21-MAR-2002 (first entry)
XX
DE Glycosyltransferase genes PCR primer #2.
XX
KW Glycosyltransferase; anthocyanin; flower colour; enzyme; PCR primer; ss.
XX
OS Unidentified.
XX
PN WO200192509-A1.
XX
PD 06-DEC-2001.
XX

```
PF   01-JUN-2001; 2001WO-JP004675.
XX
PR   02-JUN-2000; 2000JP-00170436.
XX
PA   (ITFL-) INT FLOWER DEV PTY LTD.
XX
PI   Mizutani M,  Sakakibara K,  Tanaka Y,  Kusumi T,  Ono E;
XX
DR   WPI; 2002-114345/15.
XX
PT   New gene encoding protein that transfers a sugar to the 3' position of
PT   anthocyanin for changing flower color.
XX
PS   Example 3; Page 13; 50pp; Japanese.
XX
CC   The present invention provides the genes and proteins of
CC   glycosyltransferases from Gentiana triflora, Senesio cruentus and
CC   Clitoria ternatea. The protein transfers a sugar to the 3' position of
CC   anthocyanin, and can be used for changing the colour of flowers. The
CC   present sequence is a PCR primer used to isolate glycosyltransferase
CC   coding sequences of the invention
XX
SQ   Sequence 23 BP; 1 A; 2 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 23;
  Best Local Similarity   87.0%;  Pred. No. 1.2e+03;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTTTTTTT 2184
              |||   ||||||||||||||||||
Db          1 CTCGAGTTTTTTTTTTTTTTTT 23


RESULT 1327
ABA97997/c
ID   ABA97997 standard; DNA; 24 BP.
XX
AC   ABA97997;
XX
DT   26-APR-2002  (first entry)
XX
DE   Human mitochondria carrier protein 13 PCR primer SEQ ID NO 4.
XX
KW   Human; mitochondria carrier protein 13; malignant tumour; blood disease;
KW   HIV; infection; immunity disease; inflammation; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1323810-A.
XX
PD   28-NOV-2001.
XX
PF   16-MAY-2000; 2000CN-00115695.
XX
PR   16-MAY-2000; 2000CN-00115695.
XX
PA   (SHAN-) SHANGHAI BODE GENE DEV CO LTD.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-148830/20.
XX
PT   New polypeptide-human mitochondria carrier protein 13 and polynucleotide
PT   for coding same.
XX
PS   Example 2; Page 17 (Disclosure); 33pp; Chinese.
XX
CC   The invention relates to human mitochondria carrier protein 13,
CC   polynucleotide for coding this polypeptide through DNA recombination
CC   technique. This invention also discloses the method for this polypeptide
CC   to cure several diseases, such as malignant tumour, blood disease, HIV
CC   infection and immunity disease and various inflammations etc. This
CC   invention further discloses an antagonist against this polypeptide and
CC   its therapeutic action, and the application of polynucleotide for coding
CC   this new human mitochondria carrier protein 13. The present sequence is
CC   that of a PCR primer, useful to the invention
XX
SQ   Sequence 24 BP; 5 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 24;
  Best Local Similarity   87.0%;  Pred. No. 1.4e+03;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2777 TTAGAATTGAAAAAAAAAAAAAA 2799
              | | |||| ||||||||||||||
Db         23 TGAAAATTTAAAAAAAAAAAAAA 1


RESULT 1328
AAI72268/c
ID   AAI72268 standard; DNA; 25 BP.
XX
AC   AAI72268;
XX
DT   15-APR-2002  (first entry)
XX
DE   P4 primer used in differential display s-AFLP analysis.
XX
KW   Lung; cancer; metastasis; solid tumour; blood; bone marrow; syndecan 1;
KW   collagen 1 alpha 2; 7013; 7018; amplification; mammal; human; dog; cat;
KW   bile duct; colon; breast; uterus; oesophagus; larynx; liver; brain; PCR;
KW   remission; relapse; polymerase chain reaction; amplify; primer; ss.
XX
OS   Synthetic.
XX
PN   WO200198539-A2.
XX
PD   27-DEC-2001.
XX
PF   21-JUN-2001; 2001WO-US019980.
XX
PR   21-JUN-2000; 2000US-0215727P.
PR   27-OCT-2000; 2000US-0243976P.
XX
PA   (HITB ) HITACHI CHEM CO LTD.
PA   (HITB ) HITACHI CHEM RES CENT INC.
PA   (HITA ) HITACHI LTD.
XX
PI   Mitsuhashi M,  Kambara H,  Matsunaga H,  Kawamura M;
XX
DR   WPI; 2002-098233/13.
XX
PT   Identifying lung cancer/metastasis of solid tumor in patient by isolating
PT   blood or non-lung tissue, or bone marrow from patient and identifying
PT   presence of marker e.g. syndecan 1, collagen 1 alpha 2, 7013, or 7018.
XX
PS   Example 1; Page 6; 29pp; English.
XX
CC   The sequences given in AAI72265-69 are oligonucleotides which were used
CC   in the method of the invention for identifying lung cancer or metastasis
CC   of a solid tumour. The method comprises isolating blood (or non-lung
CC   tissue in the case of identifying lung cancer, or bone marrow in case of
CC   identifying metastasis) from a patient, and identifying the presence of
CC   at least one marker (M) such as syndecan 1, collagen 1 alpha 2, 7013, or
CC   7018. These oligos lead to the amplification of cDNA's which were more
CC   abundant in lung cancer RNA than in normal blood. The method is useful
CC   for identifying lung cancer in a mammal e.g., human, dog or cat, and
CC   identifying metastasis of solid tumour in a patient, where the solid
CC   tumour is of bile duct, colon, breast, uterus, oesophagus or larynx. The
CC   method is useful for identifying presence of lung cancer cells in the
CC   blood or bone marrow, and also for identifying metastasis and thus for
CC   identifying lung cancer cells in an organ such as liver or brain. The
CC   method is useful to identify the presence of lung cancer cells at a very
CC   early stage in the disease, or after remission or to identify a relapse
XX
SQ   Sequence 25 BP; 0 A; 3 C; 0 G; 20 T; 0 U; 2 Other;
```

```
  Query Match             0.6%;  Score 18.2;  DB 1;  Length 25;
  Best Local Similarity   94.7%;  Pred. No. 1.5e+03;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              :||||||||||||||||||
Db         24 BAAAAAAAAAAAAAAAAAA 6


RESULT 1329
ACF79235/c
ID   ACF79235 standard; DNA; 25 BP.
XX
AC   ACF79235;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Calix(a)arene-oligonucleotide hybrid.
XX
KW   Calix(4)arene; triplex; gene therapy; DNA sensor; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   stem_loop       1. .25
FT                   /*tag=  a
FT   modified_base   13
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER= calix(4)arene nucleoside"
XX
PN   WO2003059925-A1.
XX
PD   24-JUL-2003.
XX
PF   19-JUN-2002; 2002WO-KR001160.
XX
PR   15-JAN-2002; 2002KR-00002316.
XX
PA   (POST-) POSTECH FOUND.
XX
PI   Kim BH,  Kim SJ;
XX
DR   WPI; 2003-627375/59.
XX
PT   New calix(4)arene-nucleoside hybrid useful in gene therapy has at least
PT   one nucleoside attached to a calix(4)arene group through amide bonding,
PT   and is derived from a calix(4)arene having amino groups.
XX
PS   Claim 7; Page 20; 16pp; English.
XX
CC   The present sequence is that of a calix(4)arene-oligonucleotide hybrid of
CC   the invention, which includes a calix(4)arene-nucleoside (preferably
CC   thymidine) derivative. The calix(4)arene-oligonucleotide hybrid functions
CC   as a DNA hairpin structure mimic. It effectively recognises DNA or RNA
CC   through triplex formation by bonding between the calix(4)arene-containing
CC   cavity and a biologically active substance. The hybrid has a certain
CC   level of both rigidity and flexibility, is stable in vivo, has high cell
CC   permeability and can be mass-produced. It can be used as a DNA sensor or
CC   for gene therapy
XX
SQ   Sequence 25 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 25;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||| ||||||||||
Db         25 AAAAAAAAAAAAANAAAAAAAAAA 2
```

```
RESULT 1330
AAC96079/c
ID   AAC96079 standard; DNA; 25 BP.
XX
AC   AAC96079;
XX
DT   26-FEB-2001  (first entry)
XX
DE   16s rRNA gene PCR primer #46.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 45; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 3 A; 2 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 25;
  Best Local Similarity   87.0%;  Pred. No. 1.5e+03;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2776 GTTAGAATTGAAAAAAAAAAAAA 2798
              |||| || | ||||||||||||||
Db         23 GTTAAAACTCAAAAAAAAAAAAA 1


RESULT 1331
AAT27193
ID   AAT27193 standard; DNA; 25 BP.
XX
AC   AAT27193;
XX
DT   20-NOV-1996  (first entry)
XX
DE   Stem loop oligonucleotide targeted to p53 chromosomal binding site.
XX
KW   Stem loop; target; secondary structure; parallel binding domain;
KW   antiparallel; replication inhibitor; cell growth inhibitor; p53;
KW   detection; stable; strong affinity; nuclease resistant;
KW   Watson-Crick bonding; Hoogsteen bonding; ss.
XX
OS   Synthetic.
XX
```

```
FH   Key             Location/Qualifiers
FT   stem_loop       1. .25
FT                   /*tag=  a
FT                   /note= "loop without stem structure"
FT   misc_binding    3. .10
FT                   /*tag=  b
FT                   /note= "target binding area"
FT   misc_binding    16. .23
FT                   /*tag=  c
FT                   /note= "target binding area"
XX
PN   US5514546-A.
XX
PD   07-MAY-1996.
XX
PF   01-SEP-1993;   93US-00115497.
XX
PR   01-SEP-1993;   93CA-02105364.
XX
PA   (RESE ) RESEARCH CORP TECHNOLOGIES INC.
XX
PI   Kool ET;
XX
DR   WPI; 1995-162088/22.
XX
PT   Stem-loop oligo:nucleotide(s) contain parallel and antiparallel binding
PT   domains - for binding target nucleic acids, to regulate biosynthesis of
PT   nucleic acid or protein in a cell, for treating e.g. cancer.
XX
PS   Example 1; Col 30; 34pp; English.
XX
CC   AAT27193-T27198 and AAT27200 are stem loop oligonucleotides directed
CC   towards chromosomal sites normally bound by p53 (see AAT35519) The stem
CC   loop oligonucleotides bind with strong affinity and high selectivity to
CC   their target nucleic acids, they are also nuclease resistant. They are
CC   used to inhibit cell growth and DNA replication and other processes
CC   involving a nucleic acid template. In addition to this the
CC   oligonucleotides may be used for the detection and isolation of target
CC   nucleic acids and for cell type-specific drug delivery. The stem loops
CC   bind to their target via a system of co- operative Watson-Crick bonding
CC   and Hoogsteen bonding
XX
SQ   Sequence 25 BP; 0 A; 7 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 25;
  Best Local Similarity   87.0%;  Pred. No. 1.5e+03;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTTTTTTTTT 2186
                ||||||||||| | | ||||||||
Db          1 CCTTTTTTTTCTCTCTTTTTTTT 23


RESULT 1332
AAC96418
ID   AAC96418 standard; DNA; 25 BP.
XX
AC   AAC96418;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DQA1 gene PCR primer #20.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 51; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 3 A; 3 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 25;
  Best Local Similarity   87.0%;  Pred. No. 1.5e+03;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTAACTTTGA 2194
                ||||||||||||| |||  |||||
Db          1 TTTTTTTTTTTTCTTAGATTTGA 23


RESULT 1333
AAC96060
ID   AAC96060 standard; DNA; 25 BP.
XX
AC   AAC96060;
XX
DT   26-FEB-2001  (first entry)
XX
DE   16s rRNA gene PCR primer #27.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 44; 66pp; English.
XX
```

CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 3 A; 3 C; 3 G; 16 T; 0 U; 0 Other;

Query Match 0.6%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 1.5e+03;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2171 TTTTTTTTTTTTTTTTAACTTTG 2193
||||||||||||||| ||| ||
Db 1 TTTTTTTTTTTTTTTAAACGCTG 23

RESULT 1334
AAH38315
ID AAH38315 standard; DNA; 25 BP.
XX
AC AAH38315;
XX
DT 14-AUG-2001 (first entry)
XX
DE SNP specific SNPE primer SEQ ID 1111.
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW inflammation; forensic investigation; paternity analysis; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200129262-A2.
XX
PD 26-APR-2001.
XX
PF 13-OCT-2000; 2000WO-US028436.
XX
PR 15-OCT-1999; 99US-0160096P.
XX
PA (ORCH-) ORCHID BIOSCIENCES INC.
XX
PI Picoult-Newburg L, Pohl M;
XX
DR WPI; 2001-290930/30.
XX
PT New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample.
XX
PS Claim 1; Page 55; 83pp; English.
XX
CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a single nucleotide
CC primer extension (SNPE) primer specific for a human SNP containing DNA
CC sequence
XX
SQ Sequence 25 BP; 2 A; 2 C; 2 G; 19 T; 0 U; 0 Other;

Query Match 0.6%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 1.5e+03;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2164 CCTTTTTTTTTTTTTTTTTTT 2186
||| |||||||||| ||||||
Db 2 CCTAGTTTTTTTTTTGTTTTTT 24

RESULT 1335
AAX89364
ID AAX89364 standard; DNA; 26 BP.
XX
AC AAX89364;
XX
DT 24-SEP-1999 (first entry)
XX
DE Chromosomal binding site for p53 protein (Seq ID No: 10 of US5936079).
XX
KW Cell growth inhibition; chromosomal binding site; p53 protein;
KW cellular replication; cancer; ss.
XX
OS Synthetic.
XX
PN US5936079-A.
XX
PD 10-AUG-1999.
XX
PF 15-AUG-1994; 94US-00291011.
XX
PR 06-APR-1992; 92US-00863661.
PR 01-MAY-1992; 92US-00879618.
XX
PA (ALTO-) ALTON OCHSNER MEDICAL FOUND.
XX
PI Cook J, Re R;
XX
DR WPI; 1999-457628/38.
XX
PT New oligonucleotide useful for treating and preventing cancer.
XX
PS Example 1; Col 12; 12pp; English.
XX
CC The invention provides methods for inhibiting cell growth by providing a
CC growing cell with an oligonucleotide capable of binding to a chromosomal
CC binding site for p53 protein. Sequences AAX89362, AAX89363 and AAX89366
CC represent oligonucleotides that are derived from the sequence AAX89355.
CC The oligonucleotides are used for inhibiting mammalian cellular
CC replication and the treatment and prevention of cancer in a human. The
CC oligonucleotides can be used in vitro to inhibit the growth of cultured
CC mammalian cells e.g. human, monkey, mouse, rat and hamster cells which
CC have chromosomal DNA encoding a binding site for p53 protein. Sequences
CC AAX89356-366 represent oligonucleotides that are based on chromosomal
CC binding sites for p53 protein
XX
SQ Sequence 26 BP; 0 A; 7 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 0.6%; Score 18.2; DB 1; Length 26;
Best Local Similarity 87.0%; Pred. No. 1.6e+03;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       2164 CCTTTTTTTTTTTTTTTTTTTT 2186
              ||||||||  |||||||  |||||
Db          2 CCTTTTTTCCTTTTTTTCTTTTT 24


RESULT 1336
ABS54659
ID   ABS54659 standard; DNA; 26 BP.
XX
AC   ABS54659;
XX
DT   03-DEC-2002  (first entry)
XX
DE   Human p53 protein chromosomal binding region oligonucleotide Hoog3.
XX
KW   ss; p53; chromosomal binding region; cancer; carcinoma; sarcoma;
KW   breast cancer; adrenal cortex cancer; colon cancer; bladder cancer;
KW   prostate cancer; lung cancer; leukaemic cancer.
XX
OS   Synthetic.
XX
PN   US2002103153-A1.
XX
PD   01-AUG-2002.
XX
PF   22-AUG-2001; 2001US-00935247.
XX
PR   06-APR-1992;   92US-00863661.
PR   01-MAY-1992;   92US-00879618.
PR   15-AUG-1994;   94US-00291011.
PR   10-MAR-1999;   99US-00266065.
XX
PA   (RERR/) RE R.
PA   (COOK/) COOK J.
XX
PI   Re R,  Cook J;
XX
DR   WPI; 2002-674027/72.
XX
PT   Composition for treating cancer comprises an oligonucleotide that binds a
PT   chromosomal binding site for p53.
XX
PS   Example 1; Page 7; 13pp; English.
XX
CC   The invention relates to composition comprising an oligonucleotide that
CC   can bind a chromosomal binding site for p53 protein, and a
CC   pharmaceutically acceptable carrier. The composition is useful for
CC   inhibiting mammalian (e.g. human, ape, monkey, cow, mouse, rat, hamster,
CC   rabbit, cat, sheep or bull, dog, horse) cell growth and replication,
CC   especially cancer (e.g. carcinoma, sarcoma, breast cancer, adrenal cortex
CC   cancer, colon cancer, bladder cancer, prostate cancer, lung cancer or
CC   leukaemic cancer). The present sequence is human p53 protein chromosomal
CC   binding region scrambled control oligonucleotide Hoog3
XX
SQ   Sequence 26 BP; 0 A; 7 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 26;
  Best Local Similarity   87.0%;  Pred. No. 1.6e+03;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTTTTTTTT 2186
              ||||||||  |||||||  |||||
Db          2 CCTTTTTTCCTTTTTTTCTTTTT 24


RESULT 1337
ADC75075/c
ID   ADC75075 standard; DNA; 27 BP.
XX
AC   ADC75075;
XX
DT   01-JAN-2004  (first entry)
XX
DE   Biosensor related oligonucleotide of the invention SEQ ID NO:3.
XX
KW   ss; biosensor; hybridisation.
XX
OS   Synthetic.
XX
PN   JP2003172737-A.
XX
PD   20-JUN-2003.
XX
PF   07-DEC-2001; 2001JP-00374764.
XX
PR   07-DEC-2001; 2001JP-00374764.
XX
PA   (TOJO ) TOYO KOHAN CO LTD.
XX
DR   WPI; 2003-819164/77.
XX
PT   Solid support body comprising crystal resonator on which a surface
PT   treatment layer is formed, and a substrate whose surface treatment layer
PT   is chemically modified, useful as biosensor.
XX
PS   Disclosure; SEQ ID NO 3; 7pp; Japanese.
XX
CC   The invention relates to a novel solid support body comprising a crystal
CC   resonator on which a surface treatment layer is formed. The biosensor is
CC   useful for analysing biological samples e.g., gene, a protein, and a
CC   peptide, and for analysing bioactive substances. Preferably, the
CC   biosensor is useful for analysing base sequences by carrying out
CC   hybridisation. The present sequence is used in the exemplification of the
CC   invention.
XX
SQ   Sequence 27 BP; 19 A; 3 C; 0 G; 5 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 27;
  Best Local Similarity   87.0%;  Pred. No. 1.8e+03;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTAACT 2190
              |||||||||  ||||||||  || |
Db         23 TTTTTTTTTATTTTTTTGAATT 1


RESULT 1338
AAT90275
ID   AAT90275 standard; DNA; 27 BP.
XX
AC   AAT90275;
XX
DT   25-MAR-2003  (revised)
DT   03-DEC-1997  (first entry)
XX
DE   Pyrimidine ring modified triplex forming oligonucleotide ON-41.
XX
KW   Modification; triplex; duplex; nucleomonomer analogue; T antigen;
KW   unsaturated group; pyrimidine ring; inhibition; gene expression;
KW   antisense; therapy; research; diagnosis; probe; primer; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .27
FT                    /*tag=  a
FT                    /note= "all C are 5-methyl-2'-deoxycytidine all U are 5-
FT                    (1-propynyl)-2'-deoxyuridine"
FT   misc_feature     20. .21
FT                    /*tag=  b
FT                    /note= "switchback linker synthon"
XX
PN   US5645985-A.
XX
PD   08-JUL-1997.
XX
```

```
PF   25-NOV-1992;   92US-00976103.
XX
PR   26-NOV-1991;   91US-00799824.
PR   25-AUG-1992;   92US-00935444.
PR   23-OCT-1992;   92US-00965941.
XX
PA   (GILE-) GILEAD SCI INC.
XX
PI   Froehler B,  Jones RJ,  Gutierrez AJ,  Matteucci M,  Pudlo J;
PI   Wagner R;
XX
DR   WPI; 1997-362920/33.
XX
PT   Nucleo:monomers containing unsaturated pyrimidine base analogues - form
PT   oligomer duplexes or triplexes with nucleic acid under physiological
PT   conditions, and used in gene expression inhibition, diagnosis and assay.
XX
PS   Example 19; Col 133-134; 104pp; English.
XX
CC   The present sequence is a 5-methyl-2'-deoxycytidine/5-(1-propynyl)-
CC   2'deoxyuridine modified, T antigen, triplex forming oligonucleotide,
CC   comprising a switchback linker synthon and nucleomonomer analogues of
CC   cytosine and uridine containing an unsaturated group in the pyrimidine
CC   ring. The 5-substituent provides enhanced binding capacity in the
CC   formation of duplexes and triplexes with single and double stranded RNA
CC   and DNA. Triplexes can be formed at pH 7.0, i.e. under physiological pH
CC   conditions. The lipophilic groups can also enhance cell permeation and
CC   uptake. The oligomer, which also shows enhanced nuclease resistance, can
CC   be used to form duplexes and triplexes as a normal oligomer, to inhibit
CC   gene expression, e.g. by its antisense configuration, for therapeutic or
CC   research purposes, and for diagnosis by providing probes or primers for
CC   specific RNA or DNA. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 27 BP; 0 A; 6 C; 0 G; 0 T; 21 U; 0 Other;

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 27;
  Best Local Similarity   8.7%;  Pred. No. 1.8e+03;
  Matches    2;  Conservative   18;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTTTTTTTTT 2178
              ::::::|: |: ::: :::::::
Db          5 UUUUUUCUUCUCUUUCUUUUUUU 27


RESULT 1339
ADC75076
ID   ADC75076 standard; DNA; 27 BP.
XX
AC   ADC75076;
XX
DT   01-JAN-2004  (first entry)
XX
DE   Biosensor related oligonucleotide of the invention SEQ ID NO:4.
XX
KW   ss; biosensor; hybridisation.
XX
OS   Synthetic.
XX
PN   JP2003172737-A.
XX
PD   20-JUN-2003.
XX
PF   07-DEC-2001; 2001JP-00374764.
XX
PR   07-DEC-2001; 2001JP-00374764.
XX
PA   (TOJO ) TOYO KOHAN CO LTD.
XX
DR   WPI; 2003-819164/77.
XX
PT   Solid support body comprising crystal resonator on which a surface
PT   treatment layer is formed, and a substrate whose surface treatment layer
PT   is chemically modified, useful as biosensor.
XX
PS   Disclosure; SEQ ID NO 4; 7pp; Japanese.
XX
CC   The invention relates to a novel solid support body comprising a crystal
CC   resonator on which a surface treatment layer is formed. The biosensor is
CC   useful for analysing biological samples e.g., gene, a protein, and a
CC   peptide, and for analysing bioactive substances. Preferably, the
CC   biosensor is useful for analysing base sequences by carrying out
CC   hybridisation. The present sequence is used in the exemplification of the
CC   invention.
XX
SQ   Sequence 27 BP; 18 A; 3 C; 0 G; 6 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 27;
  Best Local Similarity   87.0%;  Pred. No. 1.8e+03;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAA 2803
              |||| |||||||| ||| |||||
Db          1 AATTCAAAAAAAATAAATAAAAA 23


RESULT 1340
AAF60450/c
ID   AAF60450 standard; DNA; 28 BP.
XX
AC   AAF60450;
XX
DT   27-APR-2001  (first entry)
XX
DE   RNA oligonucleotide #7.
XX
KW   Protein-RNA fusion; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "C6-psoralen-2-OMe-U"
FT   modified_base   28
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "A-TEG2"
XX
PN   WO200107657-A1.
XX
PD   01-FEB-2001.
XX
PF   19-JUL-2000; 2000WO-US019653.
XX
PR   27-JUL-1999;   99US-0145834P.
XX
PA   (PHYL-) PHYLOS INC.
XX
PI   Kurz M,  Lohse P,  Wagner R;
XX
DR   WPI; 2001-182803/18.
XX
PT   Affixing a peptide acceptor to an RNA molecule useful for producing
PT   fusion proteins for isolating proteins or nucleic acids with desired
PT   properties through attachment of a peptide acceptor to the 3' end of an
PT   RNA molecule.
XX
PS   Example 6; Page 29; 56pp; English.
XX
CC   The present invention relates to a method for affixing a peptide acceptor
CC   to an RNA molecule through the formation of a covalent bond, noncovalent
CC   bond, or by chemical ligation. The method is useful for producing RNA-
CC   protein fusions which can be used for the isolation of proteins or
CC   nucleic aids with desired properties from large pools of partially or
CC   completely random amino acid or nucleic acid sequences. The present
```

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CC   sequence is an RNA oligonucleotide used in the present invention
XX
SQ   Sequence 28 BP; 20 A; 2 C; 4 G; 0 T; 2 U; 0 Other;

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 28;
  Best Local Similarity   87.0%;  Pred. No. 1.9e+03;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTTAAC 2189
              ||||||||||||||||||  | |
Db         28 TTTTTTTTTTTTTTTTTTGCATC 6


RESULT 1341
AAL45359/c
ID   AAL45359 standard; RNA; 28 BP.
XX
AC   AAL45359;
XX
DT   06-JUN-2002  (first entry)
XX
DE   Puromycin linker DNA sequence.
XX
KW   Peptide cleavage; chemical active ingredient targeted release; diagnosis;
KW   antiasthmatic; osteopathic; cytostatic; asthma; osteoporosis; cancer;
KW   stroke; neuronal disease; arthritis; pancreatitis; hypertension;
KW   thrombosis; infection; schistosomiasis; herbicide; insecticide;
KW   fungicide; cerebroprotective; neurological; antiarthritic; pancreatic;
KW   hypotensive; antithrombotic; virucide; protozoacide; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "modified by psoralen and 2'-O-methyl"
FT   modified_base    28
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "modified by (PEG)2 CC (Puromycin linker)"
XX
PN   WO200216574-A2.
XX
PD   28-FEB-2002.
XX
PF   07-AUG-2001; 2001WO-EP009102.
XX
PR   22-AUG-2000; 2000DE-01041238.
XX
PA   (XZIL-) XZILLION GMBH & CO KG.
XX
PI   Reimholz R,  Ploeger F;
XX
DR   WPI; 2002-269356/31.
XX
PT   Identifying specifically cleavable peptide, useful for targeted drug
PT   delivery and developing protease inhibitors, by incubating test compound
PT   with peptide-nucleic acid fusion.
XX
PS   Example 1; Page 19; 38pp; German.
XX
CC   The present invention relates to the identification of specific
CC   proteolytically cleavable peptides by incubating a library of fusion
CC   molecules, comprising a peptide and nucleic acid encoding said peptide,
CC   with a proteolytically active sample, then isolating the cleavage
CC   fragments and determining the coding sequences in the separated fusion
CC   molecules. The coding sequences identified by the method are used for
CC   production of specifically proteolytically cleavable substances, which
CC   are useful in the treatment of asthma, osteoporosis, cancer, stroke,
CC   neuronal diseases, arthritis, pancreatitis, hypertension, thrombosis,
CC   viral infections and schistosomiasis. Also contemplated are similar
CC   compounds designed to release herbicides, insecticides and fungicides,
CC   when cleaved. The present sequence is a puromycin linker described in the
CC   exemplification of the invention
XX
SQ   Sequence 28 BP; 20 A; 2 C; 4 G; 0 T; 2 U; 0 Other;

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 28;
  Best Local Similarity   87.0%;  Pred. No. 1.9e+03;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTTAAC 2189
              ||||||||||||||||||  | |
Db         28 TTTTTTTTTTTTTTTTTTGCATC 6


RESULT 1342
AAT70113/c
ID   AAT70113 standard; DNA; 28 BP.
XX
AC   AAT70113;
XX
DT   24-SEP-1997  (first entry)
XX
DE   PolyAB primer 2.
XX
KW   primer; polymerase chain reaction; cDNA library; anchored end; PCSUB;
KW   lock-docking; screening; PCR-based cDNA subtractive cloning; ss.
XX
OS   Synthetic.
XX
PN   WO9640998-A1.
XX
PD   19-DEC-1996.
XX
PF   05-JUN-1996;   96WO-US008582.
XX
PR   07-JUN-1995;   95US-00481687.
XX
PA   (PION-) PIONEER HI-BRED INT INC.
XX
PI   Wang X,  Duvick JP,  Briggs SP;
XX
DR   WPI; 1997-087067/08.
XX
PT   Method for prodn. of cDNA libraries with anchored ends - useful for
PT   subtractive cloning of sequences of interest.
XX
PS   Claim 1; Page 28; 56pp; English.
XX
CC   The invention provides a PCR-based method for generating a full-length
CC   cDNA library with anchored ends. The method uses lock-docking primers
CC   (AAT70106-11), where one primer, poly TV (V = G,C or A) locks over the
CC   polyA tail of eukaryotic mRNA producing first strand synthesis and a
CC   second primer, polyGH (H = A, C or T) locks onto the polyC tail added by
CC   terminal deoxynucleotidyl transferase (TdT). In the final step, AAT70112-
CC   17 (polyAB and polyCD primers; B = G, T or C; D = G, A or T) are used to
CC   amplify the first strand and produce a cDNA library with anchored ends.
CC   cDNA libraries produced may be used to identify new (unique) nucleotide
CC   sequences from PCSUB (PCR-based cDNA subtractive) libraries. The new
CC   method produces discreet sized PCR products which would not necessarily
CC   require further subcloning/screening. The method also produces full-
CC   length cDNA's obtainable from the libraries as opposed to specific cDNA
CC   clones, as produced by previously known methods. Other methods such as
CC   PCR and RACE require a knowledge of the target sequence to be amplified,
CC   by using the PCSUB method no previous knowledge is necessary
XX
SQ   Sequence 28 BP; 18 A; 4 C; 5 G; 1 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 28;
  Best Local Similarity   87.0%;  Pred. No. 1.9e+03;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||  ||
```

```
Db         28 CTTTTTTTTTTTTTTTTGCCTA 6


RESULT 1343
ABK52626
ID   ABK52626 standard; DNA; 28 BP.
XX
AC   ABK52626;
XX
DT   27-AUG-2002  (first entry)
XX
DE   Minority genome method VIH-MUT-12 DNA sequence.
XX
KW   Minority genome method; viral quasi-species; majority genome;
KW   genetic diagnosis; viral infection; human immune deficiency virus;
KW   hepatitis B; hepatitis C; antiviral therapy; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1
FT                   /*tag=  a
FT                   /label= unknown
FT                   /note= "C6 aminolinker sequence"
XX
PN   WO200183815-A1.
XX
PD   08-NOV-2001.
XX
PF   27-APR-2001; 2001WO-ES000165.
XX
PR   27-APR-2000; 2000ES-00001068.
XX
PA   (CNSJ ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
XX
PI   Arias Esteban A,  Baranowski E,  Briones Llorente C;
PI   Domingo Solans E,  Escarmis Homs C,  Gomez Castilla J;
PI   Martin Ruiz- Jarabo C,  Parro Garcia V;
XX
DR   WPI; 2002-147445/19.
XX
PT   Detecting minority genomes in viral quasi-species, useful for identifying
PT   mutants responsible for drug resistance and to individualize therapy.
XX
PS   Example 2; Page 55; 107pp; Spanish.
XX
CC   The present invention relates to a new method for detecting minority
CC   genomes, present at less than 50%, in a population of nucleic acids of a
CC   viral quasi-species and having at least one mutation with respect to the
CC   majority genome. The invention can be used for genetic diagnosis of viral
CC   infections, especially human immune deficiency virus and hepatitis B or
CC   C, particularly to detect memory minority genomes that are implicated in
CC   failure of antiviral therapy, so the method may make possible design of
CC   therapies customised for individual patients. The present nucleic acid
CC   sequence represents the VIH-MUT-12 DNA sequence that was used in the
CC   methods of the invention
XX
SQ   Sequence 28 BP; 3 A; 1 C; 4 G; 19 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 28;
  Best Local Similarity   87.0%;  Pred. No. 1.9e+03;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTAA 2188
              |||||||||||||| | | |||
Db          2 TTTTTTTTTTTTTTTGTGTGTAA 24


RESULT 1344
AAD41903
ID   AAD41903 standard; RNA; 28 BP.
XX
AC   AAD41903;
XX
DT   30-OCT-2002  (first entry)
XX
DE   ON-41 oligonucleotide used in the exemplification of the invention.
XX
KW   Antisense therapy; infection; cardiovascular disorder; immune reaction;
KW   gene therapy; virucide; cytostatic; antibacterial; antiinflammatory;
KW   cancer; cardiant; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "5-(1-propynyl)-2'-deoxyuridine; This base is
FT                   given as N in the sequence shown as SEQ ID NO: 50 in the
FT                   sequence listing"
FT   modified_base   2
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "5-methyl-2'-deoxycytidine; This base is given as
FT                   N in the sequence shown as SEQ ID NO: 50 in the sequence
FT                   listing"
FT   modified_base   3
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "5-(1-propynyl)-2'-deoxyuridine; This base is
FT                   given as N in the sequence shown as SEQ ID NO: 50 in the
FT                   sequence listing"
FT   modified_base   4
FT                   /*tag=  d
FT                   /mod_base= OTHER
FT                   /note= "5-methyl-2'-deoxycytidine; This base is given as
FT                   N in the sequence shown as SEQ ID NO: 50 in the sequence
FT                   listing"
FT   modified_base   5. .10
FT                   /*tag=  e
FT                   /mod_base= OTHER
FT                   /note= "5-(1-propynyl)-2'-deoxyuridine; This base is
FT                   given as N in the sequence shown as SEQ ID NO: 50 in the
FT                   sequence listing"
FT   modified_base   11
FT                   /*tag=  f
FT                   /mod_base= OTHER
FT                   /note= "5-methyl-2'-deoxycytidine; This base is given as
FT                   N in the sequence shown as SEQ ID NO: 50 in the sequence
FT                   listing"
FT   modified_base   12. .13
FT                   /*tag=  g
FT                   /mod_base= OTHER
FT                   /note= "5-(1-propynyl)-2'-deoxyuridine; This base is
FT                   given as N in the sequence shown as SEQ ID NO: 50 in the
FT                   sequence listing"
FT   modified_base   14
FT                   /*tag=  h
FT                   /mod_base= OTHER
FT                   /note= "5-methyl-2'-deoxycytidine; This base is given as
FT                   N in the sequence shown as SEQ ID NO: 50 in the sequence
FT                   listing"
FT   modified_base   15
FT                   /*tag=  i
FT                   /mod_base= OTHER
FT                   /note= "5-(1-propynyl)-2'-deoxyuridine; This base is
FT                   given as N in the sequence shown as SEQ ID NO: 50 in the
FT                   sequence listing"
FT   modified_base   16
FT                   /*tag=  j
FT                   /mod_base= OTHER
FT                   /note= "5-methyl-2'-deoxycytidine; This base is given as
FT                   N in the sequence shown as SEQ ID NO: 50 in the sequence
FT                   listing"
FT   modified_base   17. .19
```

```
FT                   /*tag=  k
FT                   /mod_base= OTHER
FT                   /note= "5-(1-propynyl)-2'-deoxyuridine; This base is
FT                   given as N in the sequence shown as SEQ ID NO: 50 in the
FT                   sequence listing"
FT   modified_base   20
FT                   /*tag=  l
FT                   /mod_base= OTHER
FT                   /note= "5-methyl-2'-deoxycytidine; This base is given as
FT                   N in the sequence shown as SEQ ID NO: 50 in the sequence
FT                   listing"
FT   misc_feature    21
FT                   /*tag=  m
FT                   /note= "Switchback linker synthon; This base is given as
FT                   N in the sequence shown as SEQ ID NO: 50 in the sequence
FT                   listing"
FT   modified_base   22. .28
FT                   /*tag=  n
FT                   /mod_base= OTHER
FT                   /note= "5-(1-propynyl)-2'-deoxyuridine; This base is
FT                   given as N in the sequence shown as SEQ ID NO: 50 in the
FT                   sequence listing"
XX
PN   US6380368-B1.
XX
PD   30-APR-2002.
XX
PF   12-FEB-1996;   96US-00599738.
XX
PR   26-NOV-1991;   91US-00799824.
PR   25-AUG-1992;   92US-00935444.
PR   23-OCT-1992;   92US-00965941.
PR   25-NOV-1992;   92US-00976103.
PR   14-NOV-1994;   94US-00338352.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Froehler B,  Wagner R,  Mattencci M,  Jones RJ,  Gutierrez AJ;
PI   Pudlo J;
XX
DR   WPI; 2002-535437/57.
XX
PT   New oligomers useful for binding to DNA duplex target sequence and for
PT   treating e.g. diseases caused by viruses and inflammatory conditions
PT   comprise at least three 3'-5' linked nucleosides.
XX
PS   Example 19; Col 55-56; 106pp; English.
XX
CC   The present invention relates to novel oligomers which have enhanced
CC   ability with respect to forming duplexes or triplexes. The oligomers
CC   comprise at least three 3'-5' linked nucleosides or their salts. At least
CC   one internucleoside linkage is not a phosphodiester linkage and at least
CC   one nucleoside comprises a base. Sequences of the invention are useful
CC   for binding to a DNA duplex target sequence via either CT or GT triplex
CC   helix binding motif and in antisense therapies. They are also used for
CC   treating diseases caused by viruses and for diagnostic applications to
CC   detect viral infections, bacterial infections and diseases such as
CC   cancers. The oligomers are also used as primers, in the treatment of
CC   pathological conditions associated with inflammatory conditions,
CC   cardiovascular disorders, immune reactions and bacterial infections and
CC   for modulating target gene expression. They are also useful in gene
CC   therapy. The present sequence is an oligonucleotide used in the
CC   exemplification of the invention
XX
SQ   Sequence 28 BP; 0 A; 6 C; 0 G; 0 T; 21 U; 1 Other;

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 28;
  Best Local Similarity   8.3%;  Pred. No. 1.9e+03;
  Matches    2;  Conservative   18;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTTTTTTTTT 2179
              :::::::|: |: :::  :::::::
Db          5 UUUUUUCUUCUCUUUCNUUUUUUU 28
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```
RESULT 1345
AAA71176/c
ID   AAA71176 standard; DNA; 29 BP.
XX
AC   AAA71176;
XX
DT   27-APR-2001  (first entry)
XX
DE   Molecular interaction site DNA #157.
XX
KW   Modulator; identification; molecular interaction; virtual library; ss.
XX
OS   Canis familiaris.
XX
PN   WO9958947-A2.
XX
PD   18-NOV-1999.
XX
PF   12-MAY-1999;   99WO-US010361.
XX
PR   12-MAY-1998;   98US-00076404.
PR   12-MAY-1998;   98US-0085092P.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Ecker DJ,  Griffey R,  Crooke ST,  Sampath R,  Swayze E,  Mohan V;
PI   Hofstadler S,  Mcneil J;
XX
DR   WPI; 2000-086439/07.
XX
PT   Identifying compounds which modulate activity of target biomolecules,
PT   used to provide compounds which can be used as pharmacological,
PT   agricultural and industrial compounds.
XX
PS   Example 8; Fig 134; 405pp; English.
XX
CC   This invention describes a novel method for identifying compounds which
CC   modulate the activity of a target biomolecule. The method uses 3-
CC   dimensional representations of the biomolecule and a library of compounds
CC   and comprises (a) identifying at least one molecular interaction site of
CC   the target RNA; (b) generating in silico a virtual library of compounds
CC   predicted or calculated to interact with the molecular interaction site;
CC   and (c) comparing 3-dimensional (3-D) representations of the target RNA
CC   with members of the virtual library of compounds to generate a hierarchy
CC   of the compounds ranked in accordance with their respective ability to
CC   form physical interactions with the molecular interaction site. The
CC   method also describes (1) RNA comprising a joined sequence of at least 24
CC   nucleotides but not more than 70 nucleotides and having secondary
CC   structure defined by: (a) 3 nucleotides forming a first side of a first
CC   double stranded (ds) region; (b) 2 nucleotides forming a first side of an
CC   internal loop region; (c) 4 nucleotides forming a first side of a second
CC   ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
CC   nucleotides forming a second side of the second ds region; (f) 4
CC   nucleotides forming a second side of the internal loop region; and (g) 3
CC   nucleotides forming a second side of the first ds region; (2) a purified
CC   and isolated RNA fragment comprising the human sequence
CC   UUUACAACAUAAUCUAGUUUACAGAAAAAUC (II). The methods and products can be
CC   used for identifying agents which modulate the activity of biomolecules,
CC   particularly RNA. Such agents can be used as pharmaceutical, agricultural
CC   or industrial compounds
XX
SQ   Sequence 29 BP; 21 A; 2 C; 1 G; 3 T; 0 U; 2 Other;

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 29;
  Best Local Similarity   87.0%;  Pred. No. 2e+03;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAACTTT 2192
              |||||||||||||||||  | |
Db         27 TTTTTTTTTTTTTTTTTAGGTCT 5
```

```
RESULT 1346
AAA71193/c
ID   AAA71193 standard; RNA; 29 BP.
XX
AC   AAA71193;
XX
DT   27-APR-2001  (first entry)
XX
DE   Molecular interaction site RNA #230.
XX
KW   Modulator; identification; molecular interaction; virtual library; ss.
XX
OS   Canis familiaris.
XX
PN   WO9958947-A2.
XX
PD   18-NOV-1999.
XX
PF   12-MAY-1999;   99WO-US010361.
XX
PR   12-MAY-1998;   98US-00076404.
PR   12-MAY-1998;   98US-0085092P.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Ecker DJ,  Griffey R,  Crooke ST,  Sampath R,  Swayze E,  Mohan V;
PI   Hofstadler S,  Mcneil J;
XX
DR   WPI; 2000-086439/07.
XX
PT   Identifying compounds which modulate activity of target biomolecules,
PT   used to provide compounds which can be used as pharmacological,
PT   agricultural and industrial compounds.
XX
PS   Example 8; Fig 135; 405pp; English.
XX
CC   This invention describes a novel method for identifying compounds which
CC   modulate the activity of a target biomolecule. The method uses 3-
CC   dimensional representations of the biomolecule and a library of compounds
CC   and comprises (a) identifying at least one molecular interaction site of
CC   the target RNA; (b) generating in silico a virtual library of compounds
CC   predicted or calculated to interact with the molecular interaction site;
CC   and (c) comparing 3-dimensional (3-D) representations of the target RNA
CC   with members of the virtual library of compounds to generate a hierarchy
CC   of the compounds ranked in accordance with their respective ability to
CC   form physical interactions with the molecular interaction site. The
CC   method also describes (1) RNA comprising a joined sequence of at least 24
CC   nucleotides but not more than 70 nucleotides and having secondary
CC   structure defined by: (a) 3 nucleotides forming a first side of a first
CC   double stranded (ds) region; (b) 2 nucleotides forming a first side of an
CC   internal loop region; (c) 4 nucleotides forming a first side of a second
CC   ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
CC   nucleotides forming a second side of the second ds region; (f) 4
CC   nucleotides forming a second side of the internal loop region; and (g) 3
CC   nucleotides forming a second side of the first ds region; (2) a purified
CC   and isolated RNA fragment comprising the human sequence
CC   UUUACAACAUAAUCUAGUUUACAGAAAAAUC (II). The methods and products can be
CC   used for identifying agents which modulate the activity of biomolecules,
CC   particularly RNA. Such agents can be used as pharmaceutical, agricultural
CC   or industrial compounds
XX
SQ   Sequence 29 BP; 21 A; 2 C; 1 G; 0 T; 3 U; 2 Other;

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 29;
  Best Local Similarity   87.0%;  Pred. No. 2e+03;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAACTTT 2192
              |||||||||||||||||| | |
Db         27 TTTTTTTTTTTTTTTTTAGGTCT 5
```

```
RESULT 1347
AAQ34110
ID   AAQ34110 standard; DNA; 18 BP.
XX
AC   AAQ34110;
XX
DT   25-MAR-2003  (revised)
DT   02-FEB-1993  (first entry)
XX
DE   Sequence of a microsatellite from clone TGLA60B.
XX
KW   PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW   genetic mapping; traits; amplification; ss.
XX
OS   Bos taurus.
XX
PN   WO9213102-A1.
XX
PD   06-AUG-1992.
XX
PF   15-JAN-1992;   92WO-US000340.
XX
PR   15-JAN-1991;   91US-00642342.
XX
PA   (GENM-) GENMARK.
XX
PI   Georges M,  Massey JM;
XX
DR   WPI; 1992-284684/34.
XX
PT   Polymorphic bovine DNA markers - used in genetic identification, gene
PT   mapping, and selective breeding.
XX
PS   Table 7; Page 375; 517pp; English.
XX
CC   The sequence is that of a bovine microsatellite sequence obtd. by
CC   screening a library of bovine MboI DNA fragments of between 250 and 500
CC   bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
CC   clones cross-hybridised. Assuming independent distribution of
CC   microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
CC   in the bovine genome is estimated at >100, 000. The sequence information
CC   for ca. 230 such bovine microsatellites is summarised in the
CC   specification and indexed herein (see below). The sequences upstream and
CC   downstream of the microsatellite sequence were used to generate the
CC   required PCR primers for in vitro amplification of the corresp.
CC   microsatellite (using the program OPTIPRIM). The microsatellites may be
CC   used to identify individuals, for parentage testing, and in the genetic
CC   mapping of economic trait loci, or genes involved the determinism of
CC   economically important traits esp. in cattle, to allow selective
CC   breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
CC   field.)
XX
SQ   Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAA 18
```

```
RESULT 1348
AAQ34110/c
ID   AAQ34110 standard; DNA; 18 BP.
XX
AC   AAQ34110;
XX
DT   25-MAR-2003  (revised)
DT   02-FEB-1993  (first entry)
XX
DE   Sequence of a microsatellite from clone TGLA60B.
```

```
XX
KW   PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW   genetic mapping; traits; amplification; ss.
XX
OS   Bos taurus.
XX
PN   WO9213102-A1.
XX
PD   06-AUG-1992.
XX
PF   15-JAN-1992;   92WO-US000340.
XX
PR   15-JAN-1991;   91US-00642342.
XX
PA   (GENM-) GENMARK.
XX
PI   Georges M,  Massey JM;
XX
DR   WPI; 1992-284684/34.
XX
PT   Polymorphic bovine DNA markers - used in genetic identification, gene
PT   mapping, and selective breeding.
XX
PS   Table 7; Page 375; 517pp; English.
XX
CC   The sequence is that of a bovine microsatellite sequence obtd. by
CC   screening a library of bovine MboI DNA fragments of between 250 and 500
CC   bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
CC   clones cross-hybridised. Assuming independent distribution of
CC   microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
CC   in the bovine genome is estimated at >100, 000. The sequence information
CC   for ca. 230 such bovine microsatellites is summarised in the
CC   specification and indexed herein (see below). The sequences upstream and
CC   downstream of the microsatellite sequence were used to generate the
CC   required PCR primers for in vitro amplification of the corresp.
CC   microsatellite (using the program OPTIPRIM). The microsatellites may be
CC   used to identify individuals, for parentage testing, and in the genetic
CC   mapping of economic trait loci, or genes involved the determinism of
CC   economically important traits esp. in cattle, to allow selective
CC   breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
CC   field.)
XX
SQ   Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db         18 TTTTTTTTTTTTTTTTTT 1


RESULT 1349
AAQ75025
ID   AAQ75025 standard; RNA; 18 BP.
XX
AC   AAQ75025;
XX
DT   25-MAR-2003  (revised)
DT   03-AUG-1995  (first entry)
XX
DE   PCR primer.
XX
KW   Synthetic oligo; solid phase immunoassay; ss.
XX
OS   Synthetic.
XX
PN   WO9426932-A1.
XX
PD   24-NOV-1994.
XX
PF   13-MAY-1994;   94WO-US005407.
XX
PR   13-MAY-1993;   93US-00061694.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Fields HA,  Khudyakov YE;
XX
DR   WPI; 1995-006819/01.
XX
PT   Solid phase immunoassay using oligo:nucleotide as label - also new
PT   conjugates of oligo:nucleotide coupled to antigenic peptide, partic. for
PT   diagnosing hepatitis C or E virus infection.
XX
PS   Example; Page 12; 34pp; English.
XX
CC   AAR62941 and AAR62942 are examples of synthetic immunoreactive peptides.
CC   They are used in a method for detecting an antigen in a subject. The
CC   method involves binding the antigen to a solid support and then reacting
CC   it with an immunoreactive ligand (L) bound to an oligo; removing any
CC   unreacted L, and then detecting the presence of the oligo. A similar
CC   method can be used to detect Abs, in which case the ligand is an oligo-
CC   labelled Ag. The use of an amplifiable oligo as the label allows Ag or Ab
CC   to be detected at very low levels. An exemplary olgi is AAQ75024 which
CC   can be covalently attached by the 5'- terminus to the N- or C-terminal of
CC   a synthetic peptide. In the example, peptide AAR62941 was coupled to
CC   oligo AAQ75024 using disuccinimidyl suberate. Serum samples suspected to
CC   contain HEV Abs were immobilised on plastic tubes or wells, then
CC   incubated for 30-60 mins with the peptide-oligo proruct. The vessels were
CC   washed; bound oligo was released with 0.2M glycine and amplified in a
CC   separate tube using as primers AAQ75025 and AAQ75026 in 30 cycles of PCR.
CC   The amplification product - AAQ75031 - was treated with uracil DNA
CC   glycoslase to remove the U18 fragment, and the product captured by
CC   immoblised oligo-dT. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 0 T; 18 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   0.0%;  Pred. No. 7.3e+02;
  Matches    0;  Conservative   18;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ::::::::::::::::::
Db          1 UUUUUUUUUUUUUUUUUU 18


RESULT 1350
AAQ75025/c
ID   AAQ75025 standard; RNA; 18 BP.
XX
AC   AAQ75025;
XX
DT   25-MAR-2003  (revised)
DT   03-AUG-1995  (first entry)
XX
DE   PCR primer.
XX
KW   Synthetic oligo; solid phase immunoassay; ss.
XX
OS   Synthetic.
XX
PN   WO9426932-A1.
XX
PD   24-NOV-1994.
XX
PF   13-MAY-1994;   94WO-US005407.
XX
PR   13-MAY-1993;   93US-00061694.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Fields HA,  Khudyakov YE;
XX
DR   WPI; 1995-006819/01.
```

```
XX
PT   Solid phase immunoassay using oligo:nucleotide as label - also new
PT   conjugates of oligo:nucleotide coupled to antigenic peptide, partic. for
PT   diagnosing hepatitis C or E virus infection.
XX
PS   Example; Page 12; 34pp; English.
XX
CC   AAR62941 and AAR62942 are examples of synthetic immunoreactive peptides.
CC   They are used in a method for detecting an antigen in a subject. The
CC   method involves binding the antigen to a solid support and then reacting
CC   it with an immunoreactive ligand (L) bound to an oligo; removing any
CC   unreacted L, and then detecting the presence of the oligo. A similar
CC   method can be used to detect Abs, in which case the ligand is an oligo-
CC   labelled Ag. The use of an amplifiable oligo as the label allows Ag or Ab
CC   to be detected at very low levels. An exemplary olgi is AAQ75024 which
CC   can be covalently attached by the 5'- terminus to the N- or C-terminal of
CC   a synthetic peptide. In the example, peptide AAR62941 was coupled to
CC   oligo AAQ75024 using disuccinimidyl suberate. Serum samples suspected to
CC   contain HEV Abs were immobilised on plastic tubes or wells, then
CC   incubated for 30-60 mins with the peptide-oligo proruct. The vessels were
CC   washed; bound oligo was released with 0.2M glycine and amplified in a
CC   separate tube using as primers AAQ75025 and AAQ75026 in 30 cycles of PCR.
CC   The amplification product - AAQ75031 - was treated with uracil DNA
CC   glycoslase to remove the U18 fragment, and the product captured by
CC   immoblised oligo-dT. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 0 T; 18 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1351
AAT94667
ID   AAT94667 standard; DNA; 18 BP.
XX
AC   AAT94667;
XX
DT   27-MAR-1998  (first entry)
XX
DE   Anchored poly(T) oligonucleotide polyT-AnchA.
XX
KW   Flavonoid 3' hydroxylase; pigmentation; flower colour; transgenic plant;
KW   snapdragon; primer; ss.
XX
OS   Synthetic.
XX
PN   WO9732023-A1.
XX
PD   04-SEP-1997.
XX
PF   28-FEB-1997;   97WO-AU000124.
XX
PR   01-MAR-1996;   96AU-00008386.
XX
PA   (FLOR-) FLORIGENE LTD.
XX
PI   Brugliera F,  Holton TA,  Michael MZ;
XX
DR   WPI; 1997-448691/41.
XX
PT   Novel flavonoid 3'-hydroxylase(s) from flowering plants - and
PT   corresponding DNA, used in the manipulation of pigmentation in plants.
XX
PS   Example 15; Page 59; 234pp; English.
XX
CC   Anchored poly(T) oligonucleotides polyT-anchA (AAT94667), polyT-anchC
CC   (AAT94668) and polyT-anchG (AAT94669) are complementary to the upstream
CC   region of a polyadenylation sequence. They were used to prime cDNA
CC   synthesis from snapdragon (Antirrhinum majus) petal and leaf RNA, and
CC   were also utilised in the PCR amplification of plant cytochrome P450
CC   sequences (see also AAT94670-73). A cDNA clone (see AAT94657) encoding
CC   flavonoid 3' hydroxylase (see AAW35704) was isolated using a differential
CC   display approach. This can be used to manipulate the pigmentation of
CC   transgenic plants
XX
SQ   Sequence 18 BP; 1 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTA 18


RESULT 1352
AAT94668/c
ID   AAT94668 standard; DNA; 18 BP.
XX
AC   AAT94668;
XX
DT   27-MAR-1998  (first entry)
XX
DE   Anchored poly(T) oligonucleotide polyT-AnchC.
XX
KW   Flavonoid 3' hydroxylase; pigmentation; flower colour; transgenic plant;
KW   snapdragon; primer; ss.
XX
OS   Synthetic.
XX
PN   WO9732023-A1.
XX
PD   04-SEP-1997.
XX
PF   28-FEB-1997;   97WO-AU000124.
XX
PR   01-MAR-1996;   96AU-00008386.
XX
PA   (FLOR-) FLORIGENE LTD.
XX
PI   Brugliera F,  Holton TA,  Michael MZ;
XX
DR   WPI; 1997-448691/41.
XX
PT   Novel flavonoid 3'-hydroxylase(s) from flowering plants - and
PT   corresponding DNA, used in the manipulation of pigmentation in plants.
XX
PS   Example 15; Page 59; 234pp; English.
XX
CC   Anchored poly(T) oligonucleotides polyT-anchA (AAT94667), polyT-anchC
CC   (AAT94668) and polyT-anchG (AAT94669) are complementary to the upstream
CC   region of a polyadenylation sequence. They were used to prime cDNA
CC   synthesis from snapdragon (Antirrhinum majus) petal and leaf RNA, and
CC   were also utilised in the PCR amplification of plant cytochrome P450
CC   sequences (see also AAT94670-73). A cDNA clone (see AAT94657) encoding
CC   flavonoid 3' hydroxylase (see AAW35704) was isolated using a differential
CC   display approach. This can be used to manipulate the pigmentation of
CC   transgenic plants
XX
SQ   Sequence 18 BP; 0 A; 1 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||
Db         18 GAAAAAAAAAAAAAAAAA 1
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```
RESULT 1353
AAV37712
ID   AAV37712 standard; cDNA; 18 BP.
XX
AC   AAV37712;
XX
DT   25-MAR-2003  (revised)
DT   07-SEP-1998  (first entry)
XX
DE   Human protein AQ2_1i 3'-portion and polyA tail.
XX
KW   Human; secreted protein; murine adult spleen; human foetal kidney; ovary;
KW   bone marrow; thymus; AE648_1i; AE693_1i; AK438_1i; AK609_1i; AM1060_1i;
KW   AQ2_1i; K433_1i; L256_1i; prevent; treat; ameliorate; medical; ds.
XX
OS   Homo sapiens.
XX
PN   WO9820130-A2.
XX
PD   14-MAY-1998.
XX
PF   31-OCT-1997;   97WO-US019857.
XX
PR   01-NOV-1996;   96US-00742973.
PR   29-OCT-1997;   97US-00960024.
XX
PA   (GEMY ) GENETICS INST INC.
XX
PI   Jacobs K,  Mccoy JM,  Lavallie ER,  Racie LA,  Merberg D,  Treacy M;
PI   Spaulding V,  Agostino MJ;
XX
DR   WPI; 1998-286946/25.
XX
PT   New secreted proteins and associated polynucleotides - obtained from
PT   murine adult spleen, human foetal kidney, human ovary, murine bone marrow
PT   and murine adult thymus.
XX
PS   Disclosure; Page 58; 75pp; English.
XX
CC   The present invention describes novel proteins isolated from cDNA clones:
CC   AE648_1i; AE693_1i; AK438_1i; AK609_1i; AM1060_1i; AQ2_1i; K433_1i; or
CC   L256_1i, deposited as ATCC 98237. The present sequence represents the 3'-
CC   portion of AQ2_1i isolated from a human ovary cDNA library. The proteins
CC   from the present invention may be administered in a composition to
CC   prevent, treat or ameliorate a medical condition. The proteins may
CC   exhibit biological activities such as nutritional activity, cytokine and
CC   cell proliferation/differentiation activity, immune stimulating or
CC   suppressing activity, haematopoiesis regulating activity, tissue growth
CC   activity, activin/inhibin activity, chemotactic/chemokinetic activity,
CC   haemostatic and thrombotic activity, receptor/ligand activity, anti-
CC   inflammatory activity, cadherin/tumour invasion suppressor activity,
CC   tumour inhibition activity and other activities. (Updated on 25-MAR-2003
CC   to correct PR field.)
XX
SQ   Sequence 18 BP; 17 A; 0 C; 1 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||
Db          1 GAAAAAAAAAAAAAAAAA 18


RESULT 1354
AAV21970
ID   AAV21970 standard; DNA; 18 BP.
XX
AC   AAV21970;
XX
DT   14-JUL-1998  (first entry)
XX
DE   Nuclease resistant antisense oligo NBT 13 targeted against (T)18.
XX
KW   Nuclease resistant; bacterial infection; antibiotic; target;
KW   veterinary medicine; treatment; human; industrial process;
KW   bacterial control; ss.
XX
OS   Synthetic.
XX
PN   WO9803533-A1.
XX
PD   29-JAN-1998.
XX
PF   23-JUL-1997;   97WO-US012961.
XX
PR   24-JUL-1996;   96US-00685575.
XX
PA   (OLIG-) OLIGOS ETC & OLIGOS THERAPEUTICS INC.
XX
PI   Arrow A,  Dale RMK,  Thompson TL;
XX
DR   WPI; 1998-120687/11.
XX
PT   Treating bacterial infections in humans or animals with
PT   oligo:nucleotide(s) - resistant to nuclease and targetted to bacterial
PT   nucleic acid or proteins, also conjugates of these oligo:nucleotide(s)
PT   with antibiotics.
XX
PS   Claim 49; Page 87; 163pp; English.
XX
CC   This antisense oligonucleotide is nuclease resistant and can be used in
CC   the treatment of animals, including humans, having a bacterial infection.
CC   The treatment comprises administration of such nuclease resistant
CC   oligonucleotides, targeted to a nucleic acid or protein of the bacterium,
CC   and formulated with a carrier. A compound comprising this nuclease
CC   resistant oligonucleotide can be covalently linked to an antibiotic. The
CC   method is used to treat infections by a wide variety of Gram-positive and
CC   Gram-negative, or acid-fast, bacteria, in human and veterinary medicine.
CC   The methods are particularly used in immuno-compromised individuals (e.g.
CC   patients with acquired immunodeficiency syndrome or those receiving
CC   chemotherapy or radiation therapy), optionally in combination with, or
CC   fused to, antiviral or other antimicrobial oligonucleotides. Apart from
CC   therapeutic use, the oligonucleotides can be used to control bacteria in
CC   laboratory cultures, foods, beverages and industrial processes. The
CC   oligonucleotides are specific for bacteria, without affecting metabolism
CC   in mammalian cells. They may also activate RNase H and have a general,
CC   non-specific immune-stimulating effect. The oligonucleotides can be
CC   administered orally, intranasally, rectally, topically or by injection,
CC   optionally coupled to an agent (e.g. carbohydrate or polyamine) that
CC   enhances cellular uptake
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1355
AAV21970/c
ID   AAV21970 standard; DNA; 18 BP.
XX
AC   AAV21970;
XX
DT   14-JUL-1998  (first entry)
XX
DE   Nuclease resistant antisense oligo NBT 13 targeted against (T)18.
XX
KW   Nuclease resistant; bacterial infection; antibiotic; target;
```

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KW   veterinary medicine; treatment; human; industrial process;
KW   bacterial control; ss.
XX
OS   Synthetic.
XX
PN   WO9803533-A1.
XX
PD   29-JAN-1998.
XX
PF   23-JUL-1997;   97WO-US012961.
XX
PR   24-JUL-1996;   96US-00685575.
XX
PA   (OLIG-) OLIGOS ETC & OLIGOS THERAPEUTICS INC.
XX
PI   Arrow A,  Dale RMK,  Thompson TL;
XX
DR   WPI; 1998-120687/11.
XX
PT   Treating bacterial infections in humans or animals with
PT   oligo:nucleotide(s) - resistant to nuclease and targetted to bacterial
PT   nucleic acid or proteins, also conjugates of these oligo:nucleotide(s)
PT   with antibiotics.
XX
PS   Claim 49; Page 87; 163pp; English.
XX
CC   This antisense oligonucleotide is nuclease resistant and can be used in
CC   the treatment of animals, including humans, having a bacterial infection.
CC   The treatment comprises administration of such nuclease resistant
CC   oligonucleotides, targeted to a nucleic acid or protein of the bacterium,
CC   and formulated with a carrier. A compound comprising this nuclease
CC   resistant oligonucleotide can be covalently linked to an antibiotic. The
CC   method is used to treat infections by a wide variety of Gram-positive and
CC   Gram-negative, or acid-fast, bacteria, in human and veterinary medicine.
CC   The methods are particularly used in immuno-compromised individuals (e.g.
CC   patients with acquired immunodeficiency syndrome or those receiving
CC   chemotherapy or radiation therapy), optionally in combination with, or
CC   fused to, antiviral or other antimicrobial oligonucleotides. Apart from
CC   therapeutic use, the oligonucleotides can be used to control bacteria in
CC   laboratory cultures, foods, beverages and industrial processes. The
CC   oligonucleotides are specific for bacteria, without affecting metabolism
CC   in mammalian cells. They may also activate RNase H and have a general,
CC   non-specific immune-stimulating effect. The oligonucleotides can be
CC   administered orally, intranasally, rectally, topically or by injection,
CC   optionally coupled to an agent (e.g. carbohydrate or polyamine) that
CC   enhances cellular uptake
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1356
AAX19943
ID   AAX19943 standard; DNA; 18 BP.
XX
AC   AAX19943;
XX
DT   14-JUN-1999  (first entry)
XX
DE   Primer SEQ ID NO:3 from JP11075880.
XX
KW   Primer; oligonucleotide; labelling; detection; self-priming; PCR; ss.
XX
OS   Synthetic.
XX
PN   JP11075880-A.
XX
PD   23-MAR-1999.
XX
PF   10-JUL-1998;   98JP-00195719.
XX
PR   14-JUL-1997;   97JP-00205378.
XX
PA   (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
XX
DR   WPI; 1999-257710/22.
XX
PT   Labelling of an oligonucleotide - useful for detecting genes.
XX
PS   Example 1; Page 7; 10pp; Japanese.
XX
CC   A method has been developed for labelling an oligonucleotide having a
CC   repeated sequence of (XY)n (where X and Y consists of a combination of
CC   adenine and thymine or uracil or guanine and cytosine, and n is an
CC   integer of 1 or more ) at the 3'-terminal side in which the repeated
CC   sequence is added and extended using a labelled body of the nucleotide
CC   constituting the repeated sequence and a DNA polymerase lacked in 5' to
CC   3' exonuclease activity. The method can be used for detecting a gene. The
CC   method can detect a gene in a sensitivity up to ten times higher than
CC   prior art methods. The present sequence represents a primer used in an
CC   example from the present invention
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1357
AAX19943/c
ID   AAX19943 standard; DNA; 18 BP.
XX
AC   AAX19943;
XX
DT   14-JUN-1999  (first entry)
XX
DE   Primer SEQ ID NO:3 from JP11075880.
XX
KW   Primer; oligonucleotide; labelling; detection; self-priming; PCR; ss.
XX
OS   Synthetic.
XX
PN   JP11075880-A.
XX
PD   23-MAR-1999.
XX
PF   10-JUL-1998;   98JP-00195719.
XX
PR   14-JUL-1997;   97JP-00205378.
XX
PA   (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
XX
DR   WPI; 1999-257710/22.
XX
PT   Labelling of an oligonucleotide - useful for detecting genes.
XX
PS   Example 1; Page 7; 10pp; Japanese.
XX
CC   A method has been developed for labelling an oligonucleotide having a
CC   repeated sequence of (XY)n (where X and Y consists of a combination of
CC   adenine and thymine or uracil or guanine and cytosine, and n is an
CC   integer of 1 or more ) at the 3'-terminal side in which the repeated
CC   sequence is added and extended using a labelled body of the nucleotide
CC   constituting the repeated sequence and a DNA polymerase lacked in 5' to
```

```
CC   3' exonuclease activity. The method can be used for detecting a gene. The
CC   method can detect a gene in a sensitivity up to ten times higher than
CC   prior art methods. The present sequence represents a primer used in an
CC   example from the present invention
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1358
AAX19942
ID   AAX19942 standard; DNA; 18 BP.
XX
AC   AAX19942;
XX
DT   14-JUN-1999  (first entry)
XX
DE   Primer SEQ ID NO:2 from JP11075880.
XX
KW   Primer; oligonucleotide; labelling; detection; self-priming; PCR; ss.
XX
OS   Synthetic.
XX
PN   JP11075880-A.
XX
PD   23-MAR-1999.
XX
PF   10-JUL-1998;   98JP-00195719.
XX
PR   14-JUL-1997;   97JP-00205378.
XX
PA   (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
XX
DR   WPI; 1999-257710/22.
XX
PT   Labelling of an oligonucleotide - useful for detecting genes.
XX
PS   Example 1; Page 7; 10pp; Japanese.
XX
CC   A method has been developed for labelling an oligonucleotide having a
CC   repeated sequence of (XY)n (where X and Y consists of a combination of
CC   adenine and thymine or uracil or guanine and cytosine, and n is an
CC   integer of 1 or more ) at the 3'-terminal side in which the repeated
CC   sequence is added and extended using a labelled body of the nucleotide
CC   constituting the repeated sequence and a DNA polymerase lacked in 5' to
CC   3' exonuclease activity. The method can be used for detecting a gene. The
CC   method can detect a gene in a sensitivity up to ten times higher than
CC   prior art methods. The present sequence represents a primer used in an
CC   example from the present invention
XX
SQ   Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 1359
AAX19942/c
ID   AAX19942 standard; DNA; 18 BP.
XX
AC   AAX19942;
XX
DT   14-JUN-1999  (first entry)
XX
DE   Primer SEQ ID NO:2 from JP11075880.
XX
KW   Primer; oligonucleotide; labelling; detection; self-priming; PCR; ss.
XX
OS   Synthetic.
XX
PN   JP11075880-A.
XX
PD   23-MAR-1999.
XX
PF   10-JUL-1998;   98JP-00195719.
XX
PR   14-JUL-1997;   97JP-00205378.
XX
PA   (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
XX
DR   WPI; 1999-257710/22.
XX
PT   Labelling of an oligonucleotide - useful for detecting genes.
XX
PS   Example 1; Page 7; 10pp; Japanese.
XX
CC   A method has been developed for labelling an oligonucleotide having a
CC   repeated sequence of (XY)n (where X and Y consists of a combination of
CC   adenine and thymine or uracil or guanine and cytosine, and n is an
CC   integer of 1 or more ) at the 3'-terminal side in which the repeated
CC   sequence is added and extended using a labelled body of the nucleotide
CC   constituting the repeated sequence and a DNA polymerase lacked in 5' to
CC   3' exonuclease activity. The method can be used for detecting a gene. The
CC   method can detect a gene in a sensitivity up to ten times higher than
CC   prior art methods. The present sequence represents a primer used in an
CC   example from the present invention
XX
SQ   Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          18 TTTTTTTTTTTTTTTTTT 1


RESULT 1360
AAX18372
ID   AAX18372 standard; DNA; 18 BP.
XX
AC   AAX18372;
XX
DT   11-MAY-1999  (first entry)
XX
DE   RT-PCR primer of the invention SEQ ID 13.
XX
KW   RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS   Synthetic.
XX
PN   JP11032765-A.
XX
PD   09-FEB-1999.
XX
PF   18-JUL-1997;   97JP-00208312.
XX
PR   18-JUL-1997;   97JP-00208312.
XX
PA   (TAKI ) TAKARA SHUZO CO LTD.
XX
DR   WPI; 1999-183822/16.
XX
```

PT Peptides having at least two new nucleotides - useful as primers in RT-
PT PCR.
XX
PS Disclosure; Page 11; 19pp; Japanese.
XX
CC This sequence represents a primer of the invention. The invention relates
CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC natural number indicating the repetition of alpha; beta, delta = V or N;
CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC repetition of gamma, in which thymine expressed by gamma is composed of
CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC useful as primers for RT-PCR and determination of base sequences. The new
CC sequences allow for reproductive and highly efficient analysis of gene
CC sequences
XX
SQ Sequence 18 BP; 2 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2171 TTTTTTTTTTTTTTTTAA 2188
||||||||||||||||||
Db 1 TTTTTTTTTTTTTTTTAA 18

RESULT 1361
AAA40563
ID AAA40563 standard; cDNA; 18 BP.
XX
AC AAA40563;
XX
DT 16-NOV-2000 (first entry)
XX
DE Human adult ovary cDNA fragment AQ2_1i #2.
XX
KW Secreted protein; cytostatic; immunostimulatory; antimicrobial;
KW antiviral; immunosuppressive; antiinflammatory; vulnerary; cytokine;
KW cell proliferation; differentiation; regulator; treatment; tumor;
KW autoimmune disease; inflammatory disorder; wound; microbial infection;
KW viral disease; graft versus host reaction suppression; ss.
XX
OS Homo sapiens.
XX
PN WO200037630-A1.
XX
PD 29-JUN-2000.
XX
PF 22-DEC-1999; 99WO-US031005.
XX
PR 23-DEC-1998; 98US-00220876.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Jacobs K, Mccoy JM, Lavallie ER, Collins-Racie LA, Evans C;
PI Merberg D, Treacy M, Bowman MR;
XX
DR WPI; 2000-442661/38.
DR P-PSDB; AAB10274.
XX
PT Secreted human proteins AS296-1i and AS34-1i, useful for treating tumors,
PT autoimmune diseases, inflammatory disorders, wounds, microbial infections
PT and viral diseases.
XX
PS Disclosure; Page 269; 293pp; English.
XX
CC This invention describes novel secreted human proteins (I) which have
CC cytostatic, immunostimulatory, antimicrobial, antiviral,
CC immunosuppressive, antiinflammatory and vulnerary activity and which act
CC as cytokine, cell proliferation or differentiation regulators. (I) is
CC useful for treating tumors, autoimmune diseases, inflammatory disorders,
CC wounds, microbial infections and viral diseases. (I) is also useful for
CC suppressing graft versus host reaction. AAA40490-A40580 represent cDNA
CC fragments that encode the secreted proteins AAB10226-B10288 described in
CC the method of the invention
XX
SQ Sequence 18 BP; 17 A; 0 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAAAAAAAA 2802
||||||||||||||||||
Db 1 GAAAAAAAAAAAAAAAAA 18

RESULT 1362
AAZ87161
ID AAZ87161 standard; RNA; 18 BP.
XX
AC AAZ87161;
XX
DT 08-MAY-2000 (first entry)
XX
DE Oligoarabinonucleotide SEQ ID NO:2.
XX
KW Beta-D-arabinose; antisense; inhibition; transcription; expression;
KW reverse transcription; viral replication; RNase H cleavage;
KW triple helix formation; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1. .18
FT /*tag= a
FT /note= "Ribose moiety replaced by beta-D-arabinose"
XX
PN WO9967378-A1.
XX
PD 29-DEC-1999.
XX
PF 17-JUN-1999; 99WO-CA000571.
XX
PR 19-JUN-1998; 98CA-02241361.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Damha MJ, Parniak MA, Noronha AM, Wilds C, Borkow G, Arion D;
XX
DR WPI; 2000-160584/14.
XX
PT Therapeutic composition containing antisense oligonucleotides that
PT include arabinose sugars, particularly for inhibiting viral replication.
XX
PS Example 1; Page 29; 91pp; English.
XX
CC The invention relates to a new composition for selective, sequence-
CC specific inhibition of gene transcription and expression in a host. The
CC composition comprises oligonucleotides containing arabinose sugars that
CC can hybridise to either a single-stranded (ss) RNA to induce RNase H
CC cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple
CC helix, thereby inhibiting DNA replication and/or transcription. The
CC oligoarabinonucleotides are used for antisense inhibition of gene
CC expression or to prevent DNA replication, or reverse transcription of RNA
CC by retroviruses. The compositions are therefore particularly used to
CC inhibit retroviral replication. The oligoarabinonucleotides can also be
CC used, in combination with RNase H, as reagents for sequence-specific
CC cleavage or RNA mapping, and additionally for the study and control of
CC gene expression in cells. The oligoarabinonucleotides have excellent
CC affinity for RNA, increased resistance to nucleases and show little if
CC any non-specific binding to cellular or serum proteins. They target ss
CC RNA, but not complementary ss DNA, so may be useful for targetting

```
CC   retroviral genomic RNA to inhibit the early stages of viral replication.
CC   Oligoarabinonucleotides containing pyrimidine bases form triple helices
CC   with significantly higher thermal stability than those produced by normal
CC   oligonucleotides. Sequences AAZ87160-Z87164 represent
CC   oligoarabinonucleotides containing beta-D-arabinose used in an
CC   exemplification of the present invention
XX
SQ   Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 1363
AAZ87161/c
ID   AAZ87161 standard; RNA; 18 BP.
XX
AC   AAZ87161;
XX
DT   08-MAY-2000  (first entry)
XX
DE   Oligoarabinonucleotide SEQ ID NO:2.
XX
KW   Beta-D-arabinose; antisense; inhibition; transcription; expression;
KW   reverse transcription; viral replication; RNase H cleavage;
KW   triple helix formation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .18
FT                   /*tag=  a
FT                   /note= "Ribose moiety replaced by beta-D-arabinose"
XX
PN   WO9967378-A1.
XX
PD   29-DEC-1999.
XX
PF   17-JUN-1999;   99WO-CA000571.
XX
PR   19-JUN-1998;   98CA-02241361.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Parniak MA,  Noronha AM,  Wilds C,  Borkow G,  Arion D;
XX
DR   WPI; 2000-160584/14.
XX
PT   Therapeutic composition containing antisense oligonucleotides that
PT   include arabinose sugars, particularly for inhibiting viral replication.
XX
PS   Example 1; Page 29; 91pp; English.
XX
CC   The invention relates to a new composition for selective, sequence-
CC   specific inhibition of gene transcription and expression in a host. The
CC   composition comprises oligonucleotides containing arabinose sugars that
CC   can hybridise to either a a single-stranded (ss) RNA to induce RNase H
CC   cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple
CC   helix, thereby inhibiting DNA replication and/or transcription. The
CC   oligoarabinonucleotides are used for antisense inhibition of gene
CC   expression or to prevent DNA replication, or reverse transcription of RNA
CC   by retroviruses. The compositions are therefore particularly used to
CC   inhibit retroviral replication. The oligoarabinonucleotides can also be
CC   used, in combination with RNase H, as reagents for sequence-specific
CC   cleavage or RNA mapping, and additionally for the study and control of
CC   gene expression in cells. The oligoarabinonucleotides have excellent
CC   affinity for RNA, increased resistance to nucleases and show little if
CC   any non-specific binding to cellular or serum proteins. They target ss
CC   RNA, but not complementary ss DNA, so may be useful for targetting
CC   retroviral genomic RNA to inhibit the early stages of viral replication.
CC   Oligoarabinonucleotides containing pyrimidine bases form triple helices
CC   with significantly higher thermal stability than those produced by normal
CC   oligonucleotides. Sequences AAZ87160-Z87164 represent
CC   oligoarabinonucleotides containing beta-D-arabinose used in an
CC   exemplification of the present invention
XX
SQ   Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db         18 TTTTTTTTTTTTTTTTTT 1


RESULT 1364
AAZ87162
ID   AAZ87162 standard; RNA; 18 BP.
XX
AC   AAZ87162;
XX
DT   08-MAY-2000  (first entry)
XX
DE   Oligoarabinonucleotide SEQ ID NO:3.
XX
KW   Beta-D-arabinose; antisense; inhibition; transcription; expression;
KW   reverse transcription; viral replication; RNase H cleavage;
KW   triple helix formation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .18
FT                   /*tag=  a
FT                   /note= "Ribose moiety replaced by beta-D-arabinose"
XX
PN   WO9967378-A1.
XX
PD   29-DEC-1999.
XX
PF   17-JUN-1999;   99WO-CA000571.
XX
PR   19-JUN-1998;   98CA-02241361.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Parniak MA,  Noronha AM,  Wilds C,  Borkow G,  Arion D;
XX
DR   WPI; 2000-160584/14.
XX
PT   Therapeutic composition containing antisense oligonucleotides that
PT   include arabinose sugars, particularly for inhibiting viral replication.
XX
PS   Example 1; Page 29; 91pp; English.
XX
CC   The invention relates to a new composition for selective, sequence-
CC   specific inhibition of gene transcription and expression in a host. The
CC   composition comprises oligonucleotides containing arabinose sugars that
CC   can hybridise to either a a single-stranded (ss) RNA to induce RNase H
CC   cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple
CC   helix, thereby inhibiting DNA replication and/or transcription. The
CC   oligoarabinonucleotides are used for antisense inhibition of gene
CC   expression or to prevent DNA replication, or reverse transcription of RNA
CC   by retroviruses. The compositions are therefore particularly used to
CC   inhibit retroviral replication. The oligoarabinonucleotides can also be
CC   used, in combination with RNase H, as reagents for sequence-specific
CC   cleavage or RNA mapping, and additionally for the study and control of
CC   gene expression in cells. The oligoarabinonucleotides have excellent
CC   affinity for RNA, increased resistance to nucleases and show little if
```

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CC   any non-specific binding to cellular or serum proteins. They target ss
CC   RNA, but not complementary ss DNA, so may be useful for targetting
CC   retroviral genomic RNA to inhibit the early stages of viral replication.
CC   Oligoarabinonucleotides containing pyrimidine bases form triple helices
CC   with significantly higher thermal stability than those produced by normal
CC   oligonucleotides. Sequences AAZ87160-Z87164 represent
CC   oligoarabinonucleotides containing beta-D-arabinose used in an
CC   exemplification of the present invention
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 0 T; 18 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   0.0%;  Pred. No. 7.3e+02;
  Matches    0;  Conservative   18;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2183
              :::::::::::::::::
Db          1 UUUUUUUUUUUUUUUUU 18


RESULT 1365
AAZ87162/c
ID   AAZ87162 standard; RNA; 18 BP.
XX
AC   AAZ87162;
XX
DT   08-MAY-2000  (first entry)
XX
DE   Oligoarabinonucleotide SEQ ID NO:3.
XX
KW   Beta-D-arabinose; antisense; inhibition; transcription; expression;
KW   reverse transcription; viral replication; RNase H cleavage;
KW   triple helix formation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .18
FT                   /*tag=  a
FT                   /note= "Ribose moiety replaced by beta-D-arabinose"
XX
PN   WO9967378-A1.
XX
PD   29-DEC-1999.
XX
PF   17-JUN-1999;   99WO-CA000571.
XX
PR   19-JUN-1998;   98CA-02241361.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Parniak MA,  Noronha AM,  Wilds C,  Borkow G,  Arion D;
XX
DR   WPI; 2000-160584/14.
XX
PT   Therapeutic composition containing antisense oligonucleotides that
PT   include arabinose sugars, particularly for inhibiting viral replication.
XX
PS   Example 1; Page 29; 91pp; English.
XX
CC   The invention relates to a new composition for selective, sequence-
CC   specific inhibition of gene transcription and expression in a host. The
CC   composition comprises oligonucleotides containing arabinose sugars that
CC   can hybridise to either a a single-stranded (ss) RNA to induce RNase H
CC   cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple
CC   helix, thereby inhibiting DNA replication and/or transcription. The
CC   oligoarabinonucleotides are used for antisense inhibition of gene
CC   expression or to prevent DNA replication, or reverse transcription of RNA
CC   by retroviruses. The compositions are therefore particularly used to
CC   inhibit retroviral replication. The oligoarabinonucleotides can also be
CC   used, in combination with RNase H, as reagents for sequence-specific
CC   cleavage or RNA mapping, and additionally for the study and control of
CC   gene expression in cells. The oligoarabinonucleotides have excellent
CC   affinity for RNA, increased resistance to nucleases and show little if
CC   any non-specific binding to cellular or serum proteins. They target ss
CC   RNA, but not complementary ss DNA, so may be useful for targetting
CC   retroviral genomic RNA to inhibit the early stages of viral replication.
CC   Oligoarabinonucleotides containing pyrimidine bases form triple helices
CC   with significantly higher thermal stability than those produced by normal
CC   oligonucleotides. Sequences AAZ87160-Z87164 represent
CC   oligoarabinonucleotides containing beta-D-arabinose used in an
CC   exemplification of the present invention
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 0 T; 18 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2803
              |||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAA 1


RESULT 1366
AAZ87166
ID   AAZ87166 standard; DNA; 18 BP.
XX
AC   AAZ87166;
XX
DT   08-MAY-2000  (first entry)
XX
DE   Deoxyarabinonucleotide SEQ ID NO:7.
XX
KW   2'-deoxy-2'-fluoro-beta-D-arabinose; antisense; inhibition;
KW   transcription; expression; reverse transcription; viral replication;
KW   RNase H cleavage; triple helix formation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .18
FT                   /*tag=  a
FT                   /note= "Deoxyribose moiety replaced by 2'-deoxy-2'-
FT                   fluoro-beta-D-arabinose"
XX
PN   WO9967378-A1.
XX
PD   29-DEC-1999.
XX
PF   17-JUN-1999;   99WO-CA000571.
XX
PR   19-JUN-1998;   98CA-02241361.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Parniak MA,  Noronha AM,  Wilds C,  Borkow G,  Arion D;
XX
DR   WPI; 2000-160584/14.
XX
PT   Therapeutic composition containing antisense oligonucleotides that
PT   include arabinose sugars, particularly for inhibiting viral replication.
XX
PS   Example 2; Page 31; 91pp; English.
XX
CC   The invention relates to a new composition for selective, sequence-
CC   specific inhibition of gene transcription and expression in a host. The
CC   composition comprises oligonucleotides containing arabinose sugars that
CC   can hybridise to either a a single-stranded (ss) RNA to induce RNase H
CC   cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple
CC   helix, thereby inhibiting DNA replication and/or transcription. The
CC   oligoarabinonucleotides are used for antisense inhibition of gene
CC   expression or to prevent DNA replication, or reverse transcription of RNA
CC   by retroviruses. The compositions are therefore particularly used to
CC   inhibit retroviral replication. The oligoarabinonucleotides can also be
CC   used, in combination with RNase H, as reagents for sequence-specific
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CC cleavage or RNA mapping, and additionally for the study and control of
CC gene expression in cells. The oligoarabinonucleotides have excellent
CC affinity for RNA, increased resistance to nucleases and show little if
CC any non-specific binding to cellular or serum proteins. They target ss
CC RNA, but not complementary ss DNA, so may be useful for targetting
CC retroviral genomic RNA to inhibit the early stages of viral replication.
CC Oligoarabinonucleotides containing pyrimidine bases form triple helices
CC with significantly higher thermal stability than those produced by normal
CC oligonucleotides. Sequences AAZ87165-Z87169 represent
CC oligodeoxyarabinonucleotides containing 2'-deoxy-2'fluoro-beta-D-
CC arabinose used in an exemplification of the present invention
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTT 2183
||||||||||||||||||
Db 1 TTTTTTTTTTTTTTTTTT 18

RESULT 1367
AAZ87166/c
ID AAZ87166 standard; DNA; 18 BP.
XX
AC AAZ87166;
XX
DT 08-MAY-2000 (first entry)
XX
DE Deoxyarabinonucleotide SEQ ID NO:7.
XX
KW 2'-deoxy-2'-fluoro-beta-D-arabinose; antisense; inhibition;
KW transcription; expression; reverse transcription; viral replication;
KW RNase H cleavage; triple helix formation; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1. .18
FT /*tag= a
FT /note= "Deoxyribose moiety replaced by 2'-deoxy-2'-
FT fluoro-beta-D-arabinose"
XX
PN WO9967378-A1.
XX
PD 29-DEC-1999.
XX
PF 17-JUN-1999; 99WO-CA000571.
XX
PR 19-JUN-1998; 98CA-02241361.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Damha MJ, Parniak MA, Noronha AM, Wilds C, Borkow G, Arion D;
XX
DR WPI; 2000-160584/14.
XX
PT Therapeutic composition containing antisense oligonucleotides that
PT include arabinose sugars, particularly for inhibiting viral replication.
XX
PS Example 2; Page 31; 91pp; English.
XX
CC The invention relates to a new composition for selective, sequence-
CC specific inhibition of gene transcription and expression in a host. The
CC composition comprises oligonucleotides containing arabinose sugars that
CC can hybridise to either a a single-stranded (ss) RNA to induce RNase H
CC cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple
CC helix, thereby inhibiting DNA replication and/or transcription. The
CC oligoarabinonucleotides are used for antisense inhibition of gene
CC expression or to prevent DNA replication, or reverse transcription of RNA
CC by retroviruses. The compositions are therefore particularly used to
CC inhibit retroviral replication. The oligoarabinonucleotides can also be
CC used, in combination with RNase H, as reagents for sequence-specific
CC cleavage or RNA mapping, and additionally for the study and control of
CC gene expression in cells. The oligoarabinonucleotides have excellent
CC affinity for RNA, increased resistance to nucleases and show little if
CC any non-specific binding to cellular or serum proteins. They target ss
CC RNA, but not complementary ss DNA, so may be useful for targetting
CC retroviral genomic RNA to inhibit the early stages of viral replication.
CC Oligoarabinonucleotides containing pyrimidine bases form triple helices
CC with significantly higher thermal stability than those produced by normal
CC oligonucleotides. Sequences AAZ87165-Z87169 represent
CC oligodeoxyarabinonucleotides containing 2'-deoxy-2'fluoro-beta-D-
CC arabinose used in an exemplification of the present invention
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2803
||||||||||||||||||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1368
AAZ87167
ID AAZ87167 standard; DNA; 18 BP.
XX
AC AAZ87167;
XX
DT 08-MAY-2000 (first entry)
XX
DE Deoxyarabinonucleotide SEQ ID NO:8.
XX
KW 2'-deoxy-2'-fluoro-beta-D-arabinose; antisense; inhibition;
KW transcription; expression; reverse transcription; viral replication;
KW RNase H cleavage; triple helix formation; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1. .18
FT /*tag= a
FT /note= "Deoxyribose moiety replaced by 2'-deoxy-2'-
FT fluoro-beta-D-arabinose"
XX
PN WO9967378-A1.
XX
PD 29-DEC-1999.
XX
PF 17-JUN-1999; 99WO-CA000571.
XX
PR 19-JUN-1998; 98CA-02241361.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Damha MJ, Parniak MA, Noronha AM, Wilds C, Borkow G, Arion D;
XX
DR WPI; 2000-160584/14.
XX
PT Therapeutic composition containing antisense oligonucleotides that
PT include arabinose sugars, particularly for inhibiting viral replication.
XX
PS Example 2; Page 31; 91pp; English.
XX
CC The invention relates to a new composition for selective, sequence-
CC specific inhibition of gene transcription and expression in a host. The
CC composition comprises oligonucleotides containing arabinose sugars that
CC can hybridise to either a a single-stranded (ss) RNA to induce RNase H
CC cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple
CC helix, thereby inhibiting DNA replication and/or transcription. The
CC oligoarabinonucleotides are used for antisense inhibition of gene

```
CC   expression or to prevent DNA replication, or reverse transcription of RNA
CC   by retroviruses. The compositions are therefore particularly used to
CC   inhibit retroviral replication. The oligoarabinonucleotides can also be
CC   used, in combination with RNase H, as reagents for sequence-specific
CC   cleavage or RNA mapping, and additionally for the study and control of
CC   gene expression in cells. The oligoarabinonucleotides have excellent
CC   affinity for RNA, increased resistance to nucleases and show little if
CC   any non-specific binding to cellular or serum proteins. They target ss
CC   RNA, but not complementary ss DNA, so may be useful for targetting
CC   retroviral genomic RNA to inhibit the early stages of viral replication.
CC   Oligoarabinonucleotides containing pyrimidine bases form triple helices
CC   with significantly higher thermal stability than those produced by normal
CC   oligonucleotides. Sequences AAZ87165-Z87169 represent
CC   oligodeoxyarabinonucleotides containing 2'-deoxy-2'fluoro-beta-D-
CC   arabinose used in an exemplification of the present invention
XX
SQ   Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
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Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 1369
AAZ87167/c
ID   AAZ87167 standard; DNA; 18 BP.
XX
AC   AAZ87167;
XX
DT   08-MAY-2000  (first entry)
XX
DE   Deoxyarabinonucleotide SEQ ID NO:8.
XX
KW   2'-deoxy-2'-fluoro-beta-D-arabinose; antisense; inhibition;
KW   transcription; expression; reverse transcription; viral replication;
KW   RNase H cleavage; triple helix formation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .18
FT                    /*tag= a
FT                    /note= "Deoxyribose moiety replaced by 2'-deoxy-2'-
FT                    fluoro-beta-D-arabinose"
XX
PN   WO9967378-A1.
XX
PD   29-DEC-1999.
XX
PF   17-JUN-1999;   99WO-CA000571.
XX
PR   19-JUN-1998;   98CA-02241361.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Parniak MA,  Noronha AM,  Wilds C,  Borkow G,  Arion D;
XX
DR   WPI; 2000-160584/14.
XX
PT   Therapeutic composition containing antisense oligonucleotides that
PT   include arabinose sugars, particularly for inhibiting viral replication.
XX
PS   Example 2; Page 31; 91pp; English.
XX
CC   The invention relates to a new composition for selective, sequence-
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CC   can hybridise to either a a single-stranded (ss) RNA to induce RNase H
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CC   helix, thereby inhibiting DNA replication and/or transcription. The
CC   oligoarabinonucleotides are used for antisense inhibition of gene
CC   expression or to prevent DNA replication, or reverse transcription of RNA
CC   by retroviruses. The compositions are therefore particularly used to
CC   inhibit retroviral replication. The oligoarabinonucleotides can also be
CC   used, in combination with RNase H, as reagents for sequence-specific
CC   cleavage or RNA mapping, and additionally for the study and control of
CC   gene expression in cells. The oligoarabinonucleotides have excellent
CC   affinity for RNA, increased resistance to nucleases and show little if
CC   any non-specific binding to cellular or serum proteins. They target ss
CC   RNA, but not complementary ss DNA, so may be useful for targetting
CC   retroviral genomic RNA to inhibit the early stages of viral replication.
CC   Oligoarabinonucleotides containing pyrimidine bases form triple helices
CC   with significantly higher thermal stability than those produced by normal
CC   oligonucleotides. Sequences AAZ87165-Z87169 represent
CC   oligodeoxyarabinonucleotides containing 2'-deoxy-2'fluoro-beta-D-
CC   arabinose used in an exemplification of the present invention
XX
SQ   Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db            18 TTTTTTTTTTTTTTTTTT 1


RESULT 1370
AAD03565
ID   AAD03565 standard; DNA; 18 BP.
XX
AC   AAD03565;
XX
DT   19-JUN-2001  (first entry)
XX
DE   Oligonucleotide #6 used for the preparation of normalised cDNA libraries.
XX
KW   Rat; secreted factor; clone P00188_D12; cardiant; antiinflammatory;
KW   antiarrhythmic; antiarteriosclerotic; antiatherosclerotic; nephropathic;
KW   antidiabetic; immunosuppressive; antiasthmatic; antirheumatoid;
KW   antibacterial; osteopathic; cerebroprotective; vasotropic; antiulcer;
KW   nootropic; neuroprotective; congestive heart failure; myocarditis;
KW   hypertrophic cardiomyopathy; angina pectoris; myocardial infarction;
KW   kidney disease; acute renal failure; renal glucosuria; renal infarction;
KW   polycystic kidney disease; hereditary nephritis; inflammatory disease;
KW   tumour angiogenesis; osteoarthritis; toxic shock syndrome; psoriasis;
KW   stroke; neural trauma; cerebral malaria; Crohn's disease; osteoporosis;
KW   ulcerative colitis; Alzheimer's disease; gene therapy; ss.
XX
OS   Rattus norvegicus.
XX
PN   WO200123564-A1.
XX
PD   05-APR-2001.
XX
PF   27-SEP-2000; 2000WO-US026544.
XX
PR   27-SEP-1999;   99US-0156280P.
XX
PA   (SCIO-) SCIOS INC.
XX
PI   Stanton LW,  Kapoun AM;
XX
DR   WPI; 2001-266159/27.
XX
PT   Novel secreted factor encoded by clone P00188D12 which is differentially
PT   expressed in certain disease states, useful in diagnosing and treating
PT   cardiac, renal or inflammatory diseases.
XX
PS   Example 1; Page 42; 71pp; English.
XX
```

```
CC   The patent discloses novel secreted factor protein encoded by clone
CC   P00188_D12. The secreted factor is differentially expressed in certain
CC   disease states. Secreted protein, its antibodies, antagonists or
CC   compositions comprising them are useful in the diagnosis and treatment of
CC   cardiac diseases such as congestive heart failure, myocarditis,
CC   hypertrophic cardiomyopathy, angina pectoris, myocardial infarction,
CC   cardiac arrhythmia, arteriosclerosis, kidney diseases such as acute renal
CC   failure, renal glucosuria, renal infarction, nephrogenic diabetes
CC   insipidus, polycystic kidney disease, hereditary nephritis and
CC   inflammatory diseases such as asthma, autoimmune diabetes, tumour
CC   angiogenesis, rheumatoid arthritis, osteoarthritis, toxic shock syndrome,
CC   asthma, stroke, neural trauma, psoriasis, cerebral malaria, osteoporosis,
CC   Crohn's disease, ulcerative colitis, Alzheimer's disease. Secreted
CC   protein DNA is useful in antisense-mediated gene inhibition and in gene
CC   therapy. An array comprising one or more oligonucleotides complementary
CC   to reference RNA or DNA encoding the secreted factor is useful for
CC   detecting cardiac, kidney and inflammatory disease. The present DNA
CC   sequence is an oligonucleotide which is used in the preparation of a
CC   normalised cDNA library containing secreted factor DNAs. The normalised
CC   cDNA libraries are used in the identification of differentially expressed
CC   rat secreted factor P00188_D12 gene
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1371
AAD03565/c
ID   AAD03565 standard; DNA; 18 BP.
XX
AC   AAD03565;
XX
DT   19-JUN-2001  (first entry)
XX
DE   Oligonucleotide #6 used for the preparation of normalised cDNA libraries.
XX
KW   Rat; secreted factor; clone P00188_D12; cardiant; antiinflammatory;
KW   antiarrhythmic; antiarteriosclerotic; antiatherosclerotic; nephropathic;
KW   antidiabetic; immunosuppressive; antiasthmatic; antirheumatoid;
KW   antibacterial; osteopathic; cerebroprotective; vasotropic; antiulcer;
KW   nootropic; neuroprotective; congestive heart failure; myocarditis;
KW   hypertrophic cardiomyopathy; angina pectoris; myocardial infarction;
KW   kidney disease; acute renal failure; renal glucosuria; renal infarction;
KW   polycystic kidney disease; hereditary nephritis; inflammatory disease;
KW   tumour angiogenesis; osteoarthritis; toxic shock syndrome; psoriasis;
KW   stroke; neural trauma; cerebral malaria; Crohn's disease; osteoporosis;
KW   ulcerative colitis; Alzheimer's disease; gene therapy; ss.
XX
OS   Rattus norvegicus.
XX
PN   WO200123564-A1.
XX
PD   05-APR-2001.
XX
PF   27-SEP-2000; 2000WO-US026544.
XX
PR   27-SEP-1999;   99US-0156280P.
XX
PA   (SCIO-) SCIOS INC.
XX
PI   Stanton LW,  Kapoun AM;
XX
DR   WPI; 2001-266159/27.
XX
PT   Novel secreted factor encoded by clone P00188D12 which is differentially
PT   expressed in certain disease states, useful in diagnosing and treating
PT   cardiac, renal or inflammatory diseases.
XX
PS   Example 1; Page 42; 71pp; English.
XX
CC   The patent discloses novel secreted factor protein encoded by clone
CC   P00188_D12. The secreted factor is differentially expressed in certain
CC   disease states. Secreted protein, its antibodies, antagonists or
CC   compositions comprising them are useful in the diagnosis and treatment of
CC   cardiac diseases such as congestive heart failure, myocarditis,
CC   hypertrophic cardiomyopathy, angina pectoris, myocardial infarction,
CC   cardiac arrhythmia, arteriosclerosis, kidney diseases such as acute renal
CC   failure, renal glucosuria, renal infarction, nephrogenic diabetes
CC   insipidus, polycystic kidney disease, hereditary nephritis and
CC   inflammatory diseases such as asthma, autoimmune diabetes, tumour
CC   angiogenesis, rheumatoid arthritis, osteoarthritis, toxic shock syndrome,
CC   asthma, stroke, neural trauma, psoriasis, cerebral malaria, osteoporosis,
CC   Crohn's disease, ulcerative colitis, Alzheimer's disease. Secreted
CC   protein DNA is useful in antisense-mediated gene inhibition and in gene
CC   therapy. An array comprising one or more oligonucleotides complementary
CC   to reference RNA or DNA encoding the secreted factor is useful for
CC   detecting cardiac, kidney and inflammatory disease. The present DNA
CC   sequence is an oligonucleotide which is used in the preparation of a
CC   normalised cDNA library containing secreted factor DNAs. The normalised
CC   cDNA libraries are used in the identification of differentially expressed
CC   rat secreted factor P00188_D12 gene
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1372
AAD17014
ID   AAD17014 standard; DNA; 18 BP.
XX
AC   AAD17014;
XX
DT   29-NOV-2001  (first entry)
XX
DE   Oligonucleotide A18-2PEG linker.
XX
KW   Scaffold protein; antibody mimic; fibronectin type III domain;
KW   randomised loop; randomised beta-sheet; diagnostic purpose;
KW   protein designing; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    18
FT                   /*tag=  a
FT                   /note= "Linked to (PEG)2CCPuromycin"
XX
PN   WO200164942-A1.
XX
PD   07-SEP-2001.
XX
PF   28-FEB-2001; 2001WO-US006414.
XX
PR   29-FEB-2000; 2000US-00515260.
XX
PA   (PHYL-) PHYLOS INC.
XX
PI   Lipovsek D,  Wagner RW,  Kuimelis RG;
XX
DR   WPI; 2001-557782/62.
XX
PT   Fibronectin scaffold protein array for obtaining a protein/compound which
```

```
PT   binds to a compound/protein, comprises a fibronectin type III domain
PT   having a randomized loop, a randomized beta-sheet or their combination.
XX
PS   Disclosure; Page 25; 67pp; English.
XX
CC   The present invention relates to an array of proteins (antibody mimics)
CC   comprising a fibronectin type III domain having a randomised loop, a
CC   randomised beta-sheet, or their combination, and has the capacity to bind
CC   to a compound that is not bound by a corresponding naturally- occurring
CC   fibronectin, immobilised onto a solid support. The antibody mimics is
CC   useful for detecting a compound preferably a protein, in a biological
CC   sample. It is also useful to detect one or more different analytes
CC   simultaneously in a sample. Hence is useful for diagnostic purposes. It
CC   is also useful for the purpose of designing proteins capable of binding
CC   to virtually any compound of interest. The present sequence is an
CC   oligonucleotide A18-2PEG linker used in an exemplification of the
CC   invention
XX
SQ   Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 1373
AAD17014/c
ID   AAD17014 standard; DNA; 18 BP.
XX
AC   AAD17014;
XX
DT   29-NOV-2001  (first entry)
XX
DE   Oligonucleotide A18-2PEG linker.
XX
KW   Scaffold protein; antibody mimic; fibronectin type III domain;
KW   randomised loop; randomised beta-sheet; diagnostic purpose;
KW   protein designing; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    18
FT                   /*tag=  a
FT                   /note= "Linked to (PEG)2CCPuromycin"
XX
PN   WO200164942-A1.
XX
PD   07-SEP-2001.
XX
PF   28-FEB-2001; 2001WO-US006414.
XX
PR   29-FEB-2000; 2000US-00515260.
XX
PA   (PHYL-) PHYLOS INC.
XX
PI   Lipovsek D,  Wagner RW,  Kuimelis RG;
XX
DR   WPI; 2001-557782/62.
XX
PT   Fibronectin scaffold protein array for obtaining a protein/compound which
PT   binds to a compound/protein, comprises a fibronectin type III domain
PT   having a randomized loop, a randomized beta-sheet or their combination.
XX
PS   Disclosure; Page 25; 67pp; English.
XX
CC   The present invention relates to an array of proteins (antibody mimics)
CC   comprising a fibronectin type III domain having a randomised loop, a
CC   randomised beta-sheet, or their combination, and has the capacity to bind
CC   to a compound that is not bound by a corresponding naturally- occurring
CC   fibronectin, immobilised onto a solid support. The antibody mimics is
CC   useful for detecting a compound preferably a protein, in a biological
CC   sample. It is also useful to detect one or more different analytes
CC   simultaneously in a sample. Hence is useful for diagnostic purposes. It
CC   is also useful for the purpose of designing proteins capable of binding
CC   to virtually any compound of interest. The present sequence is an
CC   oligonucleotide A18-2PEG linker used in an exemplification of the
CC   invention
XX
SQ   Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db         18 TTTTTTTTTTTTTTTTTT 1


RESULT 1374
AAF75598/c
ID   AAF75598 standard; DNA; 18 BP.
XX
AC   AAF75598;
XX
DT   10-MAY-2001  (first entry)
XX
DE   Binary encoded sequence tag method anchored primer #3.
XX
KW   Binary encoded sequence tag; BEST; nucleic acid analysis;
KW   gene expression; adaptor; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO200112855-A2.
XX
PD   22-FEB-2001.
XX
PF   11-AUG-2000; 2000WO-US022164.
XX
PR   13-AUG-1999;   99US-0148870P.
PR   06-APR-2000; 2000US-00544713.
XX
PA   (UYYA ) UNIV YALE.
XX
PI   Kaufman JC,  Roth ME,  Lizardi PM,  Feng L,  Latimer DR;
XX
DR   WPI; 2001-202878/20.
XX
PT   Producing binary sequence tags, useful for analyzing nucleic acid
PT   sequence tags, gene expression or gene-expression patterns, involves
PT   generating nucleic acid fragments, which are mixed with offset adaptors
PT   and adaptor-indexers.
XX
PS   Disclosure; Page 101; 101pp; English.
XX
CC   The present invention describes a method of producing binary sequence
CC   tags from nucleic acid fragments in a sample, involving incubating the
CC   sample with cleaving reagents, mixing offset adaptors with the sample,
CC   incubating with more cleaving reagents and mixing the sample with adaptor
CC   -indexers where the adaptors are coupled to binary sequence tags. The
CC   method is useful in sequence analysis, including analysis and comparison
CC   of gene expression, nucleic acid samples and genomes
XX
SQ   Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAA 2801
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                  ||||||||||||||||||
Db         18 TGAAAAAAAAAAAAAAAA 1


RESULT 1375
AAF99708
ID   AAF99708 standard; DNA; 18 BP.
XX
AC   AAF99708;
XX
DT   12-JUN-2001  (first entry)
XX
DE   Immunostimulatory nucleic acid #824.
XX
KW   Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW   immunostimulatory; tumour; viral infection; bacterial infection;
KW   fungal infection; parasitic infection; cancer; asthma;
KW   infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS   Synthetic.
XX
PN   WO200122972-A2.
XX
PD   05-APR-2001.
XX
PF   25-SEP-2000; 2000WO-US026383.
XX
PR   25-SEP-1999;   99US-0156113P.
PR   27-SEP-1999;   99US-0156135P.
PR   23-AUG-2000; 2000US-0227436P.
XX
PA   (IOWA ) UNIV IOWA RES FOUND.
PA   (COLE-) COLEY PHARM GMBH.
XX
PI   Krieg AM,  Schetter C,  Vollmer J;
XX
DR   WPI; 2001-273485/28.
XX
PT   Vaccinating against tumors, infectious diseases, allergies and asthma
PT   using immunostimulatory Py-rich and TG nucleic acids.
XX
PS   Claim 101; Page 56; 338pp; English.
XX
CC   The present invention relates to a method for stimulating an immune
CC   response. The method comprises administering an immunostimulatory nucleic
CC   acid to a non-rodent subject in sufficient quantity to stimulate an
CC   immune response. The present sequence is one such immunostimulatory
CC   nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC   (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC   against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC   and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC   haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC   staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC   also useful for preventing cancer, asthma, infectious disease, allergy or
CC   immune deficiency. The present sequence can also be used to redirect a
CC   Th2 to a Th1 immune response and to activate immune cells. Note: the
CC   present sequence may have a phosphorothioate backbone
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1376
AAF99708/c
ID   AAF99708 standard; DNA; 18 BP.
XX
AC   AAF99708;
XX
DT   12-JUN-2001  (first entry)
XX
DE   Immunostimulatory nucleic acid #824.
XX
KW   Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW   immunostimulatory; tumour; viral infection; bacterial infection;
KW   fungal infection; parasitic infection; cancer; asthma;
KW   infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS   Synthetic.
XX
PN   WO200122972-A2.
XX
PD   05-APR-2001.
XX
PF   25-SEP-2000; 2000WO-US026383.
XX
PR   25-SEP-1999;   99US-0156113P.
PR   27-SEP-1999;   99US-0156135P.
PR   23-AUG-2000; 2000US-0227436P.
XX
PA   (IOWA ) UNIV IOWA RES FOUND.
PA   (COLE-) COLEY PHARM GMBH.
XX
PI   Krieg AM,  Schetter C,  Vollmer J;
XX
DR   WPI; 2001-273485/28.
XX
PT   Vaccinating against tumors, infectious diseases, allergies and asthma
PT   using immunostimulatory Py-rich and TG nucleic acids.
XX
PS   Claim 101; Page 56; 338pp; English.
XX
CC   The present invention relates to a method for stimulating an immune
CC   response. The method comprises administering an immunostimulatory nucleic
CC   acid to a non-rodent subject in sufficient quantity to stimulate an
CC   immune response. The present sequence is one such immunostimulatory
CC   nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC   (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC   against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC   and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC   haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC   staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC   also useful for preventing cancer, asthma, infectious disease, allergy or
CC   immune deficiency. The present sequence can also be used to redirect a
CC   Th2 to a Th1 immune response and to activate immune cells. Note: the
CC   present sequence may have a phosphorothioate backbone
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db          18 AAAAAAAAAAAAAAAAAA 1


RESULT 1377
AAF99734
ID   AAF99734 standard; DNA; 18 BP.
XX
AC   AAF99734;
XX
DT   12-JUN-2001  (first entry)
XX
DE   Immunostimulatory nucleic acid #850.
XX
KW   Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW   immunostimulatory; tumour; viral infection; bacterial infection;
```

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KW   fungal infection; parasitic infection; cancer; asthma;
KW   infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS   Synthetic.
XX
PN   WO200122972-A2.
XX
PD   05-APR-2001.
XX
PF   25-SEP-2000; 2000WO-US026383.
XX
PR   25-SEP-1999;   99US-0156113P.
PR   27-SEP-1999;   99US-0156135P.
PR   23-AUG-2000; 2000US-0227436P.
XX
PA   (IOWA ) UNIV IOWA RES FOUND.
PA   (COLE-) COLEY PHARM GMBH.
XX
PI   Krieg AM,  Schetter C,  Vollmer J;
XX
DR   WPI; 2001-273485/28.
XX
PT   Vaccinating against tumors, infectious diseases, allergies and asthma
PT   using immunostimulatory Py-rich and TG nucleic acids.
XX
PS   Claim 101; Page 56; 338pp; English.
XX
CC   The present invention relates to a method for stimulating an immune
CC   response. The method comprises administering an immunostimulatory nucleic
CC   acid to a non-rodent subject in sufficient quantity to stimulate an
CC   immune response. The present sequence is one such immunostimulatory
CC   nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC   (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC   against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC   and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC   haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC   staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC   also useful for preventing cancer, asthma, infectious disease, allergy or
CC   immune deficiency. The present sequence can also be used to redirect a
CC   Th2 to a Th1 immune response and to activate immune cells. Note: the
CC   present sequence may have a phosphorothioate backbone
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1378
AAF99734/c
ID   AAF99734 standard; DNA; 18 BP.
XX
AC   AAF99734;
XX
DT   12-JUN-2001  (first entry)
XX
DE   Immunostimulatory nucleic acid #850.
XX
KW   Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW   immunostimulatory; tumour; viral infection; bacterial infection;
KW   fungal infection; parasitic infection; cancer; asthma;
KW   infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS   Synthetic.
XX
PN   WO200122972-A2.
XX
PD   05-APR-2001.
XX
PF   25-SEP-2000; 2000WO-US026383.
XX
PR   25-SEP-1999;   99US-0156113P.
PR   27-SEP-1999;   99US-0156135P.
PR   23-AUG-2000; 2000US-0227436P.
XX
PA   (IOWA ) UNIV IOWA RES FOUND.
PA   (COLE-) COLEY PHARM GMBH.
XX
PI   Krieg AM,  Schetter C,  Vollmer J;
XX
DR   WPI; 2001-273485/28.
XX
PT   Vaccinating against tumors, infectious diseases, allergies and asthma
PT   using immunostimulatory Py-rich and TG nucleic acids.
XX
PS   Claim 101; Page 56; 338pp; English.
XX
CC   The present invention relates to a method for stimulating an immune
CC   response. The method comprises administering an immunostimulatory nucleic
CC   acid to a non-rodent subject in sufficient quantity to stimulate an
CC   immune response. The present sequence is one such immunostimulatory
CC   nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC   (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC   against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC   and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC   haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC   staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC   also useful for preventing cancer, asthma, infectious disease, allergy or
CC   immune deficiency. The present sequence can also be used to redirect a
CC   Th2 to a Th1 immune response and to activate immune cells. Note: the
CC   present sequence may have a phosphorothioate backbone
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1379
AAF82472
ID   AAF82472 standard; DNA; 18 BP.
XX
AC   AAF82472;
XX
DT   29-JUN-2001  (first entry)
XX
DE   Phagemid vector pCR2.1 polylinker oligonucleotide #6.
XX
KW   Phagemid vector; pCR2.1; rat; secreted factor; P00210D09; cardiant;
KW   nephrotropic; antiinflammatory; gene therapy; cardiac disease;
KW   renal disease; inflammatory disease; polylinker; ss.
XX
OS   Synthetic.
XX
PN   WO200123419-A2.
XX
PD   05-APR-2001.
XX
PF   27-SEP-2000; 2000WO-US026582.
XX
PR   27-SEP-1999;   99US-0156277P.
XX
PA   (SCIO-) SCIOS INC.
XX
PI   Stanton LW,  Kapoun AM;
XX
```

```
DR   WPI; 2001-328177/34.
XX
PT   Novel secreted factor encoded by clone P00210D09 useful for diagnosing,
PT   treating and/or preventing various cardiac, renal and inflammatory
PT   diseases.
XX
PS   Example 1; Page 41; 69pp; English.
XX
CC   The present sequence corresponds to polylinker DNA of the phagemid vector
CC   pCR2.1. It was used in the construction of a normalised rat cDNA library,
CC   which was used in an example demonstrating differential expression of a
CC   rat gene referred to as clone P00210D09. The invention relates to a
CC   polypeptide comprising a sequence of at least 80% identity to residues 22
CC   -122 of the present sequence, or a sequence encoded by a nucleic acid
CC   hybridising under stringent conditions to the complement of the coding
CC   region comprising 1031 nucleotides, and having at least one biological
CC   activity of the polypeptide encoded by clone P00210D09. The polypeptides
CC   and polynucleotides of the invention are useful for the treatment of
CC   cardiac, renal and inflammatory diseases. The polynucleotides are useful
CC   in antisense mediated gene inhibition and in gene therapy. The
CC   polypeptides are useful in assays for identifying lead compounds that may
CC   be used as therapeutic agents in the treatment of cardiac, kidney or
CC   inflammatory diseases
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match              0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1380
AAF82472/c
ID   AAF82472 standard; DNA; 18 BP.
XX
AC   AAF82472;
XX
DT   29-JUN-2001  (first entry)
XX
DE   Phagemid vector pCR2.1 polylinker oligonucleotide #6.
XX
KW   Phagemid vector; pCR2.1; rat; secreted factor; P00210D09; cardiant;
KW   nephrotropic; antiinflammatory; gene therapy; cardiac disease;
KW   renal disease; inflammatory disease; polylinker; ss.
XX
OS   Synthetic.
XX
PN   WO200123419-A2.
XX
PD   05-APR-2001.
XX
PF   27-SEP-2000; 2000WO-US026582.
XX
PR   27-SEP-1999;   99US-0156277P.
XX
PA   (SCIO-) SCIOS INC.
XX
PI   Stanton LW,  Kapoun AM;
XX
DR   WPI; 2001-328177/34.
XX
PT   Novel secreted factor encoded by clone P00210D09 useful for diagnosing,
PT   treating and/or preventing various cardiac, renal and inflammatory
PT   diseases.
XX
PS   Example 1; Page 41; 69pp; English.
XX
CC   The present sequence corresponds to polylinker DNA of the phagemid vector
CC   pCR2.1. It was used in the construction of a normalised rat cDNA library,
CC   which was used in an example demonstrating differential expression of a
CC   rat gene referred to as clone P00210D09. The invention relates to a
CC   polypeptide comprising a sequence of at least 80% identity to residues 22
CC   -122 of the present sequence, or a sequence encoded by a nucleic acid
CC   hybridising under stringent conditions to the complement of the coding
CC   region comprising 1031 nucleotides, and having at least one biological
CC   activity of the polypeptide encoded by clone P00210D09. The polypeptides
CC   and polynucleotides of the invention are useful for the treatment of
CC   cardiac, renal and inflammatory diseases. The polynucleotides are useful
CC   in antisense mediated gene inhibition and in gene therapy. The
CC   polypeptides are useful in assays for identifying lead compounds that may
CC   be used as therapeutic agents in the treatment of cardiac, kidney or
CC   inflammatory diseases
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match              0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1381
AAS94743
ID   AAS94743 standard; DNA; 18 BP.
XX
AC   AAS94743;
XX
DT   12-MAR-2002  (first entry)
XX
DE   Rat secreted factor DNA oligonucleotide probe #6.
XX
KW   Rat; secreted factor polypeptide; cardiac disease; renal disease; kidney;
KW   inflammatory disease; congestive heart failure; myocarditis; asthma; ss;
KW   dilated congestive cardiomyopathy; angina pectoris; cardiac arrhythmia;
KW   myocardial infarction; pulmonary hypertension; arteriosclerosis; stroke;
KW   atherosclerosis; cardiac tumour; glomerulonephritis; nephrotic syndrome;
KW   renal infarction; hereditary nephritis; polycystic kidney disease;
KW   chronic renal failure; renal vein thrombosis; medullary sponge kidney;
KW   rheumatoid arthritis; osteoarthritis; psoriasis; restenosis; PCR primer;
KW   graft versus host reaction; Crohn's disease; ulcerative colitis; probe;
KW   Alzheimer's disease; gene therapy.
XX
OS   Synthetic.
XX
PN   WO200174901-A2.
XX
PD   11-OCT-2001.
XX
PF   23-MAR-2001; 2001WO-US009555.
XX
PR   31-MAR-2000; 2000US-0193548P.
PR   14-MAR-2001; 2001US-00809545.
XX
PA   (SCIO-) SCIOS INC.
XX
PI   Stanton LW,  White RT;
XX
DR   WPI; 2002-010779/01.
XX
PT   Novel secreted factor polypeptide useful for treating cardiac diseases
PT   such as arteriosclerosis, myocardial infarction, inflammatory diseases
PT   such as asthma, stroke, and rheumatoid arthritis and renal diseases.
XX
PS   Example 1; Page 51; 189pp; English.
XX
CC   The invention relates to rat secreted factor polypeptides and the
CC   polynucleotides encoding them. The sequences are useful for treating
CC   cardiac, renal or inflammatory diseases. These include cardiac diseases
CC   such as congestive heart failure, myocarditis, dilated congestive
```

```
CC   cardiomyopathy, angina pectoris, myocardial infarction, cardiac
CC   arrhythmia, pulmonary hypertension, arteriosclerosis, atherosclerosis and
CC   cardiac tumours, renal diseases such as glomerulonephritis, nephrotic
CC   syndrome, renal infarction, hereditary nephritis, polycystic kidney
CC   disease, chronic renal failure, renal vein thrombosis and medullary
CC   sponge kidney and inflammatory diseases such as asthma, rheumatoid
CC   arthritis, osteoarthritis, stroke, psoriasis, restenosis, graft versus
CC   host reaction, Crohn's disease, ulcerative colitis and Alzheimer's
CC   disease. Sequences AAS94693-AAS94745 represent cDNA clones, which encode
CC   the secreted factor polypeptides of the invention, and oligonucleotide
CC   probes and PCR primers
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1382
AAS94743/c
ID   AAS94743 standard; DNA; 18 BP.
XX
AC   AAS94743;
XX
DT   12-MAR-2002  (first entry)
XX
DE   Rat secreted factor DNA oligonucleotide probe #6.
XX
KW   Rat; secreted factor polypeptide; cardiac disease; renal disease; kidney;
KW   inflammatory disease; congestive heart failure; myocarditis; asthma; ss;
KW   dilated congestive cardiomyopathy; angina pectoris; cardiac arrhythmia;
KW   myocardial infarction; pulmonary hypertension; arteriosclerosis; stroke;
KW   atherosclerosis; cardiac tumour; glomerulonephritis; nephrotic syndrome;
KW   renal infarction; hereditary nephritis; polycystic kidney disease;
KW   chronic renal failure; renal vein thrombosis; medullary sponge kidney;
KW   rheumatoid arthritis; osteoarthritis; psoriasis; restenosis; PCR primer;
KW   graft versus host reaction; Crohn's disease; ulcerative colitis; probe;
KW   Alzheimer's disease; gene therapy.
XX
OS   Synthetic.
XX
PN   WO200174901-A2.
XX
PD   11-OCT-2001.
XX
PF   23-MAR-2001; 2001WO-US009555.
XX
PR   31-MAR-2000; 2000US-0193548P.
PR   14-MAR-2001; 2001US-00809545.
XX
PA   (SCIO-) SCIOS INC.
XX
PI   Stanton LW,  White RT;
XX
DR   WPI; 2002-010779/01.
XX
PT   Novel secreted factor polypeptide useful for treating cardiac diseases
PT   such as arteriosclerosis, myocardial infarction, inflammatory diseases
PT   such as asthma, stroke, and rheumatoid arthritis and renal diseases.
XX
PS   Example 1; Page 51; 189pp; English.
XX
CC   The invention relates to rat secreted factor polypeptides and the
CC   polynucleotides encoding them. The sequences are useful for treating
CC   cardiac, renal or inflammatory diseases. These include cardiac diseases
CC   such as congestive heart failure, myocarditis, dilated congestive
CC   cardiomyopathy, angina pectoris, myocardial infarction, cardiac
CC   arrhythmia, pulmonary hypertension, arteriosclerosis, atherosclerosis and
CC   cardiac tumours, renal diseases such as glomerulonephritis, nephrotic
CC   syndrome, renal infarction, hereditary nephritis, polycystic kidney
CC   disease, chronic renal failure, renal vein thrombosis and medullary
CC   sponge kidney and inflammatory diseases such as asthma, rheumatoid
CC   arthritis, osteoarthritis, stroke, psoriasis, restenosis, graft versus
CC   host reaction, Crohn's disease, ulcerative colitis and Alzheimer's
CC   disease. Sequences AAS94693-AAS94745 represent cDNA clones, which encode
CC   the secreted factor polypeptides of the invention, and oligonucleotide
CC   probes and PCR primers
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1383
ABS78455
ID   ABS78455 standard; DNA; 18 BP.
XX
AC   ABS78455;
XX
DT   13-DEC-2002  (first entry)
XX
DE   Angiogenesis inhibitory oligonucleotide #939.
XX
KW   Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW   tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW   diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW   corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW   rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW   plaque neovascularisation; telangiectasia; haemophiliac joint;
KW   angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW   scleroderma; hypertrophic scar.
XX
OS   Synthetic.
XX
PN   WO200253141-A2.
XX
PD   11-JUL-2002.
XX
PF   14-DEC-2001; 2001WO-US048458.
XX
PR   14-DEC-2000; 2000US-0255534P.
XX
PA   (COLE-) COLEY PHARM GROUP INC.
XX
PI   Bratzler RL;
XX
DR   WPI; 2002-566690/60.
XX
PT   Inhibiting angiogenesis in a subject, involves administering at least one
PT   antiangiogenic nucleic acid molecule to the subject.
XX
PS   Claim 2; Page 36; 276pp; English.
XX
CC   The invention relates to inhibiting angiogenesis in a subject, comprising
CC   administering at least one antiangiogenic nucleic acid molecule. Also
CC   included is a kit comprising a first container housing the antiangiogenic
CC   nucleic acids, and instructions for administering them to a subject
CC   having a condition characterised by unwanted angiogenesis. The method is
CC   useful for inhibiting angiogenesis associated with solid tumour growth,
CC   tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC   diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC   corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC   rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC   neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,
CC   wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
```

```
CC   hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC   acid of the invention
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1384
ABS78455/c
ID   ABS78455 standard; DNA; 18 BP.
XX
AC   ABS78455;
XX
DT   13-DEC-2002  (first entry)
XX
DE   Angiogenesis inhibitory oligonucleotide #939.
XX
KW   Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW   tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW   diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW   corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW   rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW   plaque neovascularisation; telangiectasia; haemophiliac joint;
KW   angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW   scleroderma; hypertrophic scar.
XX
OS   Synthetic.
XX
PN   WO200253141-A2.
XX
PD   11-JUL-2002.
XX
PF   14-DEC-2001; 2001WO-US048458.
XX
PR   14-DEC-2000; 2000US-0255534P.
XX
PA   (COLE-) COLEY PHARM GROUP INC.
XX
PI   Bratzler RL;
XX
DR   WPI; 2002-566690/60.
XX
PT   Inhibiting angiogenesis in a subject, involves administering at least one
PT   antiangiogenic nucleic acid molecule to the subject.
XX
PS   Claim 2; Page 36; 276pp; English.
XX
CC   The invention relates to inhibiting angiogenesis in a subject, comprising
CC   administering at least one antiangiogenic nucleic acid molecule. Also
CC   included is a kit comprising a first container housing the antiangiogenic
CC   nucleic acids, and instructions for administering them to a subject
CC   having a condition characterised by unwanted angiogenesis. The method is
CC   useful for inhibiting angiogenesis associated with solid tumour growth,
CC   tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC   diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC   corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC   rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC   neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,
CC   wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC   hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC   acid of the invention
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1385
ABS78429
ID   ABS78429 standard; DNA; 18 BP.
XX
AC   ABS78429;
XX
DT   13-DEC-2002  (first entry)
XX
DE   Angiogenesis inhibitory oligonucleotide #913.
XX
KW   Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW   tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW   diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW   corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW   rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW   plaque neovascularisation; telangiectasia; haemophiliac joint;
KW   angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW   scleroderma; hypertrophic scar.
XX
OS   Synthetic.
XX
PN   WO200253141-A2.
XX
PD   11-JUL-2002.
XX
PF   14-DEC-2001; 2001WO-US048458.
XX
PR   14-DEC-2000; 2000US-0255534P.
XX
PA   (COLE-) COLEY PHARM GROUP INC.
XX
PI   Bratzler RL;
XX
DR   WPI; 2002-566690/60.
XX
PT   Inhibiting angiogenesis in a subject, involves administering at least one
PT   antiangiogenic nucleic acid molecule to the subject.
XX
PS   Claim 2; Page 35; 276pp; English.
XX
CC   The invention relates to inhibiting angiogenesis in a subject, comprising
CC   administering at least one antiangiogenic nucleic acid molecule. Also
CC   included is a kit comprising a first container housing the antiangiogenic
CC   nucleic acids, and instructions for administering them to a subject
CC   having a condition characterised by unwanted angiogenesis. The method is
CC   useful for inhibiting angiogenesis associated with solid tumour growth,
CC   tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC   diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC   corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC   rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC   neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,
CC   wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC   hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC   acid of the invention
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18
```

```
RESULT 1386
ABS78429/c
ID   ABS78429 standard; DNA; 18 BP.
XX
AC   ABS78429;
XX
DT   13-DEC-2002  (first entry)
XX
DE   Angiogenesis inhibitory oligonucleotide #913.
XX
KW   Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW   tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW   diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW   corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW   rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW   plaque neovascularisation; telangiectasia; haemophiliac joint;
KW   angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW   scleroderma; hypertrophic scar.
XX
OS   Synthetic.
XX
PN   WO200253141-A2.
XX
PD   11-JUL-2002.
XX
PF   14-DEC-2001; 2001WO-US048458.
XX
PR   14-DEC-2000; 2000US-0255534P.
XX
PA   (COLE-) COLEY PHARM GROUP INC.
XX
PI   Bratzler RL;
XX
DR   WPI; 2002-566690/60.
XX
PT   Inhibiting angiogenesis in a subject, involves administering at least one
PT   antiangiogenic nucleic acid molecule to the subject.
XX
PS   Claim 2; Page 35; 276pp; English.
XX
CC   The invention relates to inhibiting angiogenesis in a subject, comprising
CC   administering at least one antiangiogenic nucleic acid molecule. Also
CC   included is a kit comprising a first container housing the antiangiogenic
CC   nucleic acids, and instructions for administering them to a subject
CC   having a condition characterised by unwanted angiogenesis. The method is
CC   useful for inhibiting angiogenesis associated with solid tumour growth,
CC   tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC   diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC   corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC   rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC   neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,
CC   wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC   hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC   acid of the invention
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1387
ABL39401
ID   ABL39401 standard; DNA; 18 BP.
XX
AC   ABL39401;
XX
DT   16-APR-2002  (first entry)
XX
DE   Immunostimulatory nucleic acid SEQ ID NO: 837.
XX
KW   Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
KW   angiogenesis; metastasis; cytostatic; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .18
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "phosphorothioate backbone"
XX
PN   WO200197843-A2.
XX
PD   27-DEC-2001.
XX
PF   22-JUN-2001; 2001WO-US020154.
XX
PR   22-JUN-2000; 2000US-0213346P.
XX
PA   (IOWA ) UNIV IOWA RES FOUND.
XX
PI   Weiner G,  Hartmann G;
XX
DR   WPI; 2002-154611/20.
XX
PT   Treating or preventing cancer, such as basal cell carcinoma, comprises
PT   administering immunostimulatory nucleic acids that induce expression of
PT   cell surface antigens and antibodies to a subject having or at risk of
PT   developing cancer.
XX
PS   Disclosure; Page 308; 312pp; English.
XX
CC   The present invention relates to methods for treating or preventing
CC   cancer, involving administering to a subject having or at risk of
CC   developing cancer immunostimulatory nucleic acids that induce expression
CC   of cell surface antigens and antibodies. The methods are useful for
CC   treating or preventing cancer such as basal cell carcinoma, bladder
CC   cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC   breast cancer, cervical cancer, colon and rectum cancer, connective
CC   tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx
CC   cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
CC   Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC   cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC   cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC   present sequence is an immunostimulatory oligonucleotide described in the
CC   exemplification of the invention
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1388
ABL39401/c
ID   ABL39401 standard; DNA; 18 BP.
XX
AC   ABL39401;
XX
DT   16-APR-2002  (first entry)
XX
DE   Immunostimulatory nucleic acid SEQ ID NO: 837.
XX
KW   Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
KW   angiogenesis; metastasis; cytostatic; ss.
```

```
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .18
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate backbone"
XX
PN   WO200197843-A2.
XX
PD   27-DEC-2001.
XX
PF   22-JUN-2001; 2001WO-US020154.
XX
PR   22-JUN-2000; 2000US-0213346P.
XX
PA   (IOWA ) UNIV IOWA RES FOUND.
XX
PI   Weiner G,  Hartmann G;
XX
DR   WPI; 2002-154611/20.
XX
PT   Treating or preventing cancer, such as basal cell carcinoma, comprises
PT   administering immunostimulatory nucleic acids that induce expression of
PT   cell surface antigens and antibodies to a subject having or at risk of
PT   developing cancer.
XX
PS   Disclosure; Page 308; 312pp; English.
XX
CC   The present invention relates to methods for treating or preventing
CC   cancer, involving administering to a subject having or at risk of
CC   developing cancer immunostimulatory nucleic acids that induce expression
CC   of cell surface antigens and antibodies. The methods are useful for
CC   treating or preventing cancer such as basal cell carcinoma, bladder
CC   cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC   breast cancer, cervical cancer, colon and rectum cancer, connective
CC   tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx
CC   cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
CC   Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC   cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC   cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC   present sequence is an immunostimulatory oligonucleotide described in the
CC   exemplification of the invention
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1389
AAD41497
ID   AAD41497 standard; DNA; 18 BP.
XX
AC   AAD41497;
XX
DT   30-OCT-2002  (first entry)
XX
DE   Oligonucleotide used for amplifying sea hare cyplasin L DNA.
XX
KW   Apoptosis; ion channel modulator; hyperproliferative disease; tumour;
KW   therapy; leukaemia; carcinoma; sarcoma; degenerative disease; melanoma;
KW   Alzheimer's disease; Parkinson's disease; arteriosclerosis;
KW   heart disease; stroke; vascular disease; nootropic; neuroprotective;
KW   cerebroprotective; cardiant; cytotoxic protein; cyplasin L; ss.
XX
OS   Unidentified.
XX
PN   WO200231144-A2.
XX
PD   18-APR-2002.
XX
PF   12-OCT-2001; 2001WO-EP011837.
XX
PR   13-OCT-2000; 2000EP-00122466.
XX
PA   (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI   Butzke D,  Machuy N,  Rudel T,  Meyer TF;
XX
DR   WPI; 2002-537205/57.
XX
PT   Novel polypeptide having cytotoxic activity obtainable from Aplysia,
PT   useful for destroying tumors, for identifying novel targets for the
PT   development of anti-tumor agents, and as specific ion channel modulators.
XX
PS   Example 5; Page 37; 87pp; English.
XX
CC   The present invention relates to novel polypeptides having cytotoxic
CC   activity obtainable from sea hare Aplysia. Sequences of the invention are
CC   useful for the manufacture of cytotoxic agents against apoptosis-
CC   resistant cells, where the agents are useful for diagnosis, prevention,
CC   treatment of disorders associated with dysfunctions of GAP-SH3 binding
CC   protein, factors for generating or detoxifying reactive oxygen species
CC   (ROS) and factors for blocking and/or by-passing of caspases. They are
CC   useful for tumour therapy. Cytotoxic proteins of the invention are useful
CC   for destroying tumours and/or selectively killing cells in tissues, for
CC   identifying novel targets for the development of pharmaceutical agents,
CC   preferably anti-tumour agents and as specific ion channel modulators,
CC   e.g., blockers or openers for therapy, diagnostic or research. They are
CC   useful for the diagnosis and therapy of hyperproliferative diseases,
CC   preferably tumours, e.g., leukaemia, carcinoma, sarcoma and melanoma.
CC   They are also useful for development of drugs for the treatment of
CC   degenerative diseases such as Alzheimer's disease, Parkinson's disease,
CC   arteriosclerosis, heart diseases, stroke and vascular diseases. The
CC   present sequence is an oligonucleotide which is used for amplifying sea
CC   hare cyplasin L DNA. This sequence is used in the exemplification of the
CC   invention
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1390
AAD41497/c
ID   AAD41497 standard; DNA; 18 BP.
XX
AC   AAD41497;
XX
DT   30-OCT-2002  (first entry)
XX
DE   Oligonucleotide used for amplifying sea hare cyplasin L DNA.
XX
KW   Apoptosis; ion channel modulator; hyperproliferative disease; tumour;
KW   therapy; leukaemia; carcinoma; sarcoma; degenerative disease; melanoma;
KW   Alzheimer's disease; Parkinson's disease; arteriosclerosis;
KW   heart disease; stroke; vascular disease; nootropic; neuroprotective;
KW   cerebroprotective; cardiant; cytotoxic protein; cyplasin L; ss.
XX
OS   Unidentified.
XX
PN   WO200231144-A2.
XX
```

PD 18-APR-2002.
XX
PF 12-OCT-2001; 2001WO-EP011837.
XX
PR 13-OCT-2000; 2000EP-00122466.
XX
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI Butzke D, Machuy N, Rudel T, Meyer TF;
XX
DR WPI; 2002-537205/57.
XX
PT Novel polypeptide having cytotoxic activity obtainable from Aplysia,
PT useful for destroying tumors, for identifying novel targets for the
PT development of anti-tumor agents, and as specific ion channel modulators.
XX
PS Example 5; Page 37; 87pp; English.
XX
CC The present invention relates to novel polypeptides having cytotoxic
CC activity obtainable from sea hare Aplysia. Sequences of the invention are
CC useful for the manufacture of cytotoxic agents against apoptosis-
CC resistant cells, where the agents are useful for diagnosis, prevention,
CC treatment of disorders associated with dysfunctions of GAP-SH3 binding
CC protein, factors for generating or detoxifying reactive oxygen species
CC (ROS) and factors for blocking and/or by-passing of caspases. They are
CC useful for tumour therapy. Cytotoxic proteins of the invention are useful
CC for destroying tumours and/or selectively killing cells in tissues, for
CC identifying novel targets for the development of pharmaceutical agents,
CC preferably anti-tumour agents and as specific ion channel modulators,
CC e.g., blockers or openers for therapy, diagnostic or research. They are
CC useful for the diagnosis and therapy of hyperproliferative diseases,
CC preferably tumours, e.g., leukaemia, carcinoma, sarcoma and melanoma.
CC They are also useful for development of drugs for the treatment of
CC degenerative diseases such as Alzheimer's disease, Parkinson's disease,
CC arteriosclerosis, heart diseases, stroke and vascular diseases. The
CC present sequence is an oligonucleotide which is used for amplifying sea
CC hare cyplasin L DNA. This sequence is used in the exemplification of the
CC invention
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2803
||||||||||||||||||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1391
ABS53437
ID ABS53437 standard; DNA; 18 BP.
XX
AC ABS53437;
XX
DT 29-NOV-2002 (first entry)
XX
DE Poly d(T) primer.
XX
KW Terminal continuation; TC; ss; second strand cDNA synthesis; primer;
KW poly d(T).
XX
OS Synthetic.
XX
PN WO200265093-A2.
XX
PD 22-AUG-2002.
XX
PF 14-FEB-2002; 2002WO-US005713.
XX
PR 14-FEB-2001; 2001US-0268645P.
PR 14-FEB-2001; 2001US-0268664P.
PR 18-JUL-2001; 2001US-0306216P.
PR 07-NOV-2001; 2001US-0344557P.
PR 07-NOV-2001; 2001US-0348242P.
PR 09-NOV-2001; 2001US-0350176P.
XX
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (REME-) RES FOUND MENTAL HYGIENE INC.
XX
PI Ginsberg SD, Che S;
XX
DR WPI; 2002-567050/60.
XX
PT Increasing efficiency of second strand cDNA synthesis using terminal
PT continuation model before performing further RNA amplification by RNA
PT transcription.
XX
PS Example 7; Page 80; 128pp; English.
XX
CC This invention relates to a novel method for increasing the efficiency of
CC second strand cDNA synthesis through a mechanism of terminal
CC continuation. In the method an RNA molecule is obtained and a first
CC primer is added that comprises a region that hybridises to a
CC complementary region of the molecule before a second primer is added
CC comprising at least one riboguanine at the 3' end of the primer. A first
CC complementary nucleic acid molecule is synthesised, the RNA molecule and
CC second primer are removed and a second complementary nucleic acid
CC molecule is synthesised to form a second hybrid with an extension product
CC of the third primer bound to the first complementary molecule. The method
CC of the invention is useful for increasing the efficiency of second strand
CC cDNA synthesis and may be used for linear amplification of genetic
CC signals from histologically stained tissue. The present sequence
CC represents a poly d(T) PCR primer used in the method of the invention
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTT 2183
||||||||||||||||||
Db 1 TTTTTTTTTTTTTTTTTT 18

RESULT 1392
ABS53437/c
ID ABS53437 standard; DNA; 18 BP.
XX
AC ABS53437;
XX
DT 29-NOV-2002 (first entry)
XX
DE Poly d(T) primer.
XX
KW Terminal continuation; TC; ss; second strand cDNA synthesis; primer;
KW poly d(T).
XX
OS Synthetic.
XX
PN WO200265093-A2.
XX
PD 22-AUG-2002.
XX
PF 14-FEB-2002; 2002WO-US005713.
XX
PR 14-FEB-2001; 2001US-0268645P.
PR 14-FEB-2001; 2001US-0268664P.
PR 18-JUL-2001; 2001US-0306216P.
PR 07-NOV-2001; 2001US-0344557P.
PR 07-NOV-2001; 2001US-0348242P.
PR 09-NOV-2001; 2001US-0350176P.
XX
PA (BAYU) BAYLOR COLLEGE MEDICINE.

```
PA   (REME-) RES FOUND MENTAL HYGIENE INC.
XX
PI   Ginsberg SD,  Che S;
XX
DR   WPI; 2002-567050/60.
XX
PT   Increasing efficiency of second strand cDNA synthesis using terminal
PT   continuation model before performing further RNA amplification by RNA
PT   transcription.
XX
PS   Example 7; Page 80; 128pp; English.
XX
CC   This invention relates to a novel method for increasing the efficiency of
CC   second strand cDNA synthesis through a mechanism of terminal
CC   continuation. In the method an RNA molecule is obtained and a first
CC   primer is added that comprises a region that hybridises to a
CC   complementary region of the molecule before a second primer is added
CC   comprising at least one riboguanine at the 3' end of the primer. A first
CC   complementary nucleic acid molecule is synthesised, the RNA molecule and
CC   second primer are removed and a second complementary nucleic acid
CC   molecule is synthesised to form a second hybrid with an extension product
CC   of the third primer bound to the first complementary molecule. The method
CC   of the invention is useful for increasing the efficiency of second strand
CC   cDNA synthesis and may be used for linear amplification of genetic
CC   signals from histologically stained tissue. The present sequence
CC   represents a poly d(T) PCR primer used in the method of the invention
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1393
ABA93239
ID   ABA93239 standard; DNA; 18 BP.
XX
AC   ABA93239;
XX
DT   18-APR-2002  (first entry)
XX
DE   Adaptor oligonucleotide SEQ ID NO:2.
XX
KW   Detection; comparative detection; adaptor; ss.
XX
OS   Synthetic.
XX
PN   JP2001333800-A.
XX
PD   04-DEC-2001.
XX
PF   30-MAY-2000; 2000JP-00160324.
XX
PR   30-MAY-2000; 2000JP-00160324.
XX
PA   (UNIT-) UNITECH CO LTD.
XX
DR   WPI; 2002-135950/18.
XX
PT   Comparative detection of the amounts of RNA and DNA.
XX
PS   Disclosure; Page 9; 9pp; Japanese.
XX
CC   The present invention describes a method for the comparative detection of
CC   the amount of an RNA. The method comprises: (a) cDNAs obtained by
CC   transcribing respectively from at least two tissue RNAs are respectively
CC   fragmented by using a same restriction enzyme; (b) each different adaptor
CC   and a common adaptor are added to each of the cDNA fragments derived from
CC   the same or different tissues by the step (a); (c) the resultant adaptor-
CC   added cDNAs are mixed together; (d) an adaptor primer having the common
CC   sequence to said different adaptor and a gene-specific adaptor are used
CC   to amplify said adaptor-added cDNAs containing no region derived from
CC   polyadenylic acid of the mRNA before the addition of the adaptor among
CC   the adaptor-added cDNAs prepared by the step (b); (e) the ratios of the
CC   cDNA amounts are measured between the tissues; (f) the RNA is detected
CC   from the measured result; (g) each different adaptor and a common adaptor
CC   are added to each of the genomic DNA fragments derived from a same or
CC   different individuals; (h) the resultant adaptor-added genomic DNAs are
CC   mixed together; (i) the adaptor-added genomic DNAs are amplified by using
CC   an adaptor primer having the common sequence to the different adaptor and
CC   a sequence-specific adaptor; and (j) the ratios of the amplified amounts
CC   of the genomic DNAs are measured between the individuals. The method is
CC   used for the detection of the amounts of RNA and DNA. The present
CC   sequence represents an oligonucleotide which is used in the
CC   exemplification of the present invention
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1394
ABA93239/c
ID   ABA93239 standard; DNA; 18 BP.
XX
AC   ABA93239;
XX
DT   18-APR-2002  (first entry)
XX
DE   Adaptor oligonucleotide SEQ ID NO:2.
XX
KW   Detection; comparative detection; adaptor; ss.
XX
OS   Synthetic.
XX
PN   JP2001333800-A.
XX
PD   04-DEC-2001.
XX
PF   30-MAY-2000; 2000JP-00160324.
XX
PR   30-MAY-2000; 2000JP-00160324.
XX
PA   (UNIT-) UNITECH CO LTD.
XX
DR   WPI; 2002-135950/18.
XX
PT   Comparative detection of the amounts of RNA and DNA.
XX
PS   Disclosure; Page 9; 9pp; Japanese.
XX
CC   The present invention describes a method for the comparative detection of
CC   the amount of an RNA. The method comprises: (a) cDNAs obtained by
CC   transcribing respectively from at least two tissue RNAs are respectively
CC   fragmented by using a same restriction enzyme; (b) each different adaptor
CC   and a common adaptor are added to each of the cDNA fragments derived from
CC   the same or different tissues by the step (a); (c) the resultant adaptor-
CC   added cDNAs are mixed together; (d) an adaptor primer having the common
CC   sequence to said different adaptor and a gene-specific adaptor are used
CC   to amplify said adaptor-added cDNAs containing no region derived from
CC   polyadenylic acid of the mRNA before the addition of the adaptor among
CC   the adaptor-added cDNAs prepared by the step (b); (e) the ratios of the
CC   cDNA amounts are measured between the tissues; (f) the RNA is detected
CC   from the measured result; (g) each different adaptor and a common adaptor
CC   are added to each of the genomic DNA fragments derived from a same or
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CC   different individuals; (h) the resultant adaptor-added genomic DNAs are
CC   mixed together; (i) the adaptor-added genomic DNAs are amplified by using
CC   an adaptor primer having the common sequence to the different adaptor and
CC   a sequence-specific adaptor; and (j) the ratios of the amplified amounts
CC   of the genomic DNAs are measured between the individuals. The method is
CC   used for the detection of the amounts of RNA and DNA. The present
CC   sequence represents an oligonucleotide which is used in the
CC   exemplification of the present invention
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1395
AAD56466
ID   AAD56466 standard; RNA; 18 BP.
XX
AC   AAD56466;
XX
DT   07-AUG-2003  (first entry)
XX
DE   Target RNA #1 used in the exemplification of the invention.
XX
KW   Acyclic linker; gene expression; gene therapy; ss.
XX
OS   Unidentified.
XX
PN   WO2003037909-A1.
XX
PD   08-MAY-2003.
XX
PF   29-OCT-2002; 2002WO-CA001628.
XX
PR   29-OCT-2001; 2001US-0330719P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Viazovkina E,  Mangos MM,  Parniak MA,  Min K;
XX
DR   WPI; 2003-421516/39.
XX
PT   Novel acyclic linker-containing oligonucleotide useful for preventing or
PT   decreasing translation, reverse transcription and/or replication of a
PT   target RNA in a system, comprises a modified deoxyribonucleotide.
XX
PS   Example 2; Fig 5; 104pp; English.
XX
CC   The invention relates to an acyclic linker-containing oligonucleotide
CC   comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC   the invention are useful for preventing or decreasing translation,
CC   reverse transcription and/or replication of a target RNA in a system.
CC   They are useful for selectively preventing gene expression in a sequence-
CC   specific manner, for hybridising to complementary RNA such as cellular
CC   mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC   RNA. They are also useful therapeutically in formulations or medicaments
CC   to prevent or treat a disease characterised by the expression of a
CC   particular target RNA. The invention is used in gene therapy. The present
CC   sequence is a target RNA, used in the exemplification of the invention
XX
SQ   Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1396
AAD56466/c
ID   AAD56466 standard; RNA; 18 BP.
XX
AC   AAD56466;
XX
DT   07-AUG-2003  (first entry)
XX
DE   Target RNA #1 used in the exemplification of the invention.
XX
KW   Acyclic linker; gene expression; gene therapy; ss.
XX
OS   Unidentified.
XX
PN   WO2003037909-A1.
XX
PD   08-MAY-2003.
XX
PF   29-OCT-2002; 2002WO-CA001628.
XX
PR   29-OCT-2001; 2001US-0330719P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Viazovkina E,  Mangos MM,  Parniak MA,  Min K;
XX
DR   WPI; 2003-421516/39.
XX
PT   Novel acyclic linker-containing oligonucleotide useful for preventing or
PT   decreasing translation, reverse transcription and/or replication of a
PT   target RNA in a system, comprises a modified deoxyribonucleotide.
XX
PS   Example 2; Fig 5; 104pp; English.
XX
CC   The invention relates to an acyclic linker-containing oligonucleotide
CC   comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC   the invention are useful for preventing or decreasing translation,
CC   reverse transcription and/or replication of a target RNA in a system.
CC   They are useful for selectively preventing gene expression in a sequence-
CC   specific manner, for hybridising to complementary RNA such as cellular
CC   mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC   RNA. They are also useful therapeutically in formulations or medicaments
CC   to prevent or treat a disease characterised by the expression of a
CC   particular target RNA. The invention is used in gene therapy. The present
CC   sequence is a target RNA, used in the exemplification of the invention
XX
SQ   Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db         18 TTTTTTTTTTTTTTTTTT 1


RESULT 1397
AAD56440
ID   AAD56440 standard; DNA; 18 BP.
XX
AC   AAD56440;
XX
DT   07-AUG-2003  (first entry)
XX
DE   Antisense oligo #1, to elicit RNase H degradation of target RNA.
XX
KW   Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
KW   antisense; ss.
```

```
XX
OS   Unidentified.
XX
PN   WO2003037909-A1.
XX
PD   08-MAY-2003.
XX
PF   29-OCT-2002; 2002WO-CA001628.
XX
PR   29-OCT-2001; 2001US-0330719P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Viazovkina E,  Mangos MM,  Parniak MA,  Min K;
XX
DR   WPI; 2003-421516/39.
XX
PT   Novel acyclic linker-containing oligonucleotide useful for preventing or
PT   decreasing translation, reverse transcription and/or replication of a
PT   target RNA in a system, comprises a modified deoxyribonucleotide.
XX
PS   Example 2; Fig 9; 104pp; English.
XX
CC   The invention relates to an acyclic linker-containing oligonucleotide
CC   comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC   the invention are useful for preventing or decreasing translation,
CC   reverse transcription and/or replication of a target RNA in a system.
CC   They are useful for selectively preventing gene expression in a sequence-
CC   specific manner, for hybridising to complementary RNA such as cellular
CC   mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC   RNA. They are also useful therapeutically in formulations or medicaments
CC   to prevent or treat a disease characterised by the expression of a
CC   particular target RNA. The invention is used in gene therapy. The present
CC   sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC   H degradation of target RNA. This sequence is used in the exemplification
CC   of the invention
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1398
AAD56440/c
ID   AAD56440 standard; DNA; 18 BP.
XX
AC   AAD56440;
XX
DT   07-AUG-2003  (first entry)
XX
DE   Antisense oligo #1, to elicit RNase H degradation of target RNA.
XX
KW   Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
KW   antisense; ss.
XX
OS   Unidentified.
XX
PN   WO2003037909-A1.
XX
PD   08-MAY-2003.
XX
PF   29-OCT-2002; 2002WO-CA001628.
XX
PR   29-OCT-2001; 2001US-0330719P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Viazovkina E,  Mangos MM,  Parniak MA,  Min K;
XX
DR   WPI; 2003-421516/39.
XX
PT   Novel acyclic linker-containing oligonucleotide useful for preventing or
PT   decreasing translation, reverse transcription and/or replication of a
PT   target RNA in a system, comprises a modified deoxyribonucleotide.
XX
PS   Example 2; Fig 9; 104pp; English.
XX
CC   The invention relates to an acyclic linker-containing oligonucleotide
CC   comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC   the invention are useful for preventing or decreasing translation,
CC   reverse transcription and/or replication of a target RNA in a system.
CC   They are useful for selectively preventing gene expression in a sequence-
CC   specific manner, for hybridising to complementary RNA such as cellular
CC   mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC   RNA. They are also useful therapeutically in formulations or medicaments
CC   to prevent or treat a disease characterised by the expression of a
CC   particular target RNA. The invention is used in gene therapy. The present
CC   sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC   H degradation of target RNA. This sequence is used in the exemplification
CC   of the invention
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1399
AAD56446
ID   AAD56446 standard; DNA; 18 BP.
XX
AC   AAD56446;
XX
DT   07-AUG-2003  (first entry)
XX
DE   2'F-ANA antisense oligo #1, to elicit RNase H degradation of target RNA.
XX
KW   Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
KW   antisense; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .18
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "2'-deoxy-2'-fluoroarabinothymidine"
XX
PN   WO2003037909-A1.
XX
PD   08-MAY-2003.
XX
PF   29-OCT-2002; 2002WO-CA001628.
XX
PR   29-OCT-2001; 2001US-0330719P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Viazovkina E,  Mangos MM,  Parniak MA,  Min K;
XX
DR   WPI; 2003-421516/39.
XX
PT   Novel acyclic linker-containing oligonucleotide useful for preventing or
PT   decreasing translation, reverse transcription and/or replication of a
PT   target RNA in a system, comprises a modified deoxyribonucleotide.
```

```
XX
PS   Example 2; Fig 7; 104pp; English.
XX
CC   The invention relates to an acyclic linker-containing oligonucleotide
CC   comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC   the invention are useful for preventing or decreasing translation,
CC   reverse transcription and/or replication of a target RNA in a system.
CC   They are useful for selectively preventing gene expression in a sequence-
CC   specific manner, for hybridising to complementary RNA such as cellular
CC   mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC   RNA. They are also useful therapeutically in formulations or medicaments
CC   to prevent or treat a disease characterised by the expression of a
CC   particular target RNA. The invention is used in gene therapy. The present
CC   sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC   H degradation of target RNA. This sequence is used in the exemplification
CC   of the invention
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1400
AAD56446/c
ID   AAD56446 standard; DNA; 18 BP.
XX
AC   AAD56446;
XX
DT   07-AUG-2003  (first entry)
XX
DE   2'F-ANA antisense oligo #1, to elicit RNase H degradation of target RNA.
XX
KW   Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
KW   antisense; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .18
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-deoxy-2'-fluoroarabinothymidine"
XX
PN   WO2003037909-A1.
XX
PD   08-MAY-2003.
XX
PF   29-OCT-2002; 2002WO-CA001628.
XX
PR   29-OCT-2001; 2001US-0330719P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Viazovkina E,  Mangos MM,  Parniak MA,  Min K;
XX
DR   WPI; 2003-421516/39.
XX
PT   Novel acyclic linker-containing oligonucleotide useful for preventing or
PT   decreasing translation, reverse transcription and/or replication of a
PT   target RNA in a system, comprises a modified deoxyribonucleotide.
XX
PS   Example 2; Fig 7; 104pp; English.
XX
CC   The invention relates to an acyclic linker-containing oligonucleotide
CC   comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC   the invention are useful for preventing or decreasing translation,
CC   reverse transcription and/or replication of a target RNA in a system.
CC   They are useful for selectively preventing gene expression in a sequence-
CC   specific manner, for hybridising to complementary RNA such as cellular
CC   mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC   RNA. They are also useful therapeutically in formulations or medicaments
CC   to prevent or treat a disease characterised by the expression of a
CC   particular target RNA. The invention is used in gene therapy. The present
CC   sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC   H degradation of target RNA. This sequence is used in the exemplification
CC   of the invention
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1401
ACH03247
ID   ACH03247 standard; DNA; 18 BP.
XX
AC   ACH03247;
XX
DT   25-SEP-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #882.
XX
KW   Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW   antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW   psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW   inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS   Synthetic.
XX
PN   US2003050268-A1.
XX
PD   13-MAR-2003.
XX
PF   29-MAR-2002; 2002US-00112653.
XX
PR   29-MAR-2001; 2001US-0279642P.
XX
PA   (KRIE/) KRIEG A M.
PA   (BERG/) BERG D J.
XX
PI   Krieg AM,  Berg DJ;
XX
DR   WPI; 2003-521815/49.
XX
PT   Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT   allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT   disease by administering an immunostimulatory nucleic acid.
XX
PS   Disclosure; Page 33; 229pp; English.
XX
CC   The invention describes a method of treating non-allergic inflammatory
CC   disease comprising administering to a subject having or at risk of
CC   developing a non-allergic inflammatory disease an immunostimulatory
CC   nucleic acid for prevention or treatment of the disease. The method is
CC   useful for treating non-allergic inflammatory diseases, such as
CC   psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC   inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC   This sequence represents an immunostimulatory nucleic acid
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy       2166 TTTTTTTTTTTTTTTTT 2183
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 18


RESULT 1402
ACH03247/c
ID   ACH03247 standard; DNA; 18 BP.
XX
AC   ACH03247;
XX
DT   25-SEP-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #882.
XX
KW   Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW   antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW   psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW   inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS   Synthetic.
XX
PN   US2003050268-A1.
XX
PD   13-MAR-2003.
XX
PF   29-MAR-2002; 2002US-00112653.
XX
PR   29-MAR-2001; 2001US-0279642P.
XX
PA   (KRIE/) KRIEG A M.
PA   (BERG/) BERG D J.
XX
PI   Krieg AM,  Berg DJ;
XX
DR   WPI; 2003-521815/49.
XX
PT   Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT   allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT   disease by administering an immunostimulatory nucleic acid.
XX
PS   Disclosure; Page 33; 229pp; English.
XX
CC   The invention describes a method of treating non-allergic inflammatory
CC   disease comprising administering to a subject having or at risk of
CC   developing a non-allergic inflammatory disease an immunostimulatory
CC   nucleic acid for prevention or treatment of the disease. The method is
CC   useful for treating non-allergic inflammatory diseases, such as
CC   psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC   inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC   This sequence represents an immunostimulatory nucleic acid
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1403
AAD57871
ID   AAD57871 standard; DNA; 18 BP.
XX
AC   AAD57871;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Antisense oligo #1 used in the exemplification of the invention.
XX
KW   Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;
KW   hepatitis B; gene therapy; virucide; anti-HIV; antisense; ss.
XX
OS   Unidentified.
XX
PN   WO2003064441-A2.
XX
PD   07-AUG-2003.
XX
PF   31-JAN-2003; 2003WO-CA000129.
XX
PR   01-FEB-2002; 2002US-0352873P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Parniak MA;
XX
DR   WPI; 2003-689523/65.
XX
PT   New oligonucleotide, useful for preventing or treating a disease related
PT   to a target RNA in a system, e.g., AIDS or hepatitis B.
XX
PS   Example 2; Page 35; 73pp; English.
XX
CC   The present invention relates to a new oligonucleoside which comprises
CC   alternating first and second segments. The first segment comprises at
CC   least one sugar modified nucleoside. The second segment comprises at
CC   least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of
CC   each of the first and second segments, so that it comprises at least 4
CC   alternating segments. The oligonucleotide is useful for preparing a
CC   composition for inducing RNase H-mediated cleavage of a target RNA in a
CC   system, preventing or decreasing translation, transcription or
CC   replication of a target RNA in a system, detecting the presence of a
CC   target RNA in a system, validating a gene target corresponding to a
CC   target RNA in a system or preventing or treating a disease related to a
CC   target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)
CC   or hepatitis B. The invention is useful in gene therapy. The present
CC   sequence is an antisense oligonucleotide used in the exemplification of
CC   the invention
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2183
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 18


RESULT 1404
AAD57871/c
ID   AAD57871 standard; DNA; 18 BP.
XX
AC   AAD57871;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Antisense oligo #1 used in the exemplification of the invention.
XX
KW   Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;
KW   hepatitis B; gene therapy; virucide; anti-HIV; antisense; ss.
XX
OS   Unidentified.
XX
PN   WO2003064441-A2.
XX
PD   07-AUG-2003.
XX
PF   31-JAN-2003; 2003WO-CA000129.
XX
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```
PR   01-FEB-2002; 2002US-0352873P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Parniak MA;
XX
DR   WPI; 2003-689523/65.
XX
PT   New oligonucleotide, useful for preventing or treating a disease related
PT   to a target RNA in a system, e.g., AIDS or hepatitis B.
XX
PS   Example 2; Page 35; 73pp; English.
XX
CC   The present invention relates to a new oligonucleoside which comprises
CC   alternating first and second segments. The first segment comprises at
CC   least one sugar modified nucleoside. The second segment comprises at
CC   least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of
CC   each of the first and second segments, so that it comprises at least 4
CC   alternating segments. The oligonucleotide is useful for preparing a
CC   composition for inducing RNase H-mediated cleavage of a target RNA in a
CC   system, preventing or decreasing translation, transcription or
CC   replication of a target RNA in a system, detecting the presence of a
CC   target RNA in a system, validating a gene target corresponding to a
CC   target RNA in a system or preventing or treating a disease related to a
CC   target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)
CC   or hepatitis B. The invention is useful in gene therapy. The present
CC   sequence is an antisense oligonucleotide used in the exemplification of
CC   the invention
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1405
AAD57878
ID   AAD57878 standard; DNA; 18 BP.
XX
AC   AAD57878;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Antisense DNA-RNA hybrid #2 used in the exemplification of the invention.
XX
KW   Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;
KW   hepatitis B; gene therapy; virucide; anti-HIV; antisense; DNA-RNA hybrid;
KW   ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        1. .3
FT                   /*tag=  a
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
FT   misc_RNA        7. .9
FT                   /*tag=  b
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
FT   misc_RNA        13. .15
FT                   /*tag=  c
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
XX
PN   WO2003064441-A2.
XX
PD   07-AUG-2003.
XX
PF   31-JAN-2003; 2003WO-CA000129.
XX
PR   01-FEB-2002; 2002US-0352873P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Parniak MA;
XX
DR   WPI; 2003-689523/65.
XX
PT   New oligonucleotide, useful for preventing or treating a disease related
PT   to a target RNA in a system, e.g., AIDS or hepatitis B.
XX
PS   Example 2; Page 35; 73pp; English.
XX
CC   The present invention relates to a new oligonucleoside which comprises
CC   alternating first and second segments. The first segment comprises at
CC   least one sugar modified nucleoside. The second segment comprises at
CC   least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of
CC   each of the first and second segments, so that it comprises at least 4
CC   alternating segments. The oligonucleotide is useful for preparing a
CC   composition for inducing RNase H-mediated cleavage of a target RNA in a
CC   system, preventing or decreasing translation, transcription or
CC   replication of a target RNA in a system, detecting the presence of a
CC   target RNA in a system, validating a gene target corresponding to a
CC   target RNA in a system or preventing or treating a disease related to a
CC   target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)
CC   or hepatitis B. The invention is useful in gene therapy. The present
CC   sequence is an antisense DNA-RNA hybrid used in the exemplification of
CC   the invention
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 9 T; 9 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   50.0%;  Pred. No. 7.3e+02;
  Matches    9;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              :::|||:::|||:::|||
Db          1 UUUTTTUUUTTTUUUTTT 18


RESULT 1406
AAD57878/c
ID   AAD57878 standard; DNA; 18 BP.
XX
AC   AAD57878;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Antisense DNA-RNA hybrid #2 used in the exemplification of the invention.
XX
KW   Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;
KW   hepatitis B; gene therapy; virucide; anti-HIV; antisense; DNA-RNA hybrid;
KW   ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        1. .3
FT                   /*tag=  a
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
FT   misc_RNA        7. .9
FT                   /*tag=  b
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
FT   misc_RNA        13. .15
FT                   /*tag=  c
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
XX
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PN   WO2003064441-A2.
XX
PD   07-AUG-2003.
XX
PF   31-JAN-2003; 2003WO-CA000129.
XX
PR   01-FEB-2002; 2002US-0352873P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Parniak MA;
XX
DR   WPI; 2003-689523/65.
XX
PT   New oligonucleotide, useful for preventing or treating a disease related
PT   to a target RNA in a system, e.g., AIDS or hepatitis B.
XX
PS   Example 2; Page 35; 73pp; English.
XX
CC   The present invention relates to a new oligonucleoside which comprises
CC   alternating first and second segments. The first segment comprises at
CC   least one sugar modified nucleoside. The second segment comprises at
CC   least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of
CC   each of the first and second segments, so that it comprises at least 4
CC   alternating segments. The oligonucleotide is useful for preparing a
CC   composition for inducing RNase H-mediated cleavage of a target RNA in a
CC   system, preventing or decreasing translation, transcription or
CC   replication of a target RNA in a system, detecting the presence of a
CC   target RNA in a system, validating a gene target corresponding to a
CC   target RNA in a system or preventing or treating a disease related to a
CC   target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)
CC   or hepatitis B. The invention is useful in gene therapy. The present
CC   sequence is an antisense DNA-RNA hybrid used in the exemplification of
CC   the invention
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 9 T; 9 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1407
AAD57879
ID   AAD57879 standard; DNA; 18 BP.
XX
AC   AAD57879;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Antisense DNA-RNA hybrid #3 used in the exemplification of the invention.
XX
KW   Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;
KW   hepatitis B; gene therapy; virucide; anti-HIV; antisense; DNA-RNA hybrid;
KW   ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        1. .6
FT                   /*tag=  a
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
FT   misc_RNA        13. .18
FT                   /*tag=  b
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
XX
PN   WO2003064441-A2.
XX
PD   07-AUG-2003.
XX
PF   31-JAN-2003; 2003WO-CA000129.
XX
PR   01-FEB-2002; 2002US-0352873P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Parniak MA;
XX
DR   WPI; 2003-689523/65.
XX
PT   New oligonucleotide, useful for preventing or treating a disease related
PT   to a target RNA in a system, e.g., AIDS or hepatitis B.
XX
PS   Example 2; Page 35; 73pp; English.
XX
CC   The present invention relates to a new oligonucleoside which comprises
CC   alternating first and second segments. The first segment comprises at
CC   least one sugar modified nucleoside. The second segment comprises at
CC   least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of
CC   each of the first and second segments, so that it comprises at least 4
CC   alternating segments. The oligonucleotide is useful for preparing a
CC   composition for inducing RNase H-mediated cleavage of a target RNA in a
CC   system, preventing or decreasing translation, transcription or
CC   replication of a target RNA in a system, detecting the presence of a
CC   target RNA in a system, validating a gene target corresponding to a
CC   target RNA in a system or preventing or treating a disease related to a
CC   target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)
CC   or hepatitis B. The invention is useful in gene therapy. The present
CC   sequence is an antisense DNA-RNA hybrid used in the exemplification of
CC   the invention
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 6 T; 12 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   33.3%;  Pred. No. 7.3e+02;
  Matches    6;  Conservative   12;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ::::::||||||::::::
Db          1 UUUUUUTTTTTTUUUUUU 18


RESULT 1408
AAD57879/c
ID   AAD57879 standard; DNA; 18 BP.
XX
AC   AAD57879;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Antisense DNA-RNA hybrid #3 used in the exemplification of the invention.
XX
KW   Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;
KW   hepatitis B; gene therapy; virucide; anti-HIV; antisense; DNA-RNA hybrid;
KW   ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        1. .6
FT                   /*tag=  a
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
FT   misc_RNA        13. .18
FT                   /*tag=  b
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
XX
PN   WO2003064441-A2.
XX
```

```
PD   07-AUG-2003.
XX
PF   31-JAN-2003; 2003WO-CA000129.
XX
PR   01-FEB-2002; 2002US-0352873P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Parniak MA;
XX
DR   WPI; 2003-689523/65.
XX
PT   New oligonucleotide, useful for preventing or treating a disease related
PT   to a target RNA in a system, e.g., AIDS or hepatitis B.
XX
PS   Example 2; Page 35; 73pp; English.
XX
CC   The present invention relates to a new oligonucleoside which comprises
CC   alternating first and second segments. The first segment comprises at
CC   least one sugar modified nucleoside. The second segment comprises at
CC   least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of
CC   each of the first and second segments, so that it comprises at least 4
CC   alternating segments. The oligonucleotide is useful for preparing a
CC   composition for inducing RNase H-mediated cleavage of a target RNA in a
CC   system, preventing or decreasing translation, transcription or
CC   replication of a target RNA in a system, detecting the presence of a
CC   target RNA in a system, validating a gene target corresponding to a
CC   target RNA in a system or preventing or treating a disease related to a
CC   target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)
CC   or hepatitis B. The invention is useful in gene therapy. The present
CC   sequence is an antisense DNA-RNA hybrid used in the exemplification of
CC   the invention
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 6 T; 12 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1409
AAD57877
ID   AAD57877 standard; DNA; 18 BP.
XX
AC   AAD57877;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Antisense DNA-RNA hybrid #1 used in the exemplification of the invention.
XX
KW   Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;
KW   hepatitis B; gene therapy; virucide; anti-HIV; antisense; DNA-RNA hybrid;
KW   ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        1
FT                   /*tag=  a
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
FT   misc_RNA        3
FT                   /*tag=  b
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
FT   misc_RNA        5
FT                   /*tag=  c
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
FT   misc_RNA        7
FT                   /*tag=  d
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
FT   misc_RNA        9
FT                   /*tag=  e
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
FT   misc_RNA        11
FT                   /*tag=  f
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
FT   misc_RNA        13
FT                   /*tag=  g
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
FT   misc_RNA        15
FT                   /*tag=  h
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
FT   misc_RNA        17
FT                   /*tag=  i
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
XX
PN   WO2003064441-A2.
XX
PD   07-AUG-2003.
XX
PF   31-JAN-2003; 2003WO-CA000129.
XX
PR   01-FEB-2002; 2002US-0352873P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Parniak MA;
XX
DR   WPI; 2003-689523/65.
XX
PT   New oligonucleotide, useful for preventing or treating a disease related
PT   to a target RNA in a system, e.g., AIDS or hepatitis B.
XX
PS   Example 2; Page 35; 73pp; English.
XX
CC   The present invention relates to a new oligonucleoside which comprises
CC   alternating first and second segments. The first segment comprises at
CC   least one sugar modified nucleoside. The second segment comprises at
CC   least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of
CC   each of the first and second segments, so that it comprises at least 4
CC   alternating segments. The oligonucleotide is useful for preparing a
CC   composition for inducing RNase H-mediated cleavage of a target RNA in a
CC   system, preventing or decreasing translation, transcription or
CC   replication of a target RNA in a system, detecting the presence of a
CC   target RNA in a system, validating a gene target corresponding to a
CC   target RNA in a system or preventing or treating a disease related to a
CC   target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)
CC   or hepatitis B. The invention is useful in gene therapy. The present
CC   sequence is an antisense DNA-RNA hybrid used in the exemplification of
CC   the invention
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 9 T; 9 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   50.0%;  Pred. No. 7.3e+02;
  Matches    9;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              :|:|:|:|:|:|:|:|:|
Db          1 UTUTUTUTUTUTUTUTUT 18


RESULT 1410
AAD57877/c
```

```
ID   AAD57877 standard; DNA; 18 BP.
XX
AC   AAD57877;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Antisense DNA-RNA hybrid #1 used in the exemplification of the invention.
XX
KW   Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;
KW   hepatitis B; gene therapy; virucide; anti-HIV; antisense; DNA-RNA hybrid;
KW   ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        1
FT                   /*tag=  a
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
FT   misc_RNA        3
FT                   /*tag=  b
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
FT   misc_RNA        5
FT                   /*tag=  c
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
FT   misc_RNA        7
FT                   /*tag=  d
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
FT   misc_RNA        9
FT                   /*tag=  e
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
FT   misc_RNA        11
FT                   /*tag=  f
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
FT   misc_RNA        13
FT                   /*tag=  g
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
FT   misc_RNA        15
FT                   /*tag=  h
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
FT   misc_RNA        17
FT                   /*tag=  i
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
XX
PN   WO2003064441-A2.
XX
PD   07-AUG-2003.
XX
PF   31-JAN-2003; 2003WO-CA000129.
XX
PR   01-FEB-2002; 2002US-0352873P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Parniak MA;
XX
DR   WPI; 2003-689523/65.
XX
PT   New oligonucleotide, useful for preventing or treating a disease related
PT   to a target RNA in a system, e.g., AIDS or hepatitis B.
XX
PS   Example 2; Page 35; 73pp; English.
XX
CC   The present invention relates to a new oligonucleoside which comprises
CC   alternating first and second segments. The first segment comprises at
CC   least one sugar modified nucleoside. The second segment comprises at
CC   least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of
CC   each of the first and second segments, so that it comprises at least 4
CC   alternating segments. The oligonucleotide is useful for preparing a
CC   composition for inducing RNase H-mediated cleavage of a target RNA in a
CC   system, preventing or decreasing translation, transcription or
CC   replication of a target RNA in a system, detecting the presence of a
CC   target RNA in a system, validating a gene target corresponding to a
CC   target RNA in a system or preventing or treating a disease related to a
CC   target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)
CC   or hepatitis B. The invention is useful in gene therapy. The present
CC   sequence is an antisense DNA-RNA hybrid used in the exemplification of
CC   the invention
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 9 T; 9 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1411
AAD57890
ID   AAD57890 standard; RNA; 18 BP.
XX
AC   AAD57890;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Target RNA #1 used in RNase H assay.
XX
KW   Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;
KW   hepatitis B; gene therapy; virucide; anti-HIV; ss.
XX
OS   Unidentified.
XX
PN   WO2003064441-A2.
XX
PD   07-AUG-2003.
XX
PF   31-JAN-2003; 2003WO-CA000129.
XX
PR   01-FEB-2002; 2002US-0352873P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Parniak MA;
XX
DR   WPI; 2003-689523/65.
XX
PT   New oligonucleotide, useful for preventing or treating a disease related
PT   to a target RNA in a system, e.g., AIDS or hepatitis B.
XX
PS   Example 4; Page 38; 73pp; English.
XX
CC   The present invention relates to a new oligonucleoside which comprises
CC   alternating first and second segments. The first segment comprises at
CC   least one sugar modified nucleoside. The second segment comprises at
CC   least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of
CC   each of the first and second segments, so that it comprises at least 4
CC   alternating segments. The oligonucleotide is useful for preparing a
CC   composition for inducing RNase H-mediated cleavage of a target RNA in a
CC   system, preventing or decreasing translation, transcription or
CC   replication of a target RNA in a system, detecting the presence of a
CC   target RNA in a system, validating a gene target corresponding to a
CC   target RNA in a system or preventing or treating a disease related to a
CC   target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)
CC   or hepatitis B. The invention is useful in gene therapy. The present
CC   sequence is a target RNA used in RNase H assay. This sequence is used in
```

```
CC   the exemplification of the invention
XX
SQ   Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 1412
AAD57890/c
ID   AAD57890 standard; RNA; 18 BP.
XX
AC   AAD57890;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Target RNA #1 used in RNase H assay.
XX
KW   Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;
KW   hepatitis B; gene therapy; virucide; anti-HIV; ss.
XX
OS   Unidentified.
XX
PN   WO2003064441-A2.
XX
PD   07-AUG-2003.
XX
PF   31-JAN-2003; 2003WO-CA000129.
XX
PR   01-FEB-2002; 2002US-0352873P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Parniak MA;
XX
DR   WPI; 2003-689523/65.
XX
PT   New oligonucleotide, useful for preventing or treating a disease related
PT   to a target RNA in a system, e.g., AIDS or hepatitis B.
XX
PS   Example 4; Page 38; 73pp; English.
XX
CC   The present invention relates to a new oligonucleoside which comprises
CC   alternating first and second segments. The first segment comprises at
CC   least one sugar modified nucleoside. The second segment comprises at
CC   least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of
CC   each of the first and second segments, so that it comprises at least 4
CC   alternating segments. The oligonucleotide is useful for preparing a
CC   composition for inducing RNase H-mediated cleavage of a target RNA in a
CC   system, preventing or decreasing translation, transcription or
CC   replication of a target RNA in a system, detecting the presence of a
CC   target RNA in a system, validating a gene target corresponding to a
CC   target RNA in a system or preventing or treating a disease related to a
CC   target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)
CC   or hepatitis B. The invention is useful in gene therapy. The present
CC   sequence is a target RNA used in RNase H assay. This sequence is used in
CC   the exemplification of the invention
XX
SQ   Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db         18 TTTTTTTTTTTTTTTTTT 1


RESULT 1413
ADB37210
ID   ADB37210 standard; DNA; 18 BP.
XX
AC   ADB37210;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #824.
XX
KW   ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW   hypo-responsive subject; immunostimulatory.
XX
OS   Synthetic.
XX
PN   US2003087848-A1.
XX
PD   08-MAY-2003.
XX
PF   02-FEB-2001; 2001US-00776479.
XX
PR   03-FEB-2000; 2000US-0179991P.
XX
PA   (BRAT/) BRATZLER R L.
PA   (PETE/) PETERSEN D M.
PA   (FOUR/) FOURON Y.
XX
PI   Bratzler RL,  Petersen DM,  Fouron Y;
XX
DR   WPI; 2003-657977/62.
XX
PT   Treating and/or preventing allergy or asthma using an immunostimulatory
PT   nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS   Disclosure; Page 17; 221pp; English.
XX
CC   The invention relates to a method of treating or preventing allergy or
CC   asthma which comprises administering to a subject a poly-G nucleic acid
CC   in an aerosol formulation. The methods and compositions of the present
CC   invention are useful for diagnosing and/or treating asthma and allergy
CC   especially in a hypo-responsive subject. The present sequence represents
CC   an immunostimulatory nucleic acid of the invention.
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1414
ADB37210/c
ID   ADB37210 standard; DNA; 18 BP.
XX
AC   ADB37210;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #824.
XX
KW   ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW   hypo-responsive subject; immunostimulatory.
XX
OS   Synthetic.
XX
PN   US2003087848-A1.
XX
PD   08-MAY-2003.
```

```
XX
PF   02-FEB-2001; 2001US-00776479.
XX
PR   03-FEB-2000; 2000US-0179991P.
XX
PA   (BRAT/) BRATZLER R L.
PA   (PETE/) PETERSEN D M.
PA   (FOUR/) FOURON Y.
XX
PI   Bratzler RL,  Petersen DM,  Fouron Y;
XX
DR   WPI; 2003-657977/62.
XX
PT   Treating and/or preventing allergy or asthma using an immunostimulatory
PT   nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS   Disclosure; Page 17; 221pp; English.
XX
CC   The invention relates to a method of treating or preventing allergy or
CC   asthma which comprises administering to a subject a poly-G nucleic acid
CC   in an aerosol formulation. The methods and compositions of the present
CC   invention are useful for diagnosing and/or treating asthma and allergy
CC   especially in a hypo-responsive subject. The present sequence represents
CC   an immunostimulatory nucleic acid of the invention.
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1415
ADB37236
ID   ADB37236 standard; DNA; 18 BP.
XX
AC   ADB37236;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #850.
XX
KW   ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW   hypo-responsive subject; immunostimulatory.
XX
OS   Synthetic.
XX
PN   US2003087848-A1.
XX
PD   08-MAY-2003.
XX
PF   02-FEB-2001; 2001US-00776479.
XX
PR   03-FEB-2000; 2000US-0179991P.
XX
PA   (BRAT/) BRATZLER R L.
PA   (PETE/) PETERSEN D M.
PA   (FOUR/) FOURON Y.
XX
PI   Bratzler RL,  Petersen DM,  Fouron Y;
XX
DR   WPI; 2003-657977/62.
XX
PT   Treating and/or preventing allergy or asthma using an immunostimulatory
PT   nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS   Disclosure; Page 18; 221pp; English.
XX
CC   The invention relates to a method of treating or preventing allergy or
CC   asthma which comprises administering to a subject a poly-G nucleic acid
CC   in an aerosol formulation. The methods and compositions of the present
CC   invention are useful for diagnosing and/or treating asthma and allergy
CC   especially in a hypo-responsive subject. The present sequence represents
CC   an immunostimulatory nucleic acid of the invention.
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1416
ADB37236/c
ID   ADB37236 standard; DNA; 18 BP.
XX
AC   ADB37236;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #850.
XX
KW   ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW   hypo-responsive subject; immunostimulatory.
XX
OS   Synthetic.
XX
PN   US2003087848-A1.
XX
PD   08-MAY-2003.
XX
PF   02-FEB-2001; 2001US-00776479.
XX
PR   03-FEB-2000; 2000US-0179991P.
XX
PA   (BRAT/) BRATZLER R L.
PA   (PETE/) PETERSEN D M.
PA   (FOUR/) FOURON Y.
XX
PI   Bratzler RL,  Petersen DM,  Fouron Y;
XX
DR   WPI; 2003-657977/62.
XX
PT   Treating and/or preventing allergy or asthma using an immunostimulatory
PT   nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS   Disclosure; Page 18; 221pp; English.
XX
CC   The invention relates to a method of treating or preventing allergy or
CC   asthma which comprises administering to a subject a poly-G nucleic acid
CC   in an aerosol formulation. The methods and compositions of the present
CC   invention are useful for diagnosing and/or treating asthma and allergy
CC   especially in a hypo-responsive subject. The present sequence represents
CC   an immunostimulatory nucleic acid of the invention.
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1417
ADE77617
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```
ID   ADE77617 standard; DNA; 18 BP.
XX
AC   ADE77617;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human probe NEG for elongation mediated multiplexed analysis of HLA-DR.
XX
KW   probe; ss; negative control; CFTR; human leukocyte antigen; HLA;
KW   genetic testing; carrier screening; genotyping; profiling; polymorphic;
KW   multiplexed elongation assay; enzymatic recognition;
KW   cystic fibrosis conductance transmembrane regulator.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO2003034029-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US033012.
XX
PR   15-OCT-2001; 2001US-0329427P.
PR   15-OCT-2001; 2001US-0329428P.
PR   15-OCT-2001; 2001US-0329619P.
PR   15-OCT-2001; 2001US-0329620P.
PR   14-MAR-2002; 2002US-0364416P.
XX
PA   (BIOA-) BIOARRAY SOLUTIONS LTD.
XX
PI   Li AX,  Hashmi G,  Seul M;
XX
DR   WPI; 2003-393553/37.
XX
PT   Concurrent interrogation of a number of polymorphic sites, useful for
PT   genetic testing, carrier screening, genetic profiling, and identity
PT   testing, comprises conducting a multiplexed elongation assay using
PT   probes.
XX
PS   Example 9; Page 46; 143pp; English.
XX
CC   This invention relates to a novel method for the concurrent interrogation
CC   of a number of polymorphic sites in the presence of, and without
CC   interference from, non-designated polymorphic sites. Specifically, it
CC   comprises conducting a multiplexed elongation assay by applying one or
CC   more temperature cycles to achieve linear amplification of the target or
CC   a combination of annealing and elongation steps under temperature-
CC   controlled conditions. Furthermore, this detection method uses probe
CC   extension or elongation and relies on enzymatic recognition, a superior
CC   technique that no longer depends on differential hybridisation. The
CC   present invention describes probes and methods useful for identifying or
CC   detecting polymorphisms at one or more designated sites, such that they
CC   can identify mutations within the cystic fibrosis conductance
CC   transmembrane regulator (CFTR) or the human leukocyte antigen (HLA)
CC   genes. In addition, concurrent interrogation of a multiplicity of
CC   polymorphic sites is useful for genetic testing, carrier screening,
CC   genotyping or genetic profiling, and identity testing. This
CC   oligonucleotide is the negative control probe used for the elongation
CC   mediated multiplexed analysis of HLA-DR, in an exemplification of the
CC   invention.
XX
SQ   Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAA 18

RESULT 1418
```

```
ADE77617/c
ID   ADE77617 standard; DNA; 18 BP.
XX
AC   ADE77617;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human probe NEG for elongation mediated multiplexed analysis of HLA-DR.
XX
KW   probe; ss; negative control; CFTR; human leukocyte antigen; HLA;
KW   genetic testing; carrier screening; genotyping; profiling; polymorphic;
KW   multiplexed elongation assay; enzymatic recognition;
KW   cystic fibrosis conductance transmembrane regulator.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO2003034029-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US033012.
XX
PR   15-OCT-2001; 2001US-0329427P.
PR   15-OCT-2001; 2001US-0329428P.
PR   15-OCT-2001; 2001US-0329619P.
PR   15-OCT-2001; 2001US-0329620P.
PR   14-MAR-2002; 2002US-0364416P.
XX
PA   (BIOA-) BIOARRAY SOLUTIONS LTD.
XX
PI   Li AX,  Hashmi G,  Seul M;
XX
DR   WPI; 2003-393553/37.
XX
PT   Concurrent interrogation of a number of polymorphic sites, useful for
PT   genetic testing, carrier screening, genetic profiling, and identity
PT   testing, comprises conducting a multiplexed elongation assay using
PT   probes.
XX
PS   Example 9; Page 46; 143pp; English.
XX
CC   This invention relates to a novel method for the concurrent interrogation
CC   of a number of polymorphic sites in the presence of, and without
CC   interference from, non-designated polymorphic sites. Specifically, it
CC   comprises conducting a multiplexed elongation assay by applying one or
CC   more temperature cycles to achieve linear amplification of the target or
CC   a combination of annealing and elongation steps under temperature-
CC   controlled conditions. Furthermore, this detection method uses probe
CC   extension or elongation and relies on enzymatic recognition, a superior
CC   technique that no longer depends on differential hybridisation. The
CC   present invention describes probes and methods useful for identifying or
CC   detecting polymorphisms at one or more designated sites, such that they
CC   can identify mutations within the cystic fibrosis conductance
CC   transmembrane regulator (CFTR) or the human leukocyte antigen (HLA)
CC   genes. In addition, concurrent interrogation of a multiplicity of
CC   polymorphic sites is useful for genetic testing, carrier screening,
CC   genotyping or genetic profiling, and identity testing. This
CC   oligonucleotide is the negative control probe used for the elongation
CC   mediated multiplexed analysis of HLA-DR, in an exemplification of the
CC   invention.
XX
SQ   Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db         18 TTTTTTTTTTTTTTTTTT 1
```

```
RESULT 1419
AAQ75553
ID   AAQ75553 standard; DNA; 19 BP.
XX
AC   AAQ75553;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 19 BP; 1 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 8.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTA 18


RESULT 1420
AAQ75558/c
ID   AAQ75558 standard; DNA; 19 BP.
XX
AC   AAQ75558;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 19 BP; 0 A; 2 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 8.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 1421
AAQ75551
ID   AAQ75551 standard; DNA; 19 BP.
XX
AC   AAQ75551;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 19 BP; 1 A; 0 C; 1 G; 17 T; 0 U; 0 Other;
```

```
  Query Match             0.6%;  Score 18;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 8.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTA 18


RESULT 1422
AAQ75554
ID   AAQ75554 standard; DNA; 19 BP.
XX
AC   AAQ75554;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 19 BP; 1 A; 1 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 8.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTA 18


RESULT 1423
AAQ75555/c
ID   AAQ75555 standard; DNA; 19 BP.
XX
AC   AAQ75555;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 19 BP; 0 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 8.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 1424
AAQ75557/c
ID   AAQ75557 standard; DNA; 19 BP.
XX
AC   AAQ75557;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
```

```
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 19 BP; 0 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 8.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 1425
ABL51521
ID   ABL51521 standard; DNA; 19 BP.
XX
AC   ABL51521;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Tailing reaction related exemplary primer dA18U SEQ ID NO:2.
XX
KW   Tailing reaction; tailed primer; primer; probe; identification;
KW   detection; linear amplification scheme; chain extending enzyme;
KW   telomerase; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        19
FT                   /*tag=  a
XX
PN   US2002031776-A1.
XX
PD   14-MAR-2002.
XX
PF   26-JUL-2001; 2001US-00917138.
XX
PR   28-MAY-1999;   99US-0136545P.
PR   25-MAY-2000; 2000US-00580358.
XX
PA   (TULL/) TULLIS R H.
PA   (STRE/) STREIFEL J A.
XX
PI   Tullis RH,  Streifel JA;
XX
DR   WPI; 2002-361176/39.
XX
PT   Identifying and detecting nucleic acids, particularly DNA hybridization
PT   probes, involves employing chain extending enzymes (e.g. telomerase) to
PT   elongate probes to render them readily detectable.
XX
PS   Example 1; Page 5; 10pp; English.
XX
CC   The present invention describes a method for detecting a nucleic acid
CC   probe, which comprises using chain extending enzymes to elongate probes.
CC   The method comprises: (a) treating the sample with a chain terminating
CC   reagent to prevent polynucleotide chain growth from the nucleic acid in
CC   the sample; (b) contacting the sample with the probe containing a
CC   terminus capable of elongation by a chain extending enzyme, where the
CC   probe hybridises to the nucleic acid in the sample; (c) contacting the
CC   sample with a chain extending enzyme and its substrates, which elongates
CC   the probe; and (d) detecting the elongated hybridised probe. Also
CC   described is a method comprising: (a) treating nucleic acid molecules or
CC   modified nucleic acids in a sample with a reagent or reagents that render
CC   the nucleic acid chains unextendable by a non-template-dependent enzyme;
CC   (b) hybridising the treated molecules with a nucleic acid probe that
CC   includes an extendable terminus, under conditions where hybrids form; and
CC   (c) treating any hybrids formed with a non-template dependent chain
CC   elongating enzyme and its substrates, where any hybridised probe is
CC   extended. The method is useful for identifying and detecting nucleic
CC   acids, particularly DNA hybridisation probes. The present sequence
CC   represents a tailing reaction exemplary primer, which is used in an
CC   example from the present invention
XX
SQ   Sequence 19 BP; 18 A; 0 C; 0 G; 0 T; 1 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 8.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 1426
ABL51521/c
ID   ABL51521 standard; DNA; 19 BP.
XX
AC   ABL51521;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Tailing reaction related exemplary primer dA18U SEQ ID NO:2.
XX
KW   Tailing reaction; tailed primer; primer; probe; identification;
KW   detection; linear amplification scheme; chain extending enzyme;
KW   telomerase; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        19
FT                   /*tag=  a
XX
PN   US2002031776-A1.
XX
PD   14-MAR-2002.
XX
PF   26-JUL-2001; 2001US-00917138.
XX
PR   28-MAY-1999;   99US-0136545P.
PR   25-MAY-2000; 2000US-00580358.
XX
PA   (TULL/) TULLIS R H.
PA   (STRE/) STREIFEL J A.
XX
PI   Tullis RH,  Streifel JA;
XX
DR   WPI; 2002-361176/39.
XX
PT   Identifying and detecting nucleic acids, particularly DNA hybridization
PT   probes, involves employing chain extending enzymes (e.g. telomerase) to
PT   elongate probes to render them readily detectable.
XX
PS   Example 1; Page 5; 10pp; English.
XX
CC   The present invention describes a method for detecting a nucleic acid
CC   probe, which comprises using chain extending enzymes to elongate probes.
CC   The method comprises: (a) treating the sample with a chain terminating
CC   reagent to prevent polynucleotide chain growth from the nucleic acid in
CC   the sample; (b) contacting the sample with the probe containing a
CC   terminus capable of elongation by a chain extending enzyme, where the
CC   probe hybridises to the nucleic acid in the sample; (c) contacting the
CC   sample with a chain extending enzyme and its substrates, which elongates
CC   the probe; and (d) detecting the elongated hybridised probe. Also
CC   described is a method comprising: (a) treating nucleic acid molecules or
```

```
CC   modified nucleic acids in a sample with a reagent or reagents that render
CC   the nucleic acid chains unextendable by a non-template-dependent enzyme;
CC   (b) hybridising the treated molecules with a nucleic acid probe that
CC   includes an extendable terminus, under conditions where hybrids form; and
CC   (c) treating any hybrids formed with a non-template dependent chain
CC   elongating enzyme and its substrates, where any hybridised probe is
CC   extended. The method is useful for identifying and detecting nucleic
CC   acids, particularly DNA hybridisation probes. The present sequence
CC   represents a tailing reaction exemplary primer, which is used in an
CC   example from the present invention
XX
SQ   Sequence 19 BP; 18 A; 0 C; 0 G; 0 T; 1 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 8.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db         18 TTTTTTTTTTTTTTTTTT 1


RESULT 1427
ABZ75398
ID   ABZ75398 standard; DNA; 19 BP.
XX
AC   ABZ75398;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Synthetic nuclease-resistant oligomeric compound #54.
XX
KW   Nuclease resistant; ds; pharmaceutical; topical administration;
KW   transdermal patch; enzymatic degradation resistant.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    19
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "phenoxazine"
XX
PN   WO2003004602-A2.
XX
PD   16-JAN-2003.
XX
PF   01-JUL-2002; 2002WO-US020934.
XX
PR   03-JUL-2001; 2001US-0302682P.
PR   28-NOV-2001; 2001US-00996292.
PR   10-DEC-2001; 2001US-00013295.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Manoharan M,  Maier MA,  Prakash TP,  Rajeev KG;
XX
DR   WPI; 2003-256318/25.
XX
PT   Nuclease-resistant oligomeric compound useful as pharmaceuticals for
PT   topical administration such as transdermal patches.
XX
PS   Disclosure; Page 234; 234pp; English.
XX
CC   The invention relates to novel nuclease-resistant oligomeric compounds.
CC   The compounds of the invention are useful as pharmaceuticals for topical
CC   administration such as transdermal patches. The oligomeric compound is
CC   resistant to enzymatic degradation. The sequences shown in ABZ75345-
CC   ABZ75399 represent the nuclease-resistant compounds of the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 8.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1428
ABZ75398/c
ID   ABZ75398 standard; DNA; 19 BP.
XX
AC   ABZ75398;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Synthetic nuclease-resistant oligomeric compound #54.
XX
KW   Nuclease resistant; ds; pharmaceutical; topical administration;
KW   transdermal patch; enzymatic degradation resistant.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    19
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "phenoxazine"
XX
PN   WO2003004602-A2.
XX
PD   16-JAN-2003.
XX
PF   01-JUL-2002; 2002WO-US020934.
XX
PR   03-JUL-2001; 2001US-0302682P.
PR   28-NOV-2001; 2001US-00996292.
PR   10-DEC-2001; 2001US-00013295.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Manoharan M,  Maier MA,  Prakash TP,  Rajeev KG;
XX
DR   WPI; 2003-256318/25.
XX
PT   Nuclease-resistant oligomeric compound useful as pharmaceuticals for
PT   topical administration such as transdermal patches.
XX
PS   Disclosure; Page 234; 234pp; English.
XX
CC   The invention relates to novel nuclease-resistant oligomeric compounds.
CC   The compounds of the invention are useful as pharmaceuticals for topical
CC   administration such as transdermal patches. The oligomeric compound is
CC   resistant to enzymatic degradation. The sequences shown in ABZ75345-
CC   ABZ75399 represent the nuclease-resistant compounds of the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 8.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1429
ABZ75399
ID   ABZ75399 standard; DNA; 19 BP.
XX
AC   ABZ75399;
XX
```

```
DT   07-MAY-2003  (first entry)
XX
DE   Synthetic nuclease-resistant oligomeric compound #55.
XX
KW   Nuclease resistant; ds; pharmaceutical; topical administration;
KW   transdermal patch; enzymatic degradation resistant.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   19
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "G-clamp modification"
XX
PN   WO2003004602-A2.
XX
PD   16-JAN-2003.
XX
PF   01-JUL-2002; 2002WO-US020934.
XX
PR   03-JUL-2001; 2001US-0302682P.
PR   28-NOV-2001; 2001US-00996292.
PR   10-DEC-2001; 2001US-00013295.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Manoharan M,  Maier MA,  Prakash TP,  Rajeev KG;
XX
DR   WPI; 2003-256318/25.
XX
PT   Nuclease-resistant oligomeric compound useful as pharmaceuticals for
PT   topical administration such as transdermal patches.
XX
PS   Disclosure; Page 234; 234pp; English.
XX
CC   The invention relates to novel nuclease-resistant oligomeric compounds.
CC   The compounds of the invention are useful as pharmaceuticals for topical
CC   administration such as transdermal patches. The oligomeric compound is
CC   resistant to enzymatic degradation. The sequences shown in ABZ75345-
CC   ABZ75399 represent the nuclease-resistant compounds of the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 8.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1430
ABZ75399/c
ID   ABZ75399 standard; DNA; 19 BP.
XX
AC   ABZ75399;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Synthetic nuclease-resistant oligomeric compound #55.
XX
KW   Nuclease resistant; ds; pharmaceutical; topical administration;
KW   transdermal patch; enzymatic degradation resistant.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   19
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "G-clamp modification"
XX
PN   WO2003004602-A2.
XX
PD   16-JAN-2003.
XX
PF   01-JUL-2002; 2002WO-US020934.
XX
PR   03-JUL-2001; 2001US-0302682P.
PR   28-NOV-2001; 2001US-00996292.
PR   10-DEC-2001; 2001US-00013295.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Manoharan M,  Maier MA,  Prakash TP,  Rajeev KG;
XX
DR   WPI; 2003-256318/25.
XX
PT   Nuclease-resistant oligomeric compound useful as pharmaceuticals for
PT   topical administration such as transdermal patches.
XX
PS   Disclosure; Page 234; 234pp; English.
XX
CC   The invention relates to novel nuclease-resistant oligomeric compounds.
CC   The compounds of the invention are useful as pharmaceuticals for topical
CC   administration such as transdermal patches. The oligomeric compound is
CC   resistant to enzymatic degradation. The sequences shown in ABZ75345-
CC   ABZ75399 represent the nuclease-resistant compounds of the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 8.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1431
AAT04916/c
ID   AAT04916 standard; cDNA; 20 BP.
XX
AC   AAT04916;
XX
DT   25-MAR-2003  (revised)
DT   15-MAY-1996  (first entry)
XX
DE   Mammalian stem cell factor (SCF) cDNA oligonucleotide primer 220-7.
XX
KW   Stem cell factor; progenitor; haematopoiesis; SCF; anaemia;
KW   thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft;
KW   transplant; neoplasia; myelosuppression; bone marrow; ss.
XX
OS   Synthetic.
XX
PN   EP676470-A1.
XX
PD   11-OCT-1995.
XX
PF   04-OCT-1990;   95EP-00105391.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   28-SEP-1990;   90WO-US005548.
PR   01-OCT-1990;   90US-00589701.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Zsebo KM,  Suggs SV,  Bosselman RA,  Martin FH;
XX
DR   WPI; 1995-346090/45.
```

```
XX
PT   New stem cell factor polypeptide(s) - for stimulating the growth of
PT   primitive progenitor cells, esp. for treating disorders involving blood
PT   cells.
XX
PS   Example 3; Fig 12C; 127pp; English.
XX
CC   AAT04915-T04922 are oligonucleotide primers and probes used for the
CC   amplification and sequencing of mammalian stem cell factor (SCF). Non-
CC   naturally occuring SCF and C-terminally truncated polypeptides, having
CC   amino acid sequences sufficiently duplicative of naturally ocurring SCF,
CC   stimulate growth of primitive progenitors such as haematopoietic
CC   progenitor cells, neural stem cells and primordial germ stem cells. The
CC   peptides can be used in a composition for treating leucopenia, anaemia or
CC   thrombocytopenia, for enhancing engraftment of bone marrow during
CC   transplantation or for bone marrow recovery after chemotherapy or
CC   radiation-induced bone marrow aplasia or myelosuppression. They can also
CC   be used for treating neoplasia, nerve damage, infertlilty, intestinal
CC   damage or myeloproliferative disorders. Antibodies may be raised against
CC   the peptides for use in detection or neutralisation of SCF in serum. SCF
CC   may be useful for the treatment of AIDS and severe combined
CC   immunodeficiency (SCID) states alone or in combination with other factors
CC   such as IL-7. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1432
AAT04918
ID   AAT04918 standard; cDNA; 20 BP.
XX
AC   AAT04918;
XX
DT   25-MAR-2003  (revised)
DT   15-MAY-1996  (first entry)
XX
DE   Mammalian stem cell factor (SCF) cDNA oligonucleotide primer 220-11.
XX
KW   Stem cell factor; progenitor; haematopoiesis; SCF; anaemia;
KW   thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft;
KW   transplant; neoplasia; myelosuppression; bone marrow; ss.
XX
OS   Synthetic.
XX
PN   EP676470-A1.
XX
PD   11-OCT-1995.
XX
PF   04-OCT-1990;   95EP-00105391.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   28-SEP-1990;   90WO-US005548.
PR   01-OCT-1990;   90US-00589701.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Zsebo KM,  Suggs SV,  Bosselman RA,  Martin FH;
XX
DR   WPI; 1995-346090/45.
XX
PT   New stem cell factor polypeptide(s) - for stimulating the growth of
PT   primitive progenitor cells, esp. for treating disorders involving blood
PT   cells.
XX
PS   Example 3; Fig 12C; 127pp; English.
XX
CC   AAT04915-T04922 are oligonucleotide primers and probes used for the
CC   amplification and sequencing of mammalian stem cell factor (SCF). Non-
CC   naturally occuring SCF and C-terminally truncated polypeptides, having
CC   amino acid sequences sufficiently duplicative of naturally ocurring SCF,
CC   stimulate growth of primitive progenitors such as haematopoietic
CC   progenitor cells, neural stem cells and primordial germ stem cells. The
CC   peptides can be used in a composition for treating leucopenia, anaemia or
CC   thrombocytopenia, for enhancing engraftment of bone marrow during
CC   transplantation or for bone marrow recovery after chemotherapy or
CC   radiation-induced bone marrow aplasia or myelosuppression. They can also
CC   be used for treating neoplasia, nerve damage, infertlilty, intestinal
CC   damage or myeloproliferative disorders. Antibodies may be raised against
CC   the peptides for use in detection or neutralisation of SCF in serum. SCF
CC   may be useful for the treatment of AIDS and severe combined
CC   immunodeficiency (SCID) states alone or in combination with other factors
CC   such as IL-7. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1433
AAA13753/c
ID   AAA13753 standard; DNA; 20 BP.
XX
AC   AAA13753;
XX
DT   27-JUL-2000  (first entry)
XX
DE   Stem cell factor universal oligonucleotide 220-7.
XX
KW   Stem cell factor; SCF; haematopoietic progenitor cell; blood forming;
KW   primitive progenitor cell; haematopoietic disorder; syngeneic;
KW   allogeneic; autologous bone marrow transplant; gene therapy;
KW   transfection; haematopoietic stem cell; acute blood loss; neoplasia;
KW   cancer; ss.
XX
OS   Synthetic.
XX
PN   EP992579-A1.
XX
PD   12-APR-2000.
XX
PF   04-OCT-1990;   99EP-00122861.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   28-SEP-1990;   90WO-US005548.
PR   01-OCT-1990;   90US-00589701.
PR   04-OCT-1990;   90EP-00310899.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Zsebo KM,  Suggs SV,  Bosselmann RA,  Martin FH;
XX
DR   WPI; 2000-259135/23.
XX
PT   Production of hematopoietic cells suitable for administration to a
PT   subject using progenitor cells and expanding the cells using stem cell
PT   factor.
XX
PS   Example 3; Fig 12C; 123pp; English.
```

```
XX
CC   A method has been developed of making haematopoietic cells suitable for
CC   administration to a subject. The method comprises: (a) obtaining
CC   haematopoietic progenitor cells from a donor; and (b) expanding the cells
CC   by adding to the cells a haematopoietically effective dose of a
CC   polypeptide product having at least part of the primary structural
CC   confirmation and one or more of the biological properties of naturally
CC   occurring stem cell factor (SCF). The method is useful for stimulating
CC   primitive progenitor cells including early haematopoietic progenitor
CC   cells which are capable of maturing to erythroid, megakaryocyte,
CC   granulocyte, lymphocyte and macrophage cells. SCF results in absolute
CC   increases in haematopoietic cells of both myeloid and lymphoid lineages.
CC   SCF is useful for treating haematopoietic disorders. The method is useful
CC   for expanding early haematopoietic progenitors in syngeneic, allogeneic
CC   or autologous bone marrow transplant. SCF is useful for enhancing the
CC   efficiency of gene therapy based on transfecting haematopoietic stem
CC   cells. SCF is also useful for combating the myelosuppressive effects of
CC   anti-HIV drugs such as AZT and for enhancing haematopoietic recovery
CC   after acute blood loss and as a boost to the immune system for fighting
CC   neoplasia (cancer). The present sequence represents a universal
CC   oligonucleotide which is used in an example from the present invention
XX
SQ   Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1434
AAA13754
ID   AAA13754 standard; DNA; 20 BP.
XX
AC   AAA13754;
XX
DT   27-JUL-2000  (first entry)
XX
DE   Stem cell factor universal oligonucleotide 220-11.
XX
KW   Stem cell factor; SCF; haematopoietic progenitor cell; blood forming;
KW   primitive progenitor cell; haematopoietic disorder; syngeneic;
KW   allogeneic; autologous bone marrow transplant; gene therapy;
KW   transfection; haematopoietic stem cell; acute blood loss; neoplasia;
KW   cancer; ss.
XX
OS   Synthetic.
XX
PN   EP992579-A1.
XX
PD   12-APR-2000.
XX
PF   04-OCT-1990;   99EP-00122861.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   28-SEP-1990;   90WO-US005548.
PR   01-OCT-1990;   90US-00589701.
PR   04-OCT-1990;   90EP-00310899.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Zsebo KM,  Suggs SV,  Bosselmann RA,  Martin FH;
XX
DR   WPI; 2000-259135/23.
XX
PT   Production of hematopoietic cells suitable for administration to a
PT   subject using progenitor cells and expanding the cells using stem cell
PT   factor.
XX
PS   Example 3; Fig 12C; 123pp; English.
XX
CC   A method has been developed of making haematopoietic cells suitable for
CC   administration to a subject. The method comprises: (a) obtaining
CC   haematopoietic progenitor cells from a donor; and (b) expanding the cells
CC   by adding to the cells a haematopoietically effective dose of a
CC   polypeptide product having at least part of the primary structural
CC   confirmation and one or more of the biological properties of naturally
CC   occurring stem cell factor (SCF). The method is useful for stimulating
CC   primitive progenitor cells including early haematopoietic progenitor
CC   cells which are capable of maturing to erythroid, megakaryocyte,
CC   granulocyte, lymphocyte and macrophage cells. SCF results in absolute
CC   increases in haematopoietic cells of both myeloid and lymphoid lineages.
CC   SCF is useful for treating haematopoietic disorders. The method is useful
CC   for expanding early haematopoietic progenitors in syngeneic, allogeneic
CC   or autologous bone marrow transplant. SCF is useful for enhancing the
CC   efficiency of gene therapy based on transfecting haematopoietic stem
CC   cells. SCF is also useful for combating the myelosuppressive effects of
CC   anti-HIV drugs such as AZT and for enhancing haematopoietic recovery
CC   after acute blood loss and as a boost to the immune system for fighting
CC   neoplasia (cancer). The present sequence represents a universal
CC   oligonucleotide which is used in an example from the present invention
XX
SQ   Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1435
AAH41332/c
ID   AAH41332 standard; DNA; 20 BP.
XX
AC   AAH41332;
XX
DT   21-AUG-2001  (first entry)
XX
DE   Universal stem cell factor (SCF) related oligonucleotide SEQ ID NO:33.
XX
KW   Stem cell factor; SCF; stem cell factor receptor; blood cell disorder;
KW   gene therapy; PCR primer; mutagenesis; probe; ss.
XX
OS   Synthetic.
XX
PN   US6207454-B1.
XX
PD   27-MAR-2001.
XX
PF   31-DEC-1998;   98US-00224681.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   01-OCT-1990;   90US-00589701.
PR   25-NOV-1992;   92US-00982255.
PR   21-DEC-1993;   93US-00172329.
PR   24-MAY-1995;   95US-00449653.
PR   12-JAN-1998;   98US-00005893.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Zsebo KM,  Bosselman RA,  Suggs SV,  Martin FH;
XX
DR   WPI; 2001-366062/38.
XX
PT   Enhancing efficiency of transfer of polynucleotide into a target
PT   mammalian cell in vitro, involves exposing cell that expresses a stem
```

PT cell factor receptor to stem cell factor, and introducing polynucleotide
PT into cell in vitro.
XX
PS Example 3; Fig 12C; 210pp; English.
XX
CC The present invention describes a method for enhancing (E) the efficiency
CC of transfer of a polynucleotide (I) into a target mammalian cell (II) in
CC vitro, comprising exposing (II) that expresses a stem cell factor (SCF)
CC receptor to a biologically active SCF, its analogue or fragment, which
CC induces cell proliferation, and introducing (I) to (II) in vitro.
CC Exposure of SCF to (II) results in increased uptake of (I) into the cell.
CC The method is useful for enhancing the efficiency of the transfer of a
CC polynucleotide into a target mammalian cell in vitro. The method is
CC useful in gene therapy techniques. AAH41301 to AAH41364 and AAB98351 to
CC AAB98390 represent sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2803
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1436
AAH41333
ID AAH41333 standard; DNA; 20 BP.
XX
AC AAH41333;
XX
DT 21-AUG-2001 (first entry)
XX
DE Universal stem cell factor (SCF) related oligonucleotide SEQ ID NO:34.
XX
KW Stem cell factor; SCF; stem cell factor receptor; blood cell disorder;
KW gene therapy; PCR primer; mutagenesis; probe; ss.
XX
OS Synthetic.
XX
PN US6207454-B1.
XX
PD 27-MAR-2001.
XX
PF 31-DEC-1998; 98US-00224681.
XX
PR 16-OCT-1989; 89US-00422383.
PR 11-JUN-1990; 90US-00537198.
PR 24-AUG-1990; 90US-00573616.
PR 01-OCT-1990; 90US-00589701.
PR 25-NOV-1992; 92US-00982255.
PR 21-DEC-1993; 93US-00172329.
PR 24-MAY-1995; 95US-00449653.
PR 12-JAN-1998; 98US-00005893.
XX
PA (AMGE-) AMGEN INC.
XX
PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX
DR WPI; 2001-366062/38.
XX
PT Enhancing efficiency of transfer of polynucleotide into a target
PT mammalian cell in vitro, involves exposing cell that expresses a stem
PT cell factor receptor to stem cell factor, and introducing polynucleotide
PT into cell in vitro.
XX
PS Example 3; Fig 12C; 210pp; English.
XX
CC The present invention describes a method for enhancing (E) the efficiency
CC of transfer of a polynucleotide (I) into a target mammalian cell (II) in
CC vitro, comprising exposing (II) that expresses a stem cell factor (SCF)
CC receptor to a biologically active SCF, its analogue or fragment, which
CC induces cell proliferation, and introducing (I) to (II) in vitro.
CC Exposure of SCF to (II) results in increased uptake of (I) into the cell.
CC The method is useful for enhancing the efficiency of the transfer of a
CC polynucleotide into a target mammalian cell in vitro. The method is
CC useful in gene therapy techniques. AAH41301 to AAH41364 and AAB98351 to
CC AAB98390 represent sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTT 2183
Db 1 TTTTTTTTTTTTTTTTTT 18

RESULT 1437
AAS04112/c
ID AAS04112 standard; DNA; 20 BP.
XX
AC AAS04112;
XX
DT 29-AUG-2001 (first entry)
XX
DE Human SCF (stem cell factor) cDNA universal PCR primer 220-7.
XX
KW Human; stem cell factor; SCF; early haematopoietic progenitor cell;
KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
KW anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
KW PCR primer; ss.
XX
OS Homo sapiens.
XX
PN US6207417-B1.
XX
PD 27-MAR-2001.
XX
PF 07-JUN-1995; 95US-00482918.
XX
PR 16-OCT-1989; 89US-00422383.
PR 11-JUN-1990; 90US-00537198.
PR 24-AUG-1990; 90US-00573616.
PR 01-OCT-1990; 90US-00589701.
PR 21-DEC-1993; 93US-00172329.
XX
PA (ZSEB/) ZSEBO K M.
PA (BOSS/) BOSSELMAN R A.
PA (SUGG/) SUGGS S V.
PA (MART/) MARTIN F H.
XX
PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX
DR WPI; 2001-298941/31.
XX
PT Novel nucleic acids encoding stem cell factor useful for treating
PT disorders involving blood cells, e.g. leukemia, splenomegaly, Hodgkin's
PT disease, Kala azar, anemia and septicemia.
XX
PS Example 3; Fig 12C; 209pp; English.
XX
CC The present sequence for universal PCR primer 220-7 is 1 of 8 universal
CC oligonucleotides (AAS04110-AAS04117) used in the isolation of the human
CC SCF (stem cell factor) cDNA sequence. The present invention relates to
CC novel stem cell factors (AAU02453-AAU02458, AAU02460, AAU02461) and the
CC polynucleotides encoding them. SCF stimulate primitive progenitor cells
CC including early haematopoietic progenitor cells. The invention also
CC describes SCF peptides (AAU02462-AAU02481) and the oligonucleotides
CC (AAS04081-AAS04117) used in the isolation of human and rat SCF sequences.

CC The polynucleotide encoding SCF is useful for producing SCF and useful in
CC gene therapy. It is useful for treating disorders involving blood cells
CC such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
CC myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
CC congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
CC disseminated fungus disease, Fulminating septicemia, malaria, vitamin B12
CC and folic acid deficiency, pyridoxine deficiency, and hypopigmentation
CC disorders such as piebaldism and vitiligo
XX
SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2803
||||||||||||||||||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1438
AAS04113
ID AAS04113 standard; DNA; 20 BP.
XX
AC AAS04113;
XX
DT 29-AUG-2001 (first entry)
XX
DE Human SCF (stem cell factor) cDNA universal PCR primer 220-11.
XX
KW Human; stem cell factor; SCF; early haematopoietic progenitor cell;
KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
KW anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
KW PCR primer; ss.
XX
OS Homo sapiens.
XX
PN US6207417-B1.
XX
PD 27-MAR-2001.
XX
PF 07-JUN-1995; 95US-00482918.
XX
PR 16-OCT-1989; 89US-00422383.
PR 11-JUN-1990; 90US-00537198.
PR 24-AUG-1990; 90US-00573616.
PR 01-OCT-1990; 90US-00589701.
PR 21-DEC-1993; 93US-00172329.
XX
PA (ZSEB/) ZSEBO K M.
PA (BOSS/) BOSSELMAN R A.
PA (SUGG/) SUGGS S V.
PA (MART/) MARTIN F H.
XX
PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX
DR WPI; 2001-298941/31.
XX
PT Novel nucleic acids encoding stem cell factor useful for treating
PT disorders involving blood cells, e.g. leukemia, splenomegaly, Hodgkin's
PT disease, Kala azar, anemia and septicemia.
XX
PS Example 3; Fig 12C; 209pp; English.
XX
CC The present sequence for universal PCR primer 220-11 is 1 of 8 universal
CC oligonucleotides (AAS04110-AAS04117) used in the isolation of the human
CC SCF (stem cell factor) cDNA sequence. The present invention relates to
CC novel stem cell factors (AAU02453-AAU02458, AAU02460, AAU02461) and the
CC polynucleotides encoding them. SCF stimulate primitive progenitor cells
CC including early haematopoietic progenitor cells. The invention also
CC describes SCF peptides (AAU02462-AAU02481) and the oligonucleotides
CC (AAS04081-AAS04117) used in the isolation of human and rat SCF sequences.
CC The polynucleotide encoding SCF is useful for producing SCF and useful in
CC gene therapy. It is useful for treating disorders involving blood cells
CC such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
CC myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
CC congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
CC disseminated fungus disease, Fulminating septicemia, malaria, vitamin B12
CC and folic acid deficiency, pyridoxine deficiency, and hypopigmentation
CC disorders such as piebaldism and vitiligo
XX
SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTT 2183
||||||||||||||||||
Db 1 TTTTTTTTTTTTTTTTTT 18

RESULT 1439
AAF89092/c
ID AAF89092 standard; DNA; 20 BP.
XX
AC AAF89092;
XX
DT 13-JUL-2001 (first entry)
XX
DE Mammalian stem cell factor PCR primer SEQ ID NO: 33.
XX
KW Human; rat; mammal; stem cell factor; SCF; cell growth stimulation;
KW gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia;
KW neurological damage; intestinal damage; infertility; AIDS; SCID;
KW severe combined immunodeficiency; PCR primer; ss.
XX
OS Mammalia.
XX
PN US6207802-B1.
XX
PD 27-MAR-2001.
XX
PF 09-NOV-1994; 94US-00336728.
XX
PR 16-OCT-1989; 89US-00422383.
PR 11-JUN-1990; 90US-00537198.
PR 24-AUG-1990; 90US-00573616.
PR 01-OCT-1990; 90US-00589701.
PR 25-NOV-1992; 92US-00982255.
XX
PA (AMGE-) AMGEN INC.
XX
PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX
DR WPI; 2001-353108/37.
XX
PT Novel isolated non-human mammalian stem cell factor polypeptide
PT stimulating growth of early hematopoietic progenitor cells, useful for
PT treating aplastic anemia, lymphoma, Letterer-Siwe disease, Kala azar,
PT sarcoidosis.
XX
PS Example 3; Fig 12C; 209pp; English.
XX
CC The present invention provides the protein and coding sequences of
CC mammalian stem cell factors (SCFs). These are capable of stimulating the
CC growth of early haematopoietic progenitor cells, neural stem cells and
CC primordial germ stem cells. The sequences are useful in the treatment of
CC leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal
CC nocturnal haemoglobinuria, malaria, pigmentation disorders, neurological
CC and intestinal damage, infertility, AIDS and severe combined
CC immunodeficiency (SCID). The present sequence is primer used to amplify
CC an SCF in the exemplification of the invention
XX
SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

```
  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1440
AAF89093
ID   AAF89093 standard; DNA; 20 BP.
XX
AC   AAF89093;
XX
DT   13-JUL-2001  (first entry)
XX
DE   Mammalian stem cell factor PCR primer SEQ ID NO: 34.
XX
KW   Human; rat; mammal; stem cell factor; SCF; cell growth stimulation;
KW   gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia;
KW   neurological damage; intestinal damage; infertility; AIDS; SCID;
KW   severe combined immunodeficiency; PCR primer; ss.
XX
OS   Mammalia.
XX
PN   US6207802-B1.
XX
PD   27-MAR-2001.
XX
PF   09-NOV-1994;   94US-00336728.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   01-OCT-1990;   90US-00589701.
PR   25-NOV-1992;   92US-00982255.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Zsebo KM,  Bosselman RA,  Suggs SV,  Martin FH;
XX
DR   WPI; 2001-353108/37.
XX
PT   Novel isolated non-human mammalian stem cell factor polypeptide
PT   stimulating growth of early hematopoietic progenitor cells, useful for
PT   treating aplastic anemia, lymphoma, Letterer-Siwe disease, Kala azar,
PT   sarcoidosis.
XX
PS   Example 3; Fig 12C; 209pp; English.
XX
CC   The present invention provides the protein and coding sequences of
CC   mammalian stem cell factors (SCFs). These are capable of stimulating the
CC   growth of early haematopoietic progenitor cells, neural stem cells and
CC   primordial germ stem cells. The sequences are useful in the treatment of
CC   leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal
CC   nocturnal haemoglobinuria, malaria, pigmentation disorders, neurological
CC   and intestinal damage, infertility, AIDS and severe combined
CC   immunodeficiency (SCID). The present sequence is primer used to amplify
CC   an SCF in the exemplification of the invention
XX
SQ   Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1441
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```
AAS05714
ID   AAS05714 standard; DNA; 20 BP.
XX
AC   AAS05714;
XX
DT   07-SEP-2001  (first entry)
XX
DE   Aminopurine substituted region of an RP-TFO.
XX
KW   reverse phase triplex forming oligonucleotide; RP-TFO;
KW   protected nucleic acid sequence; PNAS; single nucleotide polymorphism;
KW   SNP; short tandem repeat; cancer; Factor V Leiden SNP; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /label= OTHER
FT                   /note= "A is aminopurine substituted"
FT   modified_base   3
FT                   /*tag=  b
FT                   /label= OTHER
FT                   /note= "A is aminopurine substituted"
FT   modified_base   5
FT                   /*tag=  c
FT                   /label= OTHER
FT                   /note= "A is aminopurine substituted"
FT   Modified_base   7
FT                   /*tag=  d
FT                   /label= OTHER
FT                   /note= "A is aminopurine substituted"
FT   modified_base   9
FT                   /*tag=  f
FT                   /label= OTHER
FT                   /note= "A is aminopurine substituted"
FT   modified_base   11
FT                   /*tag=  g
FT                   /label= OTHER
FT                   /note= "A is aminopurine substituted"
FT   modified_base   13
FT                   /*tag=  g
FT                   /label= OTHER
FT                   /note= "A is aminopurine substituted"
FT   modified_base   15
FT                   /*tag=  h
FT                   /label= OTHER
FT                   /note= "A is aminopurine sustituted"
FT   modified_base   16
FT                   /*tag=  i
FT                   /label= OTHER
FT                   /note= "A is aminopurine substituted"
FT   modified_base   17
FT                   /*tag=  j
FT                   /label= OTHER
FT                   /note= "Other= Hypoxanthine or Inosine"
FT   modified_base   18
FT                   /*tag=  k
FT                   /label= OTHER
FT                   /note= "A is aminopurine substituted"
FT   modified_base   20
FT                   /*tag=  l
FT                   /label= OTHER
FT                   /note= "A is aminopurine substituted"
XX
PN   WO200132929-A1.
XX
PD   10-MAY-2001.
XX
PF   03-NOV-2000; 2000WO-US030534.
XX
PR   03-NOV-1999;   99US-0163356P.
PR   03-NOV-1999;   99US-0163416P.
```

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PR   21-DEC-1999;   99US-0171348P.
PR   07-JUL-2000; 2000US-0216579P.
XX
PA   (CYGE-) CYGENE INC.
PA   (OSTE/) OSTE C C.
XX
PI   Oste CC,  Ramberg ER;
XX
DR   WPI; 2001-343488/36.
XX
PT   Analyzing target nucleic acid sequences, useful for population genetics,
PT   drug development and diagnosing cancer, comprises hybridizing triple
PT   forming oligonucleotide and probe to target sequence.
XX
PS   Example 2; Page 66; 141pp; English.
XX
CC   The sequence is a second reverse phase triplex forming oligonucleotide,
CC   RP-TFO (3' to the SNP) used to analyse Factor V Leiden SNP using the
CC   method of the invention. The invention relates to analysing target
CC   nucleic acid sequences comprising restricting isolated DNA, hybridising
CC   at least one triplex forming oligonucleotide (TFO), adding a 3' to 5'
CC   exonuclease to form a protected nucleic acid sequence (PNAS) tail
CC   structure, hybridising the captured structure with a single nucleotide
CC   polymorphisms (SNP) identification probe and determining the SNP score.
CC   The methods can be used for analysing target nucleic acid sequences,
CC   especially genomic DNA sequences, to determine if they contain SNPs or
CC   short tandem repeats (STRs). The methods can be used to detect SNPs for
CC   use in population genetics, drug development, forensics, cancer, genetic
CC   disease research, genomic analysis, diagnostics and therapeutics in
CC   humans, plants and animals
XX
SQ   Sequence 20 BP; 19 A; 0 C; 0 G; 0 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||  ||
Db          1 AAAAAAAAAAAAAAAAANAA 19


RESULT 1442
AAS05715/c
ID   AAS05715 standard; DNA; 20 BP.
XX
AC   AAS05715;
XX
DT   07-SEP-2001  (first entry)
XX
DE   8-aminopurine substituted region of an RP-TFO.
XX
KW   reverse phase triplex forming oligonucleotide; RP-TFO;
KW   protected nucleic acid sequence; PNAS; single nucleotide polymorphism;
KW   SNP; short tandem repeat; cancer; Factor V Leiden SNP; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   17
FT                   /*tag=  a
FT                   /label= OTHER
FT                   /note= "Other= Hypoxanthine or Inosine"
XX
PN   WO200132929-A1.
XX
PD   10-MAY-2001.
XX
PF   03-NOV-2000; 2000WO-US030534.
XX
PR   03-NOV-1999;   99US-0163356P.
PR   03-NOV-1999;   99US-0163416P.
PR   21-DEC-1999;   99US-0171348P.
PR   07-JUL-2000; 2000US-0216579P.
XX
PA   (CYGE-) CYGENE INC.
PA   (OSTE/) OSTE C C.
XX
PI   Oste CC,  Ramberg ER;
XX
DR   WPI; 2001-343488/36.
XX
PT   Analyzing target nucleic acid sequences, useful for population genetics,
PT   drug development and diagnosing cancer, comprises hybridizing triple
PT   forming oligonucleotide and probe to target sequence.
XX
PS   Example 2; Page 66; 141pp; English.
XX
CC   The sequence is a second reverse phase triplex forming oligonucleotide,
CC   RP-TFO (3' to the SNP) used to analyse Factor V Leiden SNP using the
CC   method of the invention. The invention relates to analysing target
CC   nucleic acid sequences comprising restricting isolated DNA, hybridising
CC   at least one triplex forming oligonucleotide (TFO), adding a 3' to 5'
CC   exonuclease to form a protected nucleic acid sequence (PNAS) tail
CC   structure, hybridising the captured structure with a single nucleotide
CC   polymorphisms (SNP) identification probe and determining the SNP score.
CC   The methods can be used for analysing target nucleic acid sequences,
CC   especially genomic DNA sequences, to determine if they contain SNPs or
CC   short tandem repeats (STRs). The methods can be used to detect SNPs for
CC   use in population genetics, drug development, forensics, cancer, genetic
CC   disease research, genomic analysis, diagnostics and therapeutics in
CC   humans, plants and animals
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              ||| |||||||||||||||
Db         20 AAANAAAAAAAAAAAAAA 2


RESULT 1443
AAH23891
ID   AAH23891 standard; DNA; 20 BP.
XX
AC   AAH23891;
XX
DT   07-AUG-2001  (first entry)
XX
DE   Human SCF (stem cell factor) cDNA universal PCR primer 220-11.
XX
KW   Human; stem cell factor; SCF; early haematopoietic progenitor cell;
KW   blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
KW   anaemia; Kala azar; septicaemia; malaria; hypopigmentation disorder;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6204363-B1.
XX
PD   20-MAR-2001.
XX
PF   25-NOV-1992;   92US-00982255.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   01-OCT-1990;   90US-00589701.
PR   10-APR-1991;   91US-00684535.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Zsebo KM,  Bosselman RA,  Suggs SV,  Martin FH;
```

```
XX
DR   WPI; 2001-256683/26.
XX
PT   New stem cell factor polypeptides and their analogs which stimulate
PT   growth of early hematopoietic progenitors, useful for treating aplastic
PT   anemia, carcinoma, multiple myeloma, vitiligo, kala azar, Hodgkin's
PT   disease.
XX
PS   Example 3; Fig 12C; 166pp; English.
XX
CC   The present sequence for universal PCR primer 220-11 is 1 of 8 universal
CC   oligonucleotides (AAH23888-AAH23895) used in the isolation of the human
CC   SCF (stem cell factor) cDNA sequence. The present invention relates to
CC   novel stem cell factors (AAB73561-AAB73568, AAB73571-AAB73576) and the
CC   polynucleotides encoding them. SCF stimulate primitive progenitor cells
CC   including early haematopoietic progenitor cells. The invention also
CC   describes SCF peptides (AAB73578-AAB73597) and the oligonucleotides
CC   (AAH23859-AAH23887) used in the isolation of human and rat SCF sequences.
CC   The polynucleotide encoding SCF is useful for producing SCF and useful in
CC   gene therapy. It is useful for treating disorders involving blood cells
CC   such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
CC   myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
CC   congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
CC   disseminated fungus disease, Fulminating septicaemia, malaria, vitamin
CC   B12 and folic acid deficiency, pyridoxine deficiency, and
CC   hypopigmentation disorders such as piebaldism and vitiligo
XX
SQ   Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1444
AAH23890/c
ID   AAH23890 standard; DNA; 20 BP.
XX
AC   AAH23890;
XX
DT   07-AUG-2001  (first entry)
XX
DE   Human SCF (stem cell factor) cDNA universal PCR primer 220-7.
XX
KW   Human; stem cell factor; SCF; early haematopoietic progenitor cell;
KW   blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
KW   anaemia; Kala azar; septicaemia; malaria; hypopigmentation disorder;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6204363-B1.
XX
PD   20-MAR-2001.
XX
PF   25-NOV-1992;   92US-00982255.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   01-OCT-1990;   90US-00589701.
PR   10-APR-1991;   91US-00684535.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Zsebo KM,  Bosselman RA,  Suggs SV,  Martin FH;
XX
DR   WPI; 2001-256683/26.
XX
PT   New stem cell factor polypeptides and their analogs which stimulate
PT   growth of early hematopoietic progenitors, useful for treating aplastic
PT   anemia, carcinoma, multiple myeloma, vitiligo, kala azar, Hodgkin's
PT   disease.
XX
PS   Example 3; Fig 12C; 166pp; English.
XX
CC   The present sequence for universal PCR primer 220-7 is 1 of 8 universal
CC   oligonucleotides (AAH23888-AAH23895) used in the isolation of the human
CC   SCF (stem cell factor) cDNA sequence. The present invention relates to
CC   novel stem cell factors (AAB73561-AAB73568, AAB73571-AAB73576) and the
CC   polynucleotides encoding them. SCF stimulate primitive progenitor cells
CC   including early haematopoietic progenitor cells. The invention also
CC   describes SCF peptides (AAB73578-AAB73597) and the oligonucleotides
CC   (AAH23859-AAH23887) used in the isolation of human and rat SCF sequences.
CC   The polynucleotide encoding SCF is useful for producing SCF and useful in
CC   gene therapy. It is useful for treating disorders involving blood cells
CC   such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
CC   myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
CC   congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
CC   disseminated fungus disease, Fulminating septicaemia, malaria, vitamin
CC   B12 and folic acid deficiency, pyridoxine deficiency, and
CC   hypopigmentation disorders such as piebaldism and vitiligo
XX
SQ   Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1445
AAS04213/c
ID   AAS04213 standard; DNA; 20 BP.
XX
AC   AAS04213;
XX
DT   29-AUG-2001  (first entry)
XX
DE   Human SCF (stem cell factor) cDNA universal PCR primer 220-7.
XX
KW   Human; stem cell factor; SCF; early haematopoietic progenitor cell;
KW   blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
KW   anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6218148-B1.
XX
PD   17-APR-2001.
XX
PF   21-DEC-1993;   93US-00172329.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   01-OCT-1990;   90US-00589701.
PR   25-NOV-1992;   92US-00982255.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Zsebo KM,  Bosselman RA,  Suggs SV,  Martin FH;
XX
DR   WPI; 2001-281051/29.
XX
PT   Isolated DNA sequence, encoding polypeptide product useful for
PT   stimulating growth of early hematopoietic progenitor cells.
XX
```

PS Example 3; Fig 12C; 167pp; English.
XX
CC The present sequence for universal PCR primer 220-7 is 1 of 8 universal
CC oligonucleotides (AAS04211-AAS04218) used in the isolation of the human
CC SCF (stem cell factor) cDNA sequence. The present invention relates to
CC novel stem cell factors (AAU02761-AAU02767, AAU02770-AAU02775, AAU02797)
CC and the polynucleotides encoding them. SCF stimulate primitive progenitor
CC cells including early haematopoietic progenitor cells. The invention also
CC describes SCF peptides (AAU02777-AAU02794) and the oligonucleotides
CC (AAS04182-AAS04210) used in the isolation of human and rat SCF sequences.
CC The polynucleotide encoding SCF is useful for producing SCF and useful in
CC gene therapy. It is useful for treating disorders involving blood cells
CC such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
CC myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
CC congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
CC disseminated fungus disease, Fulminating septicemia, malaria, vitamin B12
CC and folic acid deficiency, pyridoxine deficiency, and hypopigmentation
CC disorders such as piebaldism and vitiligo
XX
SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2803
||||||||||||||||||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1446
AAS04214
ID AAS04214 standard; DNA; 20 BP.
XX
AC AAS04214;
XX
DT 29-AUG-2001 (first entry)
XX
DE Human SCF (stem cell factor) cDNA universal PCR primer 220-11.
XX
KW Human; stem cell factor; SCF; early haematopoietic progenitor cell;
KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
KW anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
KW PCR primer; ss.
XX
OS Homo sapiens.
XX
PN US6218148-B1.
XX
PD 17-APR-2001.
XX
PF 21-DEC-1993; 93US-00172329.
XX
PR 16-OCT-1989; 89US-00422383.
PR 11-JUN-1990; 90US-00537198.
PR 24-AUG-1990; 90US-00573616.
PR 01-OCT-1990; 90US-00589701.
PR 25-NOV-1992; 92US-00982255.
XX
PA (AMGE-) AMGEN INC.
XX
PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX
DR WPI; 2001-281051/29.
XX
PT Isolated DNA sequence, encoding polypeptide product useful for
PT stimulating growth of early hematopoietic progenitor cells.
XX
PS Example 3; Fig 12C; 167pp; English.
XX
CC The present sequence for universal PCR primer 220-11 is 1 of 8 universal
CC oligonucleotides (AAS04211-AAS04218) used in the isolation of the human
CC SCF (stem cell factor) cDNA sequence. The present invention relates to
CC novel stem cell factors (AAU02761-AAU02767, AAU02770-AAU02775, AAU02797)
CC and the polynucleotides encoding them. SCF stimulate primitive progenitor
CC cells including early haematopoietic progenitor cells. The invention also
CC describes SCF peptides (AAU02777-AAU02794) and the oligonucleotides
CC (AAS04182-AAS04210) used in the isolation of human and rat SCF sequences.
CC The polynucleotide encoding SCF is useful for producing SCF and useful in
CC gene therapy. It is useful for treating disorders involving blood cells
CC such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
CC myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
CC congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
CC disseminated fungus disease, Fulminating septicemia, malaria, vitamin B12
CC and folic acid deficiency, pyridoxine deficiency, and hypopigmentation
CC disorders such as piebaldism and vitiligo
XX
SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTT 2183
||||||||||||||||||
Db 1 TTTTTTTTTTTTTTTTTT 18

RESULT 1447
AAS10449
ID AAS10449 standard; DNA; 20 BP.
XX
AC AAS10449;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human stem cell factor (SCF) cDNA universal PCR primer 220-11.
XX
KW Human; stem cell factor; SCF; haematopoietic progenitor cell;
KW blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency;
KW hypopigmentation disorder; viral disorder; AIDS; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN US6248319-B1.
XX
PD 19-JUN-2001.
XX
PF 24-MAY-1995; 95US-00449653.
XX
PR 16-OCT-1989; 89US-00422383.
PR 11-JUN-1990; 90US-00537198.
PR 24-AUG-1990; 90US-00573616.
PR 01-OCT-1990; 90US-00589701.
PR 10-APR-1991; 91US-00684535.
PR 25-NOV-1992; 92US-00982255.
PR 21-DEC-1993; 93US-00172329.
XX
PA (ZSEB/) ZSEBO K M.
PA (BOSS/) BOSSELMAN R A.
PA (SUGG/) SUGGS S V.
PA (MART/) MARTIN F H.
XX
PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX
DR WPI; 2001-407312/43.
XX
PT Increasing the number of early hematopoietic progenitor cells in the
PT peripheral blood useful for the treatment of blood disorders including
PT Hodgkin's disease comprises the administration of human stem cell factor.
XX
PS Example 3; Fig 12C; 210pp; English.
XX
CC The present sequence for universal PCR primer 220-11 is 1 of 19 PCR
CC primers (AAS10435-AAS10453) used to amplify various portions of the human
CC SCF cDNA sequence. The sequence is described in an invention relating to

```
CC   novel stem cell factors, the polynucleotides encoding them and methods
CC   for producing the stem cell factors. The methods involve increasing the
CC   number of early haematopoietic progenitor cells in human peripheral blood
CC   by administering a haematopoietically effective human stem cell factor
CC   polypeptide. The methods are useful for the treatment of blood disorders,
CC   including myelofibrosis, myelosclerosis, osteopetrosis, metastatic
CC   carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease,
CC   lymphoma, Gaucher's disease, Niemann-Pick disease, refractory anaemia,
CC   malaria, vitamin B12 and folic acid deficiency, hypopigmentation
CC   disorders i.e. piebaldism and viral induced disorders, including AIDS
XX
SQ   Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1448
AAS10448/c
ID   AAS10448 standard; DNA; 20 BP.
XX
AC   AAS10448;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human stem cell factor (SCF) cDNA universal PCR primer 220-7.
XX
KW   Human; stem cell factor; SCF; haematopoietic progenitor cell;
KW   blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency;
KW   hypopigmentation disorder; viral disorder; AIDS; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6248319-B1.
XX
PD   19-JUN-2001.
XX
PF   24-MAY-1995;   95US-00449653.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   01-OCT-1990;   90US-00589701.
PR   10-APR-1991;   91US-00684535.
PR   25-NOV-1992;   92US-00982255.
PR   21-DEC-1993;   93US-00172329.
XX
PA   (ZSEB/) ZSEBO K M.
PA   (BOSS/) BOSSELMAN R A.
PA   (SUGG/) SUGGS S V.
PA   (MART/) MARTIN F H.
XX
PI   Zsebo KM,  Bosselman RA,  Suggs SV,  Martin FH;
XX
DR   WPI; 2001-407312/43.
XX
PT   Increasing the number of early hematopoietic progenitor cells in the
PT   peripheral blood useful for the treatment of blood disorders including
PT   Hodgkin's disease comprises the administration of human stem cell factor.
XX
PS   Example 3; Fig 12C; 210pp; English.
XX
CC   The present sequence for universal PCR primer 220-7 is 1 of 19 PCR
CC   primers (AAS10435-AAS10453) used to amplify various portions of the human
CC   SCF cDNA sequence. The sequence is described in an invention relating to
CC   novel stem cell factors, the polynucleotides encoding them and methods
CC   for producing the stem cell factors. The methods involve increasing the
CC   number of early haematopoietic progenitor cells in human peripheral blood
CC   by administering a haematopoietically effective human stem cell factor
CC   polypeptide. The methods are useful for the treatment of blood disorders,
CC   including myelofibrosis, myelosclerosis, osteopetrosis, metastatic
CC   carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease,
CC   lymphoma, Gaucher's disease, Niemann-Pick disease, refractory anaemia,
CC   malaria, vitamin B12 and folic acid deficiency, hypopigmentation
CC   disorders i.e. piebaldism and viral induced disorders, including AIDS
XX
SQ   Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1449
AAD35465/c
ID   AAD35465 standard; DNA; 20 BP.
XX
AC   AAD35465;
XX
DT   25-JUL-2002  (first entry)
XX
DE   Rat SCF 5' cDNA amplifying PCR primer, 220-7.
XX
KW   Rat; stem cell factor; SCF protein; leucopaenia; thrombocytopaenia;
KW   anaemia; myelosuppression; nerve damage; myeloproliferative disorder;
KW   infertility; neoplasia; myelofibrosis; myelosclerosis; osteopetrosis;
KW   metastatic carcinoma; acute leukaemia; multiple myeloma; sarcoidosis;
KW   Hodgkin's disease; lymphoma; Gaucher's disease; Niemann-Pick disease;
KW   Letterer-Siwe disease; refractory erythroblastic anaemia; Kala azar;
KW   Di Guglielmo syndrome; congestive splenomegaly; splenic pancytopaenia;
KW   disseminated fungus disease; Fulminating septicaemia; piebaldism; AIDS;
KW   acquired immune deficiency syndrome; malaria; military tuberculosis;
KW   pyridoxine deficiency; vitamin B12 deficiency; folic acid deficiency;
KW   Diamond Blackfan anaemia; hypopigmentation disorder; vitiligo; PCR;
KW   primer; ss.
XX
OS   Rattus sp.
XX
PN   US2002018763-A1.
XX
PD   14-FEB-2002.
XX
PF   12-JAN-1998;   98US-00005243.
XX
PR   24-MAY-1995;   95US-00449653.
XX
PA   (ZSEB/) ZSEBO K M.
PA   (BOSS/) BOSSELMAN R A.
PA   (SUGG/) SUGGS S V.
PA   (MART/) MARTIN F H.
XX
PI   Zsebo KM,  Bosselman RA,  Suggs SV,  Martin FH;
XX
DR   WPI; 2002-350789/38.
XX
PT   Novel non-naturally-occurring stem cell factor polypeptide, useful for
PT   treating leucopenia, thrombocytopenia, anemia and for enhancing
PT   engraftment of bone marrow during transplantation in a mammal.
XX
PS   Example 3; Fig 12C; 217pp; English.
XX
CC   The present invention relates to novel non-naturally-occurring stem cell
CC   factor (SCF) polypeptides having an amino acid sequence sufficiently
CC   duplicative of that of naturally-occurring SCF to allow possession of
CC   haematopoietic biological activity of naturally occurring SCF. Sequences
CC   of the invention are useful for treating leucopaenia, thrombocytopaenia,
CC   anaemia and for enhancing bone marrow recovery in treatment of radiation,
```

CC engraftment of bone marrow during transplantation in mammals and chemical
CC or chemotherapeutic induced bone marrow aplasia or myelosuppression. They
CC are also useful for treating acquired immune deficiency in a human, nerve
CC damage, neoplasia, infertility, myeloproliferative disorder, intestinal
CC damage in a mammal. SCF sequences are useful for preparing biologically
CC active polymer polypeptide adduct, for enhancing transfection of early
CC haematopoietic progenitor cells with a gene, and transfer of a gene into
CC a mammal. They are useful for treating myelofibrosis, myelosclerosis,
CC osteopetrosis, metastatic carcinoma, acute leukaemia, multiple myeloma,
CC Hodgkin's disease, lymphoma, Gaucher's disease, Niemann-Pick disease,
CC Letterer-Siwe disease, refractory erythroblastic anaemia, Di Guglielmo
CC syndrome, congestive splenomegaly, Kala azar, sarcoidosis, primary
CC splenic pancytopaenia, disseminated fungus disease, malaria, military
CC tuberculosis, Fulminating septicaemia, pyridoxine deficiency, vitamin B12
CC and folic acid deficiency, Diamond Blackfan anaemia, hypopigmentation
CC disorders such as piebaldism, AIDS (acquired immune deficiency syndrome)
CC and vitiligo. The present sequence is a PCR primer which is used for
CC amplifying the 5' end of rat SCF cDNA. This sequence is used in the
CC exemplification of the invention
XX
SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2803
||||||||||||||||||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1450
AAD35466
ID AAD35466 standard; DNA; 20 BP.
XX
AC AAD35466;
XX
DT 25-JUL-2002 (first entry)
XX
DE Rat SCF 5' cDNA amplifying PCR primer, 220-11.
XX
KW Rat; stem cell factor; SCF protein; leucopaenia; thrombocytopaenia;
KW anaemia; myelosuppression; nerve damage; myeloproliferative disorder;
KW infertility; neoplasia; myelofibrosis; myelosclerosis; osteopetrosis;
KW metastatic carcinoma; acute leukaemia; multiple myeloma; sarcoidosis;
KW Hodgkin's disease; lymphoma; Gaucher's disease; Niemann-Pick disease;
KW Letterer-Siwe disease; refractory erythroblastic anaemia; Kala azar;
KW Di Guglielmo syndrome; congestive splenomegaly; splenic pancytopaenia;
KW disseminated fungus disease; Fulminating septicaemia; piebaldism; AIDS;
KW acquired immune deficiency syndrome; malaria; military tuberculosis;
KW pyridoxine deficiency; vitamin B12 deficiency; folic acid deficiency;
KW Diamond Blackfan anaemia; hypopigmentation disorder; vitiligo; PCR;
KW primer; ss.
XX
OS Rattus sp.
XX
PN US2002018763-A1.
XX
PD 14-FEB-2002.
XX
PF 12-JAN-1998; 98US-00005243.
XX
PR 24-MAY-1995; 95US-00449653.
XX
PA (ZSEB/) ZSEBO K M.
PA (BOSS/) BOSSELMAN R A.
PA (SUGG/) SUGGS S V.
PA (MART/) MARTIN F H.
XX
PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX
DR WPI; 2002-350789/38.
XX
PT Novel non-naturally-occurring stem cell factor polypeptide, useful for
PT treating leucopenia, thrombocytopenia, anemia and for enhancing
PT engraftment of bone marrow during transplantation in a mammal.
XX
PS Example 3; Fig 12C; 217pp; English.
XX
CC The present invention relates to novel non-naturally-occurring stem cell
CC factor (SCF) polypeptides having an amino acid sequence sufficiently
CC duplicative of that of naturally-occurring SCF to allow possession of
CC haematopoietic biological activity of naturally occurring SCF. Sequences
CC of the invention are useful for treating leucopaenia, thrombocytopaenia,
CC anaemia and for enhancing bone marrow recovery in treatment of radiation,
CC engraftment of bone marrow during transplantation in mammals and chemical
CC or chemotherapeutic induced bone marrow aplasia or myelosuppression. They
CC are also useful for treating acquired immune deficiency in a human, nerve
CC damage, neoplasia, infertility, myeloproliferative disorder, intestinal
CC damage in a mammal. SCF sequences are useful for preparing biologically
CC active polymer polypeptide adduct, for enhancing transfection of early
CC haematopoietic progenitor cells with a gene, and transfer of a gene into
CC a mammal. They are useful for treating myelofibrosis, myelosclerosis,
CC osteopetrosis, metastatic carcinoma, acute leukaemia, multiple myeloma,
CC Hodgkin's disease, lymphoma, Gaucher's disease, Niemann-Pick disease,
CC Letterer-Siwe disease, refractory erythroblastic anaemia, Di Guglielmo
CC syndrome, congestive splenomegaly, Kala azar, sarcoidosis, primary
CC splenic pancytopaenia, disseminated fungus disease, malaria, military
CC tuberculosis, Fulminating septicaemia, pyridoxine deficiency, vitamin B12
CC and folic acid deficiency, Diamond Blackfan anaemia, hypopigmentation
CC disorders such as piebaldism, AIDS (acquired immune deficiency syndrome)
CC and vitiligo. The present sequence is a PCR primer which is used for
CC amplifying the 5' end of rat SCF cDNA. This sequence is used in the
CC exemplification of the invention
XX
SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTT 2183
||||||||||||||||||
Db 1 TTTTTTTTTTTTTTTTTT 18

RESULT 1451
ABS73849/c
ID ABS73849 standard; DNA; 20 BP.
XX
AC ABS73849;
XX
DT 05-DEC-2002 (first entry)
XX
DE SCF universal oligonucleotide 220-7.
XX
KW Stem cell factor; SCF; blood-forming system; blood cell disorder;
KW haematopoietic system; metastatic carcinoma; acute leukaemia;
KW multiple myeloma; Hodgkin's disease; lymphoma; malaria; vitiligo;
KW refractory erythroblastic anaemia; miliary tuberculosis; cytostatic;
KW disseminated fungus disease; haematopoietic; tuberculostatic;
KW antianaemic; antifungal; antimalarial; dermatological; ss.
XX
OS Synthetic.
XX
PN EP1241258-A2.
XX
PD 18-SEP-2002.
XX
PF 04-OCT-1990; 2002EP-00008587.
XX
PR 16-OCT-1989; 89US-00422383.
PR 11-JUN-1990; 90US-00537198.
PR 24-AUG-1990; 90US-00573616.
PR 28-SEP-1990; 90WO-US005548.
PR 01-OCT-1990; 90US-00589701.

```
PR   04-OCT-1990;   90EP-00310899.
PR   04-OCT-1990;   95EP-00105391.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Zsebo KM,  Suggs SV,  Bosselman RA,  Martin FH;
XX
DR   WPI; 2002-684093/74.
XX
PT   Production of a human stem cell factor (SCF) polypeptide for treating
PT   disorders involving blood cells, such as leukemia, comprises culturing
PT   mammalian cells comprising non-human SCF promoter DNA linked to DNA
PT   encoding the human SCF.
XX
PS   Example 3; Fig 12C; 120pp; English.
XX
CC   The present invention relates to novel stem cell factors (SCFs),
CC   polynucleotide sequences encoding the SCFs, and methods of producing
CC   them. SCFs are involved in the blood-forming (haematopoietic) system in
CC   mammals, particularly humans. The method of the invention is useful for
CC   the production of human SCF. The stem cell factors are useful to treat
CC   disorders involving blood cells e.g. metastatic carcinoma, acute
CC   leukaemia, multiple myeloma, Hodgkin's disease, lymphoma, refractory
CC   erythroblastic anaemia, miliary tuberculosis, disseminated fungus
CC   disease, malaria, and vitiligo. The present sequence representing a
CC   universal oligonucleotide for SCF DNA is used in the examples of the
CC   present invention
XX
SQ   Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1452
ABS73850
ID   ABS73850 standard; DNA; 20 BP.
XX
AC   ABS73850;
XX
DT   05-DEC-2002  (first entry)
XX
DE   SCF universal oligonucleotide 220-11.
XX
KW   Stem cell factor; SCF; blood-forming system; blood cell disorder;
KW   haematopoietic system; metastatic carcinoma; acute leukaemia;
KW   multiple myeloma; Hodgkin's disease; lymphoma; malaria; vitiligo;
KW   refractory erythroblastic anaemia; miliary tuberculosis; cytostatic;
KW   disseminated fungus disease; haematopoietic; tuberculostatic;
KW   antianaemic; antifungal; antimalarial; dermatological; ss.
XX
OS   Synthetic.
XX
PN   EP1241258-A2.
XX
PD   18-SEP-2002.
XX
PF   04-OCT-1990; 2002EP-00008587.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   28-SEP-1990;   90WO-US005548.
PR   01-OCT-1990;   90US-00589701.
PR   04-OCT-1990;   90EP-00310899.
PR   04-OCT-1990;   95EP-00105391.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Zsebo KM,  Suggs SV,  Bosselman RA,  Martin FH;
XX
DR   WPI; 2002-684093/74.
XX
PT   Production of a human stem cell factor (SCF) polypeptide for treating
PT   disorders involving blood cells, such as leukemia, comprises culturing
PT   mammalian cells comprising non-human SCF promoter DNA linked to DNA
PT   encoding the human SCF.
XX
PS   Example 3; Fig 12C; 120pp; English.
XX
CC   The present invention relates to novel stem cell factors (SCFs),
CC   polynucleotide sequences encoding the SCFs, and methods of producing
CC   them. SCFs are involved in the blood-forming (haematopoietic) system in
CC   mammals, particularly humans. The method of the invention is useful for
CC   the production of human SCF. The stem cell factors are useful to treat
CC   disorders involving blood cells e.g. metastatic carcinoma, acute
CC   leukaemia, multiple myeloma, Hodgkin's disease, lymphoma, refractory
CC   erythroblastic anaemia, miliary tuberculosis, disseminated fungus
CC   disease, malaria, and vitiligo. The present sequence representing a
CC   universal oligonucleotide for SCF DNA is used in the examples of the
CC   present invention
XX
SQ   Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1453
ABZ89678
ID   ABZ89678 standard; DNA; 20 BP.
XX
AC   ABZ89678;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
```

```
XX
PS   Disclosure; SEQ ID NO 4920; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 19 A; 0 C; 0 G; 0 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||  |||||||
Db          1 AAAAAAAAAAANAAAAAAA 19


RESULT 1454
ABZ89677
ID   ABZ89677 standard; DNA; 20 BP.
XX
AC   ABZ89677;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
```

```
XX
PS   Disclosure; SEQ ID NO 4919; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 19 A; 0 C; 0 G; 0 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||| |
Db          1 AAAAAAAAAAAAAAAAANA 19


RESULT 1455
ABZ89240
ID   ABZ89240 standard; DNA; 20 BP.
XX
AC   ABZ89240;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
```

```
XX
PS   Disclosure; SEQ ID NO 4482; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 18 A; 1 C; 0 G; 1 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db          3 AAAAAAAAAAAAAAAAAA 20


RESULT 1456
ADE52462
ID   ADE52462 standard; DNA; 20 BP.
XX
AC   ADE52462;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stem cell factor (SCF) related DNA #33.
XX
KW   Stem cell factor; SCF; haematopoietic activity; infertility;
KW   intestinal damage; myeloproliferative disorder; leucopenia;
KW   thrombocytopenia; anaemia; bone marrow transplant; immune deficiency;
KW   neoplasia; nerve damage; osteoporosis; metastatic carcinoma; leukaemia;
KW   miliary tuberculosis; haematopoietic progenitor cell; ss.
XX
OS   Synthetic.
XX
PN   US2002031491-A1.
XX
PD   14-MAR-2002.
XX
PF   31-DEC-1998;   98US-00224683.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   01-OCT-1990;   90US-00589701.
PR   10-APR-1991;   91US-00684535.
PR   25-NOV-1992;   92US-00982255.
PR   21-DEC-1993;   93US-00172329.
PR   24-MAY-1995;   95US-00449653.
PR   12-JAN-1998;   98US-00005893.
XX
PA   (ZSEB/) ZSEBO K M.
PA   (BOSS/) BOSSELMAN R A.
PA   (SUGG/) SUGGS S V.
PA   (MART/) MARTIN F H.
XX
PI   Zsebo KM,  Bosselman RA,  Suggs SV,  Martin FH;
XX
DR   WPI; 2003-851459/79.
XX
PT   New non-natural stem cell factor, useful for treating e.g. leucopenia or
PT   immune deficiency, also related nucleic acid and antibodies.
XX
PS   Disclosure; SEQ ID NO 34; 217pp; English.
XX
CC   The invention relates to stem cell factor (SCF) polypeptides with
CC   haematopoietic activity and the polynucleotides encoding them. The
CC   polypeptides are used for treating infertility, intestinal damage,
CC   myeloproliferative disorders, leucopenia, thrombocytopenia or anaemia,
CC   for improving engraftment of bone marrow transplants, for enhancing bone
CC   marrow recovery after radiotherapy or chemotherapy and in treatment of
CC   immune deficiency, neoplasia, nerve damage, osteoporosis, metastatic
CC   carcinoma, leukaemia and miliary tuberculosis. The SCF polypeptides are
CC   also used to expand haematopoietic progenitor cells for transplantation
CC   and to prepare such cells for transfection with a gene. The SCF
CC   polynucleotides can be used for recombinant expression of the
CC   polypeptides and also as probes for mapping of the SCF gene, for
CC   identifying SCF-related diseases and as a marker for neighbouring genes.
CC   Antibodies raised against the polypeptides are useful in diagnosis and to
CC   remove SCF from blood. This sequence represents SCF related DNA of the
CC   invention.
XX
SQ   Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1457
ADE52461/c
ID   ADE52461 standard; DNA; 20 BP.
XX
AC   ADE52461;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stem cell factor (SCF) related DNA #32.
XX
KW   Stem cell factor; SCF; haematopoietic activity; infertility;
KW   intestinal damage; myeloproliferative disorder; leucopenia;
KW   thrombocytopenia; anaemia; bone marrow transplant; immune deficiency;
KW   neoplasia; nerve damage; osteoporosis; metastatic carcinoma; leukaemia;
KW   miliary tuberculosis; haematopoietic progenitor cell; ss.
XX
OS   Synthetic.
XX
PN   US2002031491-A1.
XX
PD   14-MAR-2002.
XX
PF   31-DEC-1998;   98US-00224683.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   01-OCT-1990;   90US-00589701.
PR   10-APR-1991;   91US-00684535.
PR   25-NOV-1992;   92US-00982255.
PR   21-DEC-1993;   93US-00172329.
PR   24-MAY-1995;   95US-00449653.
PR   12-JAN-1998;   98US-00005893.
XX
PA   (ZSEB/) ZSEBO K M.
```

```
PA   (BOSS/) BOSSELMAN R A.
PA   (SUGG/) SUGGS S V.
PA   (MART/) MARTIN F H.
XX
PI   Zsebo KM,  Bosselman RA,  Suggs SV,  Martin FH;
XX
DR   WPI; 2003-851459/79.
XX
PT   New non-natural stem cell factor, useful for treating e.g. leucopenia or
PT   immune deficiency, also related nucleic acid and antibodies.
XX
PS   Disclosure; SEQ ID NO 33; 217pp; English.
XX
CC   The invention relates to stem cell factor (SCF) polypeptides with
CC   haematopoietic activity and the polynucleotides encoding them. The
CC   polypeptides are used for treating infertility, intestinal damage,
CC   myeloproliferative disorders, leucopenia, thrombocytopenia or anaemia,
CC   for improving engraftment of bone marrow transplants, for enhancing bone
CC   marrow recovery after radiotherapy or chemotherapy and in treatment of
CC   immune deficiency, neoplasia, nerve damage, osteoporosis, metastatic
CC   carcinoma, leukaemia and miliary tuberculosis. The SCF polypeptides are
CC   also used to expand haematopoietic progenitor cells for transplantation
CC   and to prepare such cells for transfection with a gene. The SCF
CC   polynucleotides can be used for recombinant expression of the
CC   polypeptides and also as probes for mapping of the SCF gene, for
CC   identifying SCF-related diseases and as a marker for neighbouring genes.
CC   Antibodies raised against the polypeptides are useful in diagnosis and to
CC   remove SCF from blood. This sequence represents SCF related DNA of the
CC   invention.
XX
SQ   Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1458
AAQ75588
ID   AAQ75588 standard; DNA; 20 BP.
XX
AC   AAQ75588;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTA 18


RESULT 1459
AAQ75601/c
ID   AAQ75601 standard; DNA; 20 BP.
XX
AC   AAQ75601;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 0 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 1460
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```
AAQ75591/c
ID   AAQ75591 standard; DNA; 20 BP.
XX
AC   AAQ75591;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 0 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 1461
AAQ75605/c
ID   AAQ75605 standard; DNA; 20 BP.
XX
AC   AAQ75605;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 0 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 1462
AAQ75575
ID   AAQ75575 standard; DNA; 20 BP.
XX
AC   AAQ75575;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 1 A; 0 C; 2 G; 17 T; 0 U; 0 Other;
```

```
  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTA 18


RESULT 1463
AAQ75577
ID   AAQ75577 standard; DNA; 20 BP.
XX
AC   AAQ75577;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTA 18


RESULT 1464
AAQ75593/c
ID   AAQ75593 standard; DNA; 20 BP.
XX
AC   AAQ75593;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 1465
AAQ75594/c
ID   AAQ75594 standard; DNA; 20 BP.
XX
AC   AAQ75594;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
```

```
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 0 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match              0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 1466
AAQ75583
ID   AAQ75583 standard; DNA; 20 BP.
XX
AC   AAQ75583;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match              0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTA 18


RESULT 1467
AAQ75606/c
ID   AAQ75606 standard; DNA; 20 BP.
XX
AC   AAQ75606;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 0 A; 3 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match              0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 1468
AAQ75603/c
ID   AAQ75603 standard; DNA; 20 BP.
XX
AC   AAQ75603;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
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PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 0 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match              0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 1469
AAQ75576
ID   AAQ75576 standard; DNA; 20 BP.
XX
AC   AAQ75576;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 2 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match              0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTA 18


RESULT 1470
AAQ75587
ID   AAQ75587 standard; DNA; 20 BP.
XX
AC   AAQ75587;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match              0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTA 18


RESULT 1471
AAQ75599/c
ID   AAQ75599 standard; DNA; 20 BP.
XX
AC   AAQ75599;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
```

OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAAAAAAAA 2802
||||||||||||||||||
Db 18 GAAAAAAAAAAAAAAAAA 1

RESULT 1472
AAT04917
ID AAT04917 standard; cDNA; 20 BP.
XX
AC AAT04917;
XX
DT 25-MAR-2003 (revised)
DT 15-MAY-1996 (first entry)
XX
DE Mammalian stem cell factor (SCF) cDNA oligonucleotide primer 220-3.
XX
KW Stem cell factor; progenitor; haematopoiesis; SCF; anaemia;
KW thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft;
KW transplant; neoplasia; myelosuppression; bone marrow; ss.
XX
OS Synthetic.
XX
PN EP676470-A1.
XX
PD 11-OCT-1995.
XX
PF 04-OCT-1990; 95EP-00105391.
XX
PR 16-OCT-1989; 89US-00422383.
PR 11-JUN-1990; 90US-00537198.
PR 24-AUG-1990; 90US-00573616.
PR 28-SEP-1990; 90WO-US005548.
PR 01-OCT-1990; 90US-00589701.
XX
PA (AMGE-) AMGEN INC.
XX
PI Zsebo KM, Suggs SV, Bosselman RA, Martin FH;
XX
DR WPI; 1995-346090/45.
XX
PT New stem cell factor polypeptide(s) - for stimulating the growth of
PT primitive progenitor cells, esp. for treating disorders involving blood
PT cells.
XX
PS Example 3; Fig 12C; 127pp; English.
XX
CC AAT04915-T04922 are oligonucleotide primers and probes used for the
CC amplification and sequencing of mammalian stem cell factor (SCF). Non-
CC naturally occuring SCF and C-terminally truncated polypeptides, having
CC amino acid sequences sufficiently duplicative of naturally ocurring SCF,
CC stimulate growth of primitive progenitors such as haematopoietic
CC progenitor cells, neural stem cells and primordial germ stem cells. The
CC peptides can be used in a composition for treating leucopenia, anaemia or
CC thrombocytopenia, for enhancing engraftment of bone marrow during
CC transplantation or for bone marrow recovery after chemotherapy or
CC radiation-induced bone marrow aplasia or myelosuppression. They can also
CC be used for treating neoplasia, nerve damage, infertlilty, intestinal
CC damage or myeloproliferative disorders. Antibodies may be raised against
CC the peptides for use in detection or neutralisation of SCF in serum. SCF
CC may be useful for the treatment of AIDS and severe combined
CC immunodeficiency (SCID) states alone or in combination with other factors
CC such as IL-7. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTT 2183
||||||||||||||||||
Db 1 TTTTTTTTTTTTTTTTTT 18

RESULT 1473
AAT04917/c
ID AAT04917 standard; cDNA; 20 BP.
XX
AC AAT04917;
XX
DT 25-MAR-2003 (revised)
DT 15-MAY-1996 (first entry)
XX
DE Mammalian stem cell factor (SCF) cDNA oligonucleotide primer 220-3.
XX
KW Stem cell factor; progenitor; haematopoiesis; SCF; anaemia;
KW thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft;
KW transplant; neoplasia; myelosuppression; bone marrow; ss.
XX
OS Synthetic.
XX
PN EP676470-A1.
XX
PD 11-OCT-1995.
XX
PF 04-OCT-1990; 95EP-00105391.
XX
PR 16-OCT-1989; 89US-00422383.
PR 11-JUN-1990; 90US-00537198.
PR 24-AUG-1990; 90US-00573616.
PR 28-SEP-1990; 90WO-US005548.
PR 01-OCT-1990; 90US-00589701.
XX
PA (AMGE-) AMGEN INC.
XX
PI Zsebo KM, Suggs SV, Bosselman RA, Martin FH;
XX
DR WPI; 1995-346090/45.
XX
PT New stem cell factor polypeptide(s) - for stimulating the growth of
PT primitive progenitor cells, esp. for treating disorders involving blood
PT cells.

```
XX
PS   Example 3; Fig 12C; 127pp; English.
XX
CC   AAT04915-T04922 are oligonucleotide primers and probes used for the
CC   amplification and sequencing of mammalian stem cell factor (SCF). Non-
CC   naturally occuring SCF and C-terminally truncated polypeptides, having
CC   amino acid sequences sufficiently duplicative of naturally ocurring SCF,
CC   stimulate growth of primitive progenitors such as haematopoietic
CC   progenitor cells, neural stem cells and primordial germ stem cells. The
CC   peptides can be used in a composition for treating leucopenia, anaemia or
CC   thrombocytopenia, for enhancing engraftment of bone marrow during
CC   transplantation or for bone marrow recovery after chemotherapy or
CC   radiation-induced bone marrow aplasia or myelosuppression. They can also
CC   be used for treating neoplasia, nerve damage, infertlilty, intestinal
CC   damage or myeloproliferative disorders. Antibodies may be raised against
CC   the peptides for use in detection or neutralisation of SCF in serum. SCF
CC   may be useful for the treatment of AIDS and severe combined
CC   immunodeficiency (SCID) states alone or in combination with other factors
CC   such as IL-7. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1474
AAA13752
ID   AAA13752 standard; DNA; 20 BP.
XX
AC   AAA13752;
XX
DT   27-JUL-2000  (first entry)
XX
DE   Stem cell factor universal oligonucleotide 220-3.
XX
KW   Stem cell factor; SCF; haematopoietic progenitor cell; blood forming;
KW   primitive progenitor cell; haematopoietic disorder; syngeneic;
KW   allogeneic; autologous bone marrow transplant; gene therapy;
KW   transfection; haematopoietic stem cell; acute blood loss; neoplasia;
KW   cancer; ss.
XX
OS   Synthetic.
XX
PN   EP992579-A1.
XX
PD   12-APR-2000.
XX
PF   04-OCT-1990;   99EP-00122861.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   28-SEP-1990;   90WO-US005548.
PR   01-OCT-1990;   90US-00589701.
PR   04-OCT-1990;   90EP-00310899.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Zsebo KM,  Suggs SV,  Bosselmann RA,  Martin FH;
XX
DR   WPI; 2000-259135/23.
XX
PT   Production of hematopoietic cells suitable for administration to a
PT   subject using progenitor cells and expanding the cells using stem cell
PT   factor.
XX
PS   Example 3; Fig 12C; 123pp; English.
XX
CC   A method has been developed of making haematopoietic cells suitable for
CC   administration to a subject. The method comprises: (a) obtaining
CC   haematopoietic progenitor cells from a donor; and (b) expanding the cells
CC   by adding to the cells a haematopoietically effective dose of a
CC   polypeptide product having at least part of the primary structural
CC   confirmation and one or more of the biological properties of naturally
CC   occurring stem cell factor (SCF). The method is useful for stimulating
CC   primitive progenitor cells including early haematopoietic progenitor
CC   cells which are capable of maturing to erythroid, megakaryocyte,
CC   granulocyte, lymphocyte and macrophage cells. SCF results in absolute
CC   increases in haematopoietic cells of both myeloid and lymphoid lineages.
CC   SCF is useful for treating haematopoietic disorders. The method is useful
CC   for expanding early haematopoietic progenitors in syngeneic, allogeneic
CC   or autologous bone marrow transplant. SCF is useful for enhancing the
CC   efficiency of gene therapy based on transfecting haematopoietic stem
CC   cells. SCF is also useful for combating the myelosuppressive effects of
CC   anti-HIV drugs such as AZT and for enhancing haematopoietic recovery
CC   after acute blood loss and as a boost to the immune system for fighting
CC   neoplasia (cancer). The present sequence represents a universal
CC   oligonucleotide which is used in an example from the present invention
XX
SQ   Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1475
AAA13752/c
ID   AAA13752 standard; DNA; 20 BP.
XX
AC   AAA13752;
XX
DT   27-JUL-2000  (first entry)
XX
DE   Stem cell factor universal oligonucleotide 220-3.
XX
KW   Stem cell factor; SCF; haematopoietic progenitor cell; blood forming;
KW   primitive progenitor cell; haematopoietic disorder; syngeneic;
KW   allogeneic; autologous bone marrow transplant; gene therapy;
KW   transfection; haematopoietic stem cell; acute blood loss; neoplasia;
KW   cancer; ss.
XX
OS   Synthetic.
XX
PN   EP992579-A1.
XX
PD   12-APR-2000.
XX
PF   04-OCT-1990;   99EP-00122861.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   28-SEP-1990;   90WO-US005548.
PR   01-OCT-1990;   90US-00589701.
PR   04-OCT-1990;   90EP-00310899.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Zsebo KM,  Suggs SV,  Bosselmann RA,  Martin FH;
XX
DR   WPI; 2000-259135/23.
XX
PT   Production of hematopoietic cells suitable for administration to a
PT   subject using progenitor cells and expanding the cells using stem cell
PT   factor.
```

```
XX
PS   Example 3; Fig 12C; 123pp; English.
XX
CC   A method has been developed of making haematopoietic cells suitable for
CC   administration to a subject. The method comprises: (a) obtaining
CC   haematopoietic progenitor cells from a donor; and (b) expanding the cells
CC   by adding to the cells a haematopoietically effective dose of a
CC   polypeptide product having at least part of the primary structural
CC   confirmation and one or more of the biological properties of naturally
CC   occurring stem cell factor (SCF). The method is useful for stimulating
CC   primitive progenitor cells including early haematopoietic progenitor
CC   cells which are capable of maturing to erythroid, megakaryocyte,
CC   granulocyte, lymphocyte and macrophage cells. SCF results in absolute
CC   increases in haematopoietic cells of both myeloid and lymphoid lineages.
CC   SCF is useful for treating haematopoietic disorders. The method is useful
CC   for expanding early haematopoietic progenitors in syngeneic, allogeneic
CC   or autologous bone marrow transplant. SCF is useful for enhancing the
CC   efficiency of gene therapy based on transfecting haematopoietic stem
CC   cells. SCF is also useful for combating the myelosuppressive effects of
CC   anti-HIV drugs such as AZT and for enhancing haematopoietic recovery
CC   after acute blood loss and as a boost to the immune system for fighting
CC   neoplasia (cancer). The present sequence represents a universal
CC   oligonucleotide which is used in an example from the present invention
XX
SQ   Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1476
AAH41331
ID   AAH41331 standard; DNA; 20 BP.
XX
AC   AAH41331;
XX
DT   21-AUG-2001  (first entry)
XX
DE   Universal stem cell factor (SCF) related oligonucleotide SEQ ID NO:32.
XX
KW   Stem cell factor; SCF; stem cell factor receptor; blood cell disorder;
KW   gene therapy; PCR primer; mutagenesis; probe; ss.
XX
OS   Synthetic.
XX
PN   US6207454-B1.
XX
PD   27-MAR-2001.
XX
PF   31-DEC-1998;   98US-00224681.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   01-OCT-1990;   90US-00589701.
PR   25-NOV-1992;   92US-00982255.
PR   21-DEC-1993;   93US-00172329.
PR   24-MAY-1995;   95US-00449653.
PR   12-JAN-1998;   98US-00005893.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Zsebo KM,  Bosselman RA,  Suggs SV,  Martin FH;
XX
DR   WPI; 2001-366062/38.
XX
PT   Enhancing efficiency of transfer of polynucleotide into a target
PT   mammalian cell in vitro, involves exposing cell that expresses a stem
PT   cell factor receptor to stem cell factor, and introducing polynucleotide
PT   into cell in vitro.
XX
PS   Example 3; Fig 12C; 210pp; English.
XX
CC   The present invention describes a method for enhancing (E) the efficiency
CC   of transfer of a polynucleotide (I) into a target mammalian cell (II) in
CC   vitro, comprising exposing (II) that expresses a stem cell factor (SCF)
CC   receptor to a biologically active SCF, its analogue or fragment, which
CC   induces cell proliferation, and introducing (I) to (II) in vitro.
CC   Exposure of SCF to (II) results in increased uptake of (I) into the cell.
CC   The method is useful for enhancing the efficiency of the transfer of a
CC   polynucleotide into a target mammalian cell in vitro. The method is
CC   useful in gene therapy techniques. AAH41301 to AAH41364 and AAB98351 to
CC   AAB98390 represent sequences used in the exemplification of the present
CC   invention
XX
SQ   Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1477
AAH41331/c
ID   AAH41331 standard; DNA; 20 BP.
XX
AC   AAH41331;
XX
DT   21-AUG-2001  (first entry)
XX
DE   Universal stem cell factor (SCF) related oligonucleotide SEQ ID NO:32.
XX
KW   Stem cell factor; SCF; stem cell factor receptor; blood cell disorder;
KW   gene therapy; PCR primer; mutagenesis; probe; ss.
XX
OS   Synthetic.
XX
PN   US6207454-B1.
XX
PD   27-MAR-2001.
XX
PF   31-DEC-1998;   98US-00224681.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   01-OCT-1990;   90US-00589701.
PR   25-NOV-1992;   92US-00982255.
PR   21-DEC-1993;   93US-00172329.
PR   24-MAY-1995;   95US-00449653.
PR   12-JAN-1998;   98US-00005893.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Zsebo KM,  Bosselman RA,  Suggs SV,  Martin FH;
XX
DR   WPI; 2001-366062/38.
XX
PT   Enhancing efficiency of transfer of polynucleotide into a target
PT   mammalian cell in vitro, involves exposing cell that expresses a stem
PT   cell factor receptor to stem cell factor, and introducing polynucleotide
PT   into cell in vitro.
XX
PS   Example 3; Fig 12C; 210pp; English.
XX
CC   The present invention describes a method for enhancing (E) the efficiency
CC   of transfer of a polynucleotide (I) into a target mammalian cell (II) in
```

```
CC   vitro, comprising exposing (II) that expresses a stem cell factor (SCF)
CC   receptor to a biologically active SCF, its analogue or fragment, which
CC   induces cell proliferation, and introducing (I) to (II) in vitro.
CC   Exposure of SCF to (II) results in increased uptake of (I) into the cell.
CC   The method is useful for enhancing the efficiency of the transfer of a
CC   polynucleotide into a target mammalian cell in vitro. The method is
CC   useful in gene therapy techniques. AAH41301 to AAH41364 and AAB98351 to
CC   AAB98390 represent sequences used in the exemplification of the present
CC   invention
XX
SQ   Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1478
AAS04111
ID   AAS04111 standard; DNA; 20 BP.
XX
AC   AAS04111;
XX
DT   29-AUG-2001  (first entry)
XX
DE   Human SCF (stem cell factor) cDNA universal PCR primer 220-3.
XX
KW   Human; stem cell factor; SCF; early haematopoietic progenitor cell;
KW   blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
KW   anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6207417-B1.
XX
PD   27-MAR-2001.
XX
PF   07-JUN-1995;   95US-00482918.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   01-OCT-1990;   90US-00589701.
PR   21-DEC-1993;   93US-00172329.
XX
PA   (ZSEB/) ZSEBO K M.
PA   (BOSS/) BOSSELMAN R A.
PA   (SUGG/) SUGGS S V.
PA   (MART/) MARTIN F H.
XX
PI   Zsebo KM,  Bosselman RA,  Suggs SV,  Martin FH;
XX
DR   WPI; 2001-298941/31.
XX
PT   Novel nucleic acids encoding stem cell factor useful for treating
PT   disorders involving blood cells, e.g. leukemia, splenomegaly, Hodgkin's
PT   disease, Kala azar, anemia and septicemia.
XX
PS   Example 3; Fig 12C; 209pp; English.
XX
CC   The present sequence for universal PCR primer 220-3 is 1 of 8 universal
CC   oligonucleotides (AAS04110-AAS04117) used in the isolation of the human
CC   SCF (stem cell factor) cDNA sequence. The present invention relates to
CC   novel stem cell factors (AAU02453-AAU02458, AAU02460, AAU02461) and the
CC   polynucleotides encoding them. SCF stimulate primitive progenitor cells
CC   including early haematopoietic progenitor cells. The invention also
CC   describes SCF peptides (AAU02462-AAU02481) and the oligonucleotides
CC   (AAS04081-AAS04117) used in the isolation of human and rat SCF sequences.
CC   The polynucleotide encoding SCF is useful for producing SCF and useful in
CC   gene therapy. It is useful for treating disorders involving blood cells
CC   such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
CC   myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
CC   congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
CC   disseminated fungus disease, Fulminating septicemia, malaria, vitamin B12
CC   and folic acid deficiency, pyridoxine deficiency, and hypopigmentation
CC   disorders such as piebaldism and vitiligo
XX
SQ   Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1479
AAS04111/c
ID   AAS04111 standard; DNA; 20 BP.
XX
AC   AAS04111;
XX
DT   29-AUG-2001  (first entry)
XX
DE   Human SCF (stem cell factor) cDNA universal PCR primer 220-3.
XX
KW   Human; stem cell factor; SCF; early haematopoietic progenitor cell;
KW   blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
KW   anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6207417-B1.
XX
PD   27-MAR-2001.
XX
PF   07-JUN-1995;   95US-00482918.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   01-OCT-1990;   90US-00589701.
PR   21-DEC-1993;   93US-00172329.
XX
PA   (ZSEB/) ZSEBO K M.
PA   (BOSS/) BOSSELMAN R A.
PA   (SUGG/) SUGGS S V.
PA   (MART/) MARTIN F H.
XX
PI   Zsebo KM,  Bosselman RA,  Suggs SV,  Martin FH;
XX
DR   WPI; 2001-298941/31.
XX
PT   Novel nucleic acids encoding stem cell factor useful for treating
PT   disorders involving blood cells, e.g. leukemia, splenomegaly, Hodgkin's
PT   disease, Kala azar, anemia and septicemia.
XX
PS   Example 3; Fig 12C; 209pp; English.
XX
CC   The present sequence for universal PCR primer 220-3 is 1 of 8 universal
CC   oligonucleotides (AAS04110-AAS04117) used in the isolation of the human
CC   SCF (stem cell factor) cDNA sequence. The present invention relates to
CC   novel stem cell factors (AAU02453-AAU02458, AAU02460, AAU02461) and the
CC   polynucleotides encoding them. SCF stimulate primitive progenitor cells
CC   including early haematopoietic progenitor cells. The invention also
CC   describes SCF peptides (AAU02462-AAU02481) and the oligonucleotides
CC   (AAS04081-AAS04117) used in the isolation of human and rat SCF sequences.
CC   The polynucleotide encoding SCF is useful for producing SCF and useful in
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```
CC   gene therapy. It is useful for treating disorders involving blood cells
CC   such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
CC   myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
CC   congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
CC   disseminated fungus disease, Fulminating septicemia, malaria, vitamin B12
CC   and folic acid deficiency, pyridoxine deficiency, and hypopigmentation
CC   disorders such as piebaldism and vitiligo
XX
SQ   Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1480
AAF89091
ID   AAF89091 standard; DNA; 20 BP.
XX
AC   AAF89091;
XX
DT   13-JUL-2001  (first entry)
XX
DE   Mammalian stem cell factor PCR primer SEQ ID NO: 32.
XX
KW   Human; rat; mammal; stem cell factor; SCF; cell growth stimulation;
KW   gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia;
KW   neurological damage; intestinal damage; infertility; AIDS; SCID;
KW   severe combined immunodeficiency; PCR primer; ss.
XX
OS   Mammalia.
XX
PN   US6207802-B1.
XX
PD   27-MAR-2001.
XX
PF   09-NOV-1994;   94US-00336728.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   01-OCT-1990;   90US-00589701.
PR   25-NOV-1992;   92US-00982255.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Zsebo KM,  Bosselman RA,  Suggs SV,  Martin FH;
XX
DR   WPI; 2001-353108/37.
XX
PT   Novel isolated non-human mammalian stem cell factor polypeptide
PT   stimulating growth of early hematopoietic progenitor cells, useful for
PT   treating aplastic anemia, lymphoma, Letterer-Siwe disease, Kala azar,
PT   sarcoidosis.
XX
PS   Example 3; Fig 12C; 209pp; English.
XX
CC   The present invention provides the protein and coding sequences of
CC   mammalian stem cell factors (SCFs). These are capable of stimulating the
CC   growth of early haematopoietic progenitor cells, neural stem cells and
CC   primordial germ stem cells. The sequences are useful in the treatment of
CC   leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal
CC   nocturnal haemoglobinuria, malaria, pigmentation disorders, neurological
CC   and intestinal damage, infertility, AIDS and severe combined
CC   immunodeficiency (SCID). The present sequence is primer used to amplify
CC   an SCF in the exemplification of the invention
XX
SQ   Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1481
AAF89091/c
ID   AAF89091 standard; DNA; 20 BP.
XX
AC   AAF89091;
XX
DT   13-JUL-2001  (first entry)
XX
DE   Mammalian stem cell factor PCR primer SEQ ID NO: 32.
XX
KW   Human; rat; mammal; stem cell factor; SCF; cell growth stimulation;
KW   gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia;
KW   neurological damage; intestinal damage; infertility; AIDS; SCID;
KW   severe combined immunodeficiency; PCR primer; ss.
XX
OS   Mammalia.
XX
PN   US6207802-B1.
XX
PD   27-MAR-2001.
XX
PF   09-NOV-1994;   94US-00336728.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   01-OCT-1990;   90US-00589701.
PR   25-NOV-1992;   92US-00982255.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Zsebo KM,  Bosselman RA,  Suggs SV,  Martin FH;
XX
DR   WPI; 2001-353108/37.
XX
PT   Novel isolated non-human mammalian stem cell factor polypeptide
PT   stimulating growth of early hematopoietic progenitor cells, useful for
PT   treating aplastic anemia, lymphoma, Letterer-Siwe disease, Kala azar,
PT   sarcoidosis.
XX
PS   Example 3; Fig 12C; 209pp; English.
XX
CC   The present invention provides the protein and coding sequences of
CC   mammalian stem cell factors (SCFs). These are capable of stimulating the
CC   growth of early haematopoietic progenitor cells, neural stem cells and
CC   primordial germ stem cells. The sequences are useful in the treatment of
CC   leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal
CC   nocturnal haemoglobinuria, malaria, pigmentation disorders, neurological
CC   and intestinal damage, infertility, AIDS and severe combined
CC   immunodeficiency (SCID). The present sequence is primer used to amplify
CC   an SCF in the exemplification of the invention
XX
SQ   Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1482
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```
AAH23889
ID   AAH23889 standard; DNA; 20 BP.
XX
AC   AAH23889;
XX
DT   07-AUG-2001  (first entry)
XX
DE   Human SCF (stem cell factor) cDNA universal PCR primer 220-3.
XX
KW   Human; stem cell factor; SCF; early haematopoietic progenitor cell;
KW   blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
KW   anaemia; Kala azar; septicaemia; malaria; hypopigmentation disorder;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6204363-B1.
XX
PD   20-MAR-2001.
XX
PF   25-NOV-1992;   92US-00982255.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   01-OCT-1990;   90US-00589701.
PR   10-APR-1991;   91US-00684535.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Zsebo KM,  Bosselman RA,  Suggs SV,  Martin FH;
XX
DR   WPI; 2001-256683/26.
XX
PT   New stem cell factor polypeptides and their analogs which stimulate
PT   growth of early hematopoietic progenitors, useful for treating aplastic
PT   anemia, carcinoma, multiple myeloma, vitiligo, kala azar, Hodgkin's
PT   disease.
XX
PS   Example 3; Fig 12C; 166pp; English.
XX
CC   The present sequence for universal PCR primer 220-3 is 1 of 8 universal
CC   oligonucleotides (AAH23888-AAH23895) used in the isolation of the human
CC   SCF (stem cell factor) cDNA sequence. The present invention relates to
CC   novel stem cell factors (AAB73561-AAB73568, AAB73571-AAB73576) and the
CC   polynucleotides encoding them. SCF stimulate primitive progenitor cells
CC   including early haematopoietic progenitor cells. The invention also
CC   describes SCF peptides (AAB73578-AAB73597) and the oligonucleotides
CC   (AAH23859-AAH23887) used in the isolation of human and rat SCF sequences.
CC   The polynucleotide encoding SCF is useful for producing SCF and useful in
CC   gene therapy. It is useful for treating disorders involving blood cells
CC   such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
CC   myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
CC   congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
CC   disseminated fungus disease, Fulminating septicaemia, malaria, vitamin
CC   B12 and folic acid deficiency, pyridoxine deficiency, and
CC   hypopigmentation disorders such as piebaldism and vitiligo
XX
SQ   Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1483
AAH23889/c
ID   AAH23889 standard; DNA; 20 BP.
XX
AC   AAH23889;
XX
DT   07-AUG-2001  (first entry)
XX
DE   Human SCF (stem cell factor) cDNA universal PCR primer 220-3.
XX
KW   Human; stem cell factor; SCF; early haematopoietic progenitor cell;
KW   blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
KW   anaemia; Kala azar; septicaemia; malaria; hypopigmentation disorder;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6204363-B1.
XX
PD   20-MAR-2001.
XX
PF   25-NOV-1992;   92US-00982255.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   01-OCT-1990;   90US-00589701.
PR   10-APR-1991;   91US-00684535.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Zsebo KM,  Bosselman RA,  Suggs SV,  Martin FH;
XX
DR   WPI; 2001-256683/26.
XX
PT   New stem cell factor polypeptides and their analogs which stimulate
PT   growth of early hematopoietic progenitors, useful for treating aplastic
PT   anemia, carcinoma, multiple myeloma, vitiligo, kala azar, Hodgkin's
PT   disease.
XX
PS   Example 3; Fig 12C; 166pp; English.
XX
CC   The present sequence for universal PCR primer 220-3 is 1 of 8 universal
CC   oligonucleotides (AAH23888-AAH23895) used in the isolation of the human
CC   SCF (stem cell factor) cDNA sequence. The present invention relates to
CC   novel stem cell factors (AAB73561-AAB73568, AAB73571-AAB73576) and the
CC   polynucleotides encoding them. SCF stimulate primitive progenitor cells
CC   including early haematopoietic progenitor cells. The invention also
CC   describes SCF peptides (AAB73578-AAB73597) and the oligonucleotides
CC   (AAH23859-AAH23887) used in the isolation of human and rat SCF sequences.
CC   The polynucleotide encoding SCF is useful for producing SCF and useful in
CC   gene therapy. It is useful for treating disorders involving blood cells
CC   such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
CC   myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
CC   congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
CC   disseminated fungus disease, Fulminating septicaemia, malaria, vitamin
CC   B12 and folic acid deficiency, pyridoxine deficiency, and
CC   hypopigmentation disorders such as piebaldism and vitiligo
XX
SQ   Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1484
AAS04212
ID   AAS04212 standard; DNA; 20 BP.
XX
AC   AAS04212;
XX
DT   29-AUG-2001  (first entry)
```

```
XX
DE   Human SCF (stem cell factor) cDNA universal PCR primer 220-3.
XX
KW   Human; stem cell factor; SCF; early haematopoietic progenitor cell;
KW   blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
KW   anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6218148-B1.
XX
PD   17-APR-2001.
XX
PF   21-DEC-1993;   93US-00172329.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   01-OCT-1990;   90US-00589701.
PR   25-NOV-1992;   92US-00982255.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Zsebo KM,  Bosselman RA,  Suggs SV,  Martin FH;
XX
DR   WPI; 2001-281051/29.
XX
PT   Isolated DNA sequence, encoding polypeptide product useful for
PT   stimulating growth of early hematopoietic progenitor cells.
XX
PS   Example 3; Fig 12C; 167pp; English.
XX
CC   The present sequence for universal PCR primer 220-3 is 1 of 8 universal
CC   oligonucleotides (AAS04211-AAS04218) used in the isolation of the human
CC   SCF (stem cell factor) cDNA sequence. The present invention relates to
CC   novel stem cell factors (AAU02761-AAU02767, AAU02770-AAU02775, AAU02797)
CC   and the polynucleotides encoding them. SCF stimulate primitive progenitor
CC   cells including early haematopoietic progenitor cells. The invention also
CC   describes SCF peptides (AAU02777-AAU02794) and the oligonucleotides
CC   (AAS04182-AAS04210) used in the isolation of human and rat SCF sequences.
CC   The polynucleotide encoding SCF is useful for producing SCF and useful in
CC   gene therapy. It is useful for treating disorders involving blood cells
CC   such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
CC   myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
CC   congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
CC   disseminated fungus disease, Fulminating septicemia, malaria, vitamin B12
CC   and folic acid deficiency, pyridoxine deficiency, and hypopigmentation
CC   disorders such as piebaldism and vitiligo
XX
SQ   Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1485
AAS04212/c
ID   AAS04212 standard; DNA; 20 BP.
XX
AC   AAS04212;
XX
DT   29-AUG-2001  (first entry)
XX
DE   Human SCF (stem cell factor) cDNA universal PCR primer 220-3.
XX
KW   Human; stem cell factor; SCF; early haematopoietic progenitor cell;
KW   blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
KW   anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6218148-B1.
XX
PD   17-APR-2001.
XX
PF   21-DEC-1993;   93US-00172329.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   01-OCT-1990;   90US-00589701.
PR   25-NOV-1992;   92US-00982255.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Zsebo KM,  Bosselman RA,  Suggs SV,  Martin FH;
XX
DR   WPI; 2001-281051/29.
XX
PT   Isolated DNA sequence, encoding polypeptide product useful for
PT   stimulating growth of early hematopoietic progenitor cells.
XX
PS   Example 3; Fig 12C; 167pp; English.
XX
CC   The present sequence for universal PCR primer 220-3 is 1 of 8 universal
CC   oligonucleotides (AAS04211-AAS04218) used in the isolation of the human
CC   SCF (stem cell factor) cDNA sequence. The present invention relates to
CC   novel stem cell factors (AAU02761-AAU02767, AAU02770-AAU02775, AAU02797)
CC   and the polynucleotides encoding them. SCF stimulate primitive progenitor
CC   cells including early haematopoietic progenitor cells. The invention also
CC   describes SCF peptides (AAU02777-AAU02794) and the oligonucleotides
CC   (AAS04182-AAS04210) used in the isolation of human and rat SCF sequences.
CC   The polynucleotide encoding SCF is useful for producing SCF and useful in
CC   gene therapy. It is useful for treating disorders involving blood cells
CC   such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
CC   myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
CC   congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
CC   disseminated fungus disease, Fulminating septicemia, malaria, vitamin B12
CC   and folic acid deficiency, pyridoxine deficiency, and hypopigmentation
CC   disorders such as piebaldism and vitiligo
XX
SQ   Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1486
AAS10447
ID   AAS10447 standard; DNA; 20 BP.
XX
AC   AAS10447;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human stem cell factor (SCF) cDNA universal PCR primer 220-3.
XX
KW   Human; stem cell factor; SCF; haematopoietic progenitor cell;
KW   blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency;
KW   hypopigmentation disorder; viral disorder; AIDS; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6248319-B1.
```

```
XX
PD   19-JUN-2001.
XX
PF   24-MAY-1995;   95US-00449653.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   01-OCT-1990;   90US-00589701.
PR   10-APR-1991;   91US-00684535.
PR   25-NOV-1992;   92US-00982255.
PR   21-DEC-1993;   93US-00172329.
XX
PA   (ZSEB/) ZSEBO K M.
PA   (BOSS/) BOSSELMAN R A.
PA   (SUGG/) SUGGS S V.
PA   (MART/) MARTIN F H.
XX
PI   Zsebo KM,  Bosselman RA,  Suggs SV,  Martin FH;
XX
DR   WPI; 2001-407312/43.
XX
PT   Increasing the number of early hematopoietic progenitor cells in the
PT   peripheral blood useful for the treatment of blood disorders including
PT   Hodgkin's disease comprises the administration of human stem cell factor.
XX
PS   Example 3; Fig 12C; 210pp; English.
XX
CC   The present sequence for universal PCR primer 220-3 is 1 of 19 PCR
CC   primers (AAS10435-AAS10453) used to amplify various portions of the human
CC   SCF cDNA sequence. The sequence is described in an invention relating to
CC   novel stem cell factors, the polynucleotides encoding them and methods
CC   for producing the stem cell factors. The methods involve increasing the
CC   number of early haematopoietic progenitor cells in human peripheral blood
CC   by administering a haematopoietically effective human stem cell factor
CC   polypeptide. The methods are useful for the treatment of blood disorders,
CC   including myelofibrosis, myelosclerosis, osteopetrosis, metastatic
CC   carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease,
CC   lymphoma, Gaucher's disease, Niemann-Pick disease, refractory anaemia,
CC   malaria, vitamin B12 and folic acid deficiency, hypopigmentation
CC   disorders i.e. piebaldism and viral induced disorders, including AIDS
XX
SQ   Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1487
AAS10447/c
ID   AAS10447 standard; DNA; 20 BP.
XX
AC   AAS10447;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human stem cell factor (SCF) cDNA universal PCR primer 220-3.
XX
KW   Human; stem cell factor; SCF; haematopoietic progenitor cell;
KW   blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency;
KW   hypopigmentation disorder; viral disorder; AIDS; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6248319-B1.
XX
PD   19-JUN-2001.
XX
PF   24-MAY-1995;   95US-00449653.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   01-OCT-1990;   90US-00589701.
PR   10-APR-1991;   91US-00684535.
PR   25-NOV-1992;   92US-00982255.
PR   21-DEC-1993;   93US-00172329.
XX
PA   (ZSEB/) ZSEBO K M.
PA   (BOSS/) BOSSELMAN R A.
PA   (SUGG/) SUGGS S V.
PA   (MART/) MARTIN F H.
XX
PI   Zsebo KM,  Bosselman RA,  Suggs SV,  Martin FH;
XX
DR   WPI; 2001-407312/43.
XX
PT   Increasing the number of early hematopoietic progenitor cells in the
PT   peripheral blood useful for the treatment of blood disorders including
PT   Hodgkin's disease comprises the administration of human stem cell factor.
XX
PS   Example 3; Fig 12C; 210pp; English.
XX
CC   The present sequence for universal PCR primer 220-3 is 1 of 19 PCR
CC   primers (AAS10435-AAS10453) used to amplify various portions of the human
CC   SCF cDNA sequence. The sequence is described in an invention relating to
CC   novel stem cell factors, the polynucleotides encoding them and methods
CC   for producing the stem cell factors. The methods involve increasing the
CC   number of early haematopoietic progenitor cells in human peripheral blood
CC   by administering a haematopoietically effective human stem cell factor
CC   polypeptide. The methods are useful for the treatment of blood disorders,
CC   including myelofibrosis, myelosclerosis, osteopetrosis, metastatic
CC   carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease,
CC   lymphoma, Gaucher's disease, Niemann-Pick disease, refractory anaemia,
CC   malaria, vitamin B12 and folic acid deficiency, hypopigmentation
CC   disorders i.e. piebaldism and viral induced disorders, including AIDS
XX
SQ   Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1488
AAD35464
ID   AAD35464 standard; DNA; 20 BP.
XX
AC   AAD35464;
XX
DT   25-JUL-2002  (first entry)
XX
DE   Rat SCF 5' cDNA amplifying PCR primer, 220-3.
XX
KW   Rat; stem cell factor; SCF protein; leucopaenia; thrombocytopaenia;
KW   anaemia; myelosuppression; nerve damage; myeloproliferative disorder;
KW   infertility; neoplasia; myelofibrosis; myelosclerosis; osteopetrosis;
KW   metastatic carcinoma; acute leukaemia; multiple myeloma; sarcoidosis;
KW   Hodgkin's disease; lymphoma; Gaucher's disease; Niemann-Pick disease;
KW   Letterer-Siwe disease; refractory erythroblastic anaemia; Kala azar;
KW   Di Guglielmo syndrome; congestive splenomegaly; splenic pancytopaenia;
KW   disseminated fungus disease; Fulminating septicaemia; piebaldism; AIDS;
KW   acquired immune deficiency syndrome; malaria; military tuberculosis;
KW   pyridoxine deficiency; vitamin B12 deficiency; folic acid deficiency;
KW   Diamond Blackfan anaemia; hypopigmentation disorder; vitiligo; PCR;
KW   primer; ss.
XX
```

OS Rattus sp.
XX
PN US2002018763-A1.
XX
PD 14-FEB-2002.
XX
PF 12-JAN-1998; 98US-00005243.
XX
PR 24-MAY-1995; 95US-00449653.
XX
PA (ZSEB/) ZSEBO K M.
PA (BOSS/) BOSSELMAN R A.
PA (SUGG/) SUGGS S V.
PA (MART/) MARTIN F H.
XX
PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX
DR WPI; 2002-350789/38.
XX
PT Novel non-naturally-occurring stem cell factor polypeptide, useful for
PT treating leucopenia, thrombocytopenia, anemia and for enhancing
PT engraftment of bone marrow during transplantation in a mammal.
XX
PS Example 3; Fig 12C; 217pp; English.
XX
CC The present invention relates to novel non-naturally-occurring stem cell
CC factor (SCF) polypeptides having an amino acid sequence sufficiently
CC duplicative of that of naturally-occurring SCF to allow possession of
CC haematopoietic biological activity of naturally occurring SCF. Sequences
CC of the invention are useful for treating leucopaenia, thrombocytopaenia,
CC anaemia and for enhancing bone marrow recovery in treatment of radiation,
CC engraftment of bone marrow during transplantation in mammals and chemical
CC or chemotherapeutic induced bone marrow aplasia or myelosuppression. They
CC are also useful for treating acquired immune deficiency in a human, nerve
CC damage, neoplasia, infertility, myeloproliferative disorder, intestinal
CC damage in a mammal. SCF sequences are useful for preparing biologically
CC active polymer polypeptide adduct, for enhancing transfection of early
CC haematopoietic progenitor cells with a gene, and transfer of a gene into
CC a mammal. They are useful for treating myelofibrosis, myelosclerosis,
CC osteopetrosis, metastatic carcinoma, acute leukaemia, multiple myeloma,
CC Hodgkin's disease, lymphoma, Gaucher's disease, Niemann-Pick disease,
CC Letterer-Siwe disease, refractory erythroblastic anaemia, Di Guglielmo
CC syndrome, congestive splenomegaly, Kala azar, sarcoidosis, primary
CC splenic pancytopaenia, disseminated fungus disease, malaria, military
CC tuberculosis, Fulminating septicaemia, pyridoxine deficiency, vitamin B12
CC and folic acid deficiency, Diamond Blackfan anaemia, hypopigmentation
CC disorders such as piebaldism, AIDS (acquired immune deficiency syndrome)
CC and vitiligo. The present sequence is a PCR primer which is used for
CC amplifying the 5' end of rat SCF cDNA. This sequence is used in the
CC exemplification of the invention
XX
SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTT 2183
||||||||||||||||||
Db 1 TTTTTTTTTTTTTTTTTT 18

RESULT 1489
AAD35464/c
ID AAD35464 standard; DNA; 20 BP.
XX
AC AAD35464;
XX
DT 25-JUL-2002 (first entry)
XX
DE Rat SCF 5' cDNA amplifying PCR primer, 220-3.
XX
KW Rat; stem cell factor; SCF protein; leucopaenia; thrombocytopaenia;
KW anaemia; myelosuppression; nerve damage; myeloproliferative disorder;
KW infertility; neoplasia; myelofibrosis; myelosclerosis; osteopetrosis;
KW metastatic carcinoma; acute leukaemia; multiple myeloma; sarcoidosis;
KW Hodgkin's disease; lymphoma; Gaucher's disease; Niemann-Pick disease;
KW Letterer-Siwe disease; refractory erythroblastic anaemia; Kala azar;
KW Di Guglielmo syndrome; congestive splenomegaly; splenic pancytopaenia;
KW disseminated fungus disease; Fulminating septicaemia; piebaldism; AIDS;
KW acquired immune deficiency syndrome; malaria; military tuberculosis;
KW pyridoxine deficiency; vitamin B12 deficiency; folic acid deficiency;
KW Diamond Blackfan anaemia; hypopigmentation disorder; vitiligo; PCR;
KW primer; ss.
XX
OS Rattus sp.
XX
PN US2002018763-A1.
XX
PD 14-FEB-2002.
XX
PF 12-JAN-1998; 98US-00005243.
XX
PR 24-MAY-1995; 95US-00449653.
XX
PA (ZSEB/) ZSEBO K M.
PA (BOSS/) BOSSELMAN R A.
PA (SUGG/) SUGGS S V.
PA (MART/) MARTIN F H.
XX
PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX
DR WPI; 2002-350789/38.
XX
PT Novel non-naturally-occurring stem cell factor polypeptide, useful for
PT treating leucopenia, thrombocytopenia, anemia and for enhancing
PT engraftment of bone marrow during transplantation in a mammal.
XX
PS Example 3; Fig 12C; 217pp; English.
XX
CC The present invention relates to novel non-naturally-occurring stem cell
CC factor (SCF) polypeptides having an amino acid sequence sufficiently
CC duplicative of that of naturally-occurring SCF to allow possession of
CC haematopoietic biological activity of naturally occurring SCF. Sequences
CC of the invention are useful for treating leucopaenia, thrombocytopaenia,
CC anaemia and for enhancing bone marrow recovery in treatment of radiation,
CC engraftment of bone marrow during transplantation in mammals and chemical
CC or chemotherapeutic induced bone marrow aplasia or myelosuppression. They
CC are also useful for treating acquired immune deficiency in a human, nerve
CC damage, neoplasia, infertility, myeloproliferative disorder, intestinal
CC damage in a mammal. SCF sequences are useful for preparing biologically
CC active polymer polypeptide adduct, for enhancing transfection of early
CC haematopoietic progenitor cells with a gene, and transfer of a gene into
CC a mammal. They are useful for treating myelofibrosis, myelosclerosis,
CC osteopetrosis, metastatic carcinoma, acute leukaemia, multiple myeloma,
CC Hodgkin's disease, lymphoma, Gaucher's disease, Niemann-Pick disease,
CC Letterer-Siwe disease, refractory erythroblastic anaemia, Di Guglielmo
CC syndrome, congestive splenomegaly, Kala azar, sarcoidosis, primary
CC splenic pancytopaenia, disseminated fungus disease, malaria, military
CC tuberculosis, Fulminating septicaemia, pyridoxine deficiency, vitamin B12
CC and folic acid deficiency, Diamond Blackfan anaemia, hypopigmentation
CC disorders such as piebaldism, AIDS (acquired immune deficiency syndrome)
CC and vitiligo. The present sequence is a PCR primer which is used for
CC amplifying the 5' end of rat SCF cDNA. This sequence is used in the
CC exemplification of the invention
XX
SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2803
||||||||||||||||||
Db 18 AAAAAAAAAAAAAAAAAA 1

```
RESULT 1490
ABS73848
ID   ABS73848 standard; DNA; 20 BP.
XX
AC   ABS73848;
XX
DT   05-DEC-2002  (first entry)
XX
DE   SCF universal oligonucleotide 220-3.
XX
KW   Stem cell factor; SCF; blood-forming system; blood cell disorder;
KW   haematopoietic system; metastatic carcinoma; acute leukaemia;
KW   multiple myeloma; Hodgkin's disease; lymphoma; malaria; vitiligo;
KW   refractory erythroblastic anaemia; miliary tuberculosis; cytostatic;
KW   disseminated fungus disease; haematopoietic; tuberculostatic;
KW   antianaemic; antifungal; antimalarial; dermatological; ss.
XX
OS   Synthetic.
XX
PN   EP1241258-A2.
XX
PD   18-SEP-2002.
XX
PF   04-OCT-1990; 2002EP-00008587.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   28-SEP-1990;   90WO-US005548.
PR   01-OCT-1990;   90US-00589701.
PR   04-OCT-1990;   90EP-00310899.
PR   04-OCT-1990;   95EP-00105391.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Zsebo KM,  Suggs SV,  Bosselman RA,  Martin FH;
XX
DR   WPI; 2002-684093/74.
XX
PT   Production of a human stem cell factor (SCF) polypeptide for treating
PT   disorders involving blood cells, such as leukemia, comprises culturing
PT   mammalian cells comprising non-human SCF promoter DNA linked to DNA
PT   encoding the human SCF.
XX
PS   Example 3; Fig 12C; 120pp; English.
XX
CC   The present invention relates to novel stem cell factors (SCFs),
CC   polynucleotide sequences encoding the SCFs, and methods of producing
CC   them. SCFs are involved in the blood-forming (haematopoietic) system in
CC   mammals, particularly humans. The method of the invention is useful for
CC   the production of human SCF. The stem cell factors are useful to treat
CC   disorders involving blood cells e.g. metastatic carcinoma, acute
CC   leukaemia, multiple myeloma, Hodgkin's disease, lymphoma, refractory
CC   erythroblastic anaemia, miliary tuberculosis, disseminated fungus
CC   disease, malaria, and vitiligo. The present sequence representing a
CC   universal oligonucleotide for SCF DNA is used in the examples of the
CC   present invention
XX
SQ   Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1491
ABS73848/c
ID   ABS73848 standard; DNA; 20 BP.
XX
AC   ABS73848;
XX
DT   05-DEC-2002  (first entry)
XX
DE   SCF universal oligonucleotide 220-3.
XX
KW   Stem cell factor; SCF; blood-forming system; blood cell disorder;
KW   haematopoietic system; metastatic carcinoma; acute leukaemia;
KW   multiple myeloma; Hodgkin's disease; lymphoma; malaria; vitiligo;
KW   refractory erythroblastic anaemia; miliary tuberculosis; cytostatic;
KW   disseminated fungus disease; haematopoietic; tuberculostatic;
KW   antianaemic; antifungal; antimalarial; dermatological; ss.
XX
OS   Synthetic.
XX
PN   EP1241258-A2.
XX
PD   18-SEP-2002.
XX
PF   04-OCT-1990; 2002EP-00008587.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   28-SEP-1990;   90WO-US005548.
PR   01-OCT-1990;   90US-00589701.
PR   04-OCT-1990;   90EP-00310899.
PR   04-OCT-1990;   95EP-00105391.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Zsebo KM,  Suggs SV,  Bosselman RA,  Martin FH;
XX
DR   WPI; 2002-684093/74.
XX
PT   Production of a human stem cell factor (SCF) polypeptide for treating
PT   disorders involving blood cells, such as leukemia, comprises culturing
PT   mammalian cells comprising non-human SCF promoter DNA linked to DNA
PT   encoding the human SCF.
XX
PS   Example 3; Fig 12C; 120pp; English.
XX
CC   The present invention relates to novel stem cell factors (SCFs),
CC   polynucleotide sequences encoding the SCFs, and methods of producing
CC   them. SCFs are involved in the blood-forming (haematopoietic) system in
CC   mammals, particularly humans. The method of the invention is useful for
CC   the production of human SCF. The stem cell factors are useful to treat
CC   disorders involving blood cells e.g. metastatic carcinoma, acute
CC   leukaemia, multiple myeloma, Hodgkin's disease, lymphoma, refractory
CC   erythroblastic anaemia, miliary tuberculosis, disseminated fungus
CC   disease, malaria, and vitiligo. The present sequence representing a
CC   universal oligonucleotide for SCF DNA is used in the examples of the
CC   present invention
XX
SQ   Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1492
ABZ89896
ID   ABZ89896 standard; DNA; 20 BP.
XX
AC   ABZ89896;
XX
DT   17-OCT-2003  (first entry)
```

XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 5138; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 18 A; 0 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAAAAAAAA 2802
||||||||||||||||||
Db 3 GAAAAAAAAAAAAAAAAA 20

RESULT 1493
ABZ89703/c
ID ABZ89703 standard; DNA; 20 BP.
XX
AC ABZ89703;
XX
DT 17-OCT-2003 (first entry)

XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4945; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 16 A; 0 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2171 TTTTTTTTTTTTTTTTAA 2188
||||||||||||||||||
Db 20 TTTTTTTTTTTTTTTTAA 3

RESULT 1494
ABZ89719/c
ID ABZ89719 standard; DNA; 20 BP.
XX
AC ABZ89719;
XX
DT 17-OCT-2003 (first entry)

```
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 4961; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||
Db         20 GAAAAAAAAAAAAAAAAA 3


RESULT 1495
ADE52460
ID   ADE52460 standard; DNA; 20 BP.
XX
AC   ADE52460;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stem cell factor (SCF) related DNA #31.
XX
KW   Stem cell factor; SCF; haematopoietic activity; infertility;
KW   intestinal damage; myeloproliferative disorder; leucopenia;
KW   thrombocytopenia; anaemia; bone marrow transplant; immune deficiency;
KW   neoplasia; nerve damage; osteoporosis; metastatic carcinoma; leukaemia;
KW   miliary tuberculosis; haematopoietic progenitor cell; ss.
XX
OS   Synthetic.
XX
PN   US2002031491-A1.
XX
PD   14-MAR-2002.
XX
PF   31-DEC-1998;   98US-00224683.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   01-OCT-1990;   90US-00589701.
PR   10-APR-1991;   91US-00684535.
PR   25-NOV-1992;   92US-00982255.
PR   21-DEC-1993;   93US-00172329.
PR   24-MAY-1995;   95US-00449653.
PR   12-JAN-1998;   98US-00005893.
XX
PA   (ZSEB/) ZSEBO K M.
PA   (BOSS/) BOSSELMAN R A.
PA   (SUGG/) SUGGS S V.
PA   (MART/) MARTIN F H.
XX
PI   Zsebo KM,  Bosselman RA,  Suggs SV,  Martin FH;
XX
DR   WPI; 2003-851459/79.
XX
PT   New non-natural stem cell factor, useful for treating e.g. leucopenia or
PT   immune deficiency, also related nucleic acid and antibodies.
XX
PS   Disclosure; SEQ ID NO 32; 217pp; English.
XX
CC   The invention relates to stem cell factor (SCF) polypeptides with
CC   haematopoietic activity and the polynucleotides encoding them. The
CC   polypeptides are used for treating infertility, intestinal damage,
CC   myeloproliferative disorders, leucopenia, thrombocytopenia or anaemia,
CC   for improving engraftment of bone marrow transplants, for enhancing bone
CC   marrow recovery after radiotherapy or chemotherapy and in treatment of
CC   immune deficiency, neoplasia, nerve damage, osteoporosis, metastatic
CC   carcinoma, leukaemia and miliary tuberculosis. The SCF polypeptides are
CC   also used to expand haematopoietic progenitor cells for transplantation
CC   and to prepare such cells for transfection with a gene. The SCF
CC   polynucleotides can be used for recombinant expression of the
CC   polypeptides and also as probes for mapping of the SCF gene, for
CC   identifying SCF-related diseases and as a marker for neighbouring genes.
CC   Antibodies raised against the polypeptides are useful in diagnosis and to
CC   remove SCF from blood. This sequence represents SCF related DNA of the
CC   invention.
XX
SQ   Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1496
ADE52460/c
ID   ADE52460 standard; DNA; 20 BP.
XX
```

```
AC   ADE52460;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stem cell factor (SCF) related DNA #31.
XX
KW   Stem cell factor; SCF; haematopoietic activity; infertility;
KW   intestinal damage; myeloproliferative disorder; leucopenia;
KW   thrombocytopenia; anaemia; bone marrow transplant; immune deficiency;
KW   neoplasia; nerve damage; osteoporosis; metastatic carcinoma; leukaemia;
KW   miliary tuberculosis; haematopoietic progenitor cell; ss.
XX
OS   Synthetic.
XX
PN   US2002031491-A1.
XX
PD   14-MAR-2002.
XX
PF   31-DEC-1998;   98US-00224683.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   01-OCT-1990;   90US-00589701.
PR   10-APR-1991;   91US-00684535.
PR   25-NOV-1992;   92US-00982255.
PR   21-DEC-1993;   93US-00172329.
PR   24-MAY-1995;   95US-00449653.
PR   12-JAN-1998;   98US-00005893.
XX
PA   (ZSEB/) ZSEBO K M.
PA   (BOSS/) BOSSELMAN R A.
PA   (SUGG/) SUGGS S V.
PA   (MART/) MARTIN F H.
XX
PI   Zsebo KM,  Bosselman RA,  Suggs SV,  Martin FH;
XX
DR   WPI; 2003-851459/79.
XX
PT   New non-natural stem cell factor, useful for treating e.g. leucopenia or
PT   immune deficiency, also related nucleic acid and antibodies.
XX
PS   Disclosure; SEQ ID NO 32; 217pp; English.
XX
CC   The invention relates to stem cell factor (SCF) polypeptides with
CC   haematopoietic activity and the polynucleotides encoding them. The
CC   polypeptides are used for treating infertility, intestinal damage,
CC   myeloproliferative disorders, leucopenia, thrombocytopenia or anaemia,
CC   for improving engraftment of bone marrow transplants, for enhancing bone
CC   marrow recovery after radiotherapy or chemotherapy and in treatment of
CC   immune deficiency, neoplasia, nerve damage, osteoporosis, metastatic
CC   carcinoma, leukaemia and miliary tuberculosis. The SCF polypeptides are
CC   also used to expand haematopoietic progenitor cells for transplantation
CC   and to prepare such cells for transfection with a gene. The SCF
CC   polynucleotides can be used for recombinant expression of the
CC   polypeptides and also as probes for mapping of the SCF gene, for
CC   identifying SCF-related diseases and as a marker for neighbouring genes.
CC   Antibodies raised against the polypeptides are useful in diagnosis and to
CC   remove SCF from blood. This sequence represents SCF related DNA of the
CC   invention.
XX
SQ   Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1497
AAQ75692
ID   AAQ75692 standard; DNA; 21 BP.
XX
AC   AAQ75692;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 3 A; 1 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTA 18


RESULT 1498
AAQ75776/c
ID   AAQ75776 standard; DNA; 21 BP.
XX
AC   AAQ75776;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
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```
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 1499
AAQ75777/c
ID   AAQ75777 standard; DNA; 21 BP.
XX
AC   AAQ75777;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 1 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 1500
AAQ75693
ID   AAQ75693 standard; DNA; 21 BP.
XX
AC   AAQ75693;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTA 18


RESULT 1501
AAQ75694
ID   AAQ75694 standard; DNA; 21 BP.
XX
AC   AAQ75694;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
```

```
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTA 18


RESULT 1502
AAQ75775/c
ID   AAQ75775 standard; DNA; 21 BP.
XX
AC   AAQ75775;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 1503
AAQ75691
ID   AAQ75691 standard; DNA; 21 BP.
XX
AC   AAQ75691;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTA 18


RESULT 1504
AAQ75735/c
```

```
ID   AAQ75735 standard; DNA; 21 BP.
XX
AC   AAQ75735;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 1 C; 3 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 1505
AAQ75738/c
ID   AAQ75738 standard; DNA; 21 BP.
XX
AC   AAQ75738;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 2 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 1506
AAQ75748/c
ID   AAQ75748 standard; DNA; 21 BP.
XX
AC   AAQ75748;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
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  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 1507
AAQ75795/c
ID   AAQ75795 standard; DNA; 21 BP.
XX
AC   AAQ75795;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 3 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 1508
AAQ75671
ID   AAQ75671 standard; DNA; 21 BP.
XX
AC   AAQ75671;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTA 18


RESULT 1509
AAQ75736/c
ID   AAQ75736 standard; DNA; 21 BP.
XX
AC   AAQ75736;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
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CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 1510
AAQ75798/c
ID   AAQ75798 standard; DNA; 21 BP.
XX
AC   AAQ75798;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 4 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 1511
AAQ75674
ID   AAQ75674 standard; DNA; 21 BP.
XX
AC   AAQ75674;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTA 18


RESULT 1512
AAQ75687
ID   AAQ75687 standard; DNA; 21 BP.
XX
AC   AAQ75687;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
```

```
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTA 18


RESULT 1513
AAQ75793/c
ID   AAQ75793 standard; DNA; 21 BP.
XX
AC   AAQ75793;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 2 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 1514
AAQ75794/c
ID   AAQ75794 standard; DNA; 21 BP.
XX
AC   AAQ75794;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 3 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 1515
AAQ75690
ID   AAQ75690 standard; DNA; 21 BP.
XX
AC   AAQ75690;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
```

```
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTA 18


RESULT 1516
AAQ75767/c
ID   AAQ75767 standard; DNA; 21 BP.
XX
AC   AAQ75767;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 1517
AAQ75688
ID   AAQ75688 standard; DNA; 21 BP.
XX
AC   AAQ75688;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTA 18


RESULT 1518
AAQ75713
ID   AAQ75713 standard; DNA; 21 BP.
XX
```

```
AC   AAQ75713;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTA 18


RESULT 1519
AAQ75747/c
ID   AAQ75747 standard; DNA; 21 BP.
XX
AC   AAQ75747;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 2 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 1520
AAQ75786/c
ID   AAQ75786 standard; DNA; 21 BP.
XX
AC   AAQ75786;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 3 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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```
Qy       2785 GAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         18 GAAAAAAAAAAAAAAAA 1


RESULT 1521
AAQ75791/c
ID   AAQ75791 standard; DNA; 21 BP.
XX
AC   AAQ75791;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         18 GAAAAAAAAAAAAAAAA 1


RESULT 1522
AAQ75743/c
ID   AAQ75743 standard; DNA; 21 BP.
XX
AC   AAQ75743;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         18 GAAAAAAAAAAAAAAAA 1


RESULT 1523
AAQ75769/c
ID   AAQ75769 standard; DNA; 21 BP.
XX
AC   AAQ75769;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
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```
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 1524
AAQ75796/c
ID   AAQ75796 standard; DNA; 21 BP.
XX
AC   AAQ75796;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 3 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 1525
AAQ75797/c
ID   AAQ75797 standard; DNA; 21 BP.
XX
AC   AAQ75797;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 3 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 1526
AAQ75689
ID   AAQ75689 standard; DNA; 21 BP.
XX
AC   AAQ75689;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
```

```
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTA 18


RESULT 1527
AAQ75703
ID   AAQ75703 standard; DNA; 21 BP.
XX
AC   AAQ75703;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 0 C; 3 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTA 18


RESULT 1528
AAQ75714
ID   AAQ75714 standard; DNA; 21 BP.
XX
AC   AAQ75714;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTA 18


RESULT 1529
AAQ75705
ID   AAQ75705 standard; DNA; 21 BP.
XX
AC   AAQ75705;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
```

```
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTA 18


RESULT 1530
AAQ75712
ID   AAQ75712 standard; DNA; 21 BP.
XX
AC   AAQ75712;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTA 18


RESULT 1531
AAQ75737/c
ID   AAQ75737 standard; DNA; 21 BP.
XX
AC   AAQ75737;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 1532
AAQ75672
ID   AAQ75672 standard; DNA; 21 BP.
XX
AC   AAQ75672;
XX
```

DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2170 TTTTTTTTTTTTTTTTTA 2187
||||||||||||||||||
Db 1 TTTTTTTTTTTTTTTTTA 18

RESULT 1533
AAQ75706
ID AAQ75706 standard; DNA; 21 BP.
XX
AC AAQ75706;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2170 TTTTTTTTTTTTTTTTA 2187
||||||||||||||||||
Db 1 TTTTTTTTTTTTTTTTA 18

RESULT 1534
AAQ75746/c
ID AAQ75746 standard; DNA; 21 BP.
XX
AC AAQ75746;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAAAAAAAA 2802

```
                    ||||||||||||||||||
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 1535
AAQ75784/c
ID   AAQ75784 standard; DNA; 21 BP.
XX
AC   AAQ75784;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match              0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
                ||||||||||||||||||
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 1536
AAQ75785/c
ID   AAQ75785 standard; DNA; 21 BP.
XX
AC   AAQ75785;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match              0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
                ||||||||||||||||||
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 1537
AAQ75704
ID   AAQ75704 standard; DNA; 21 BP.
XX
AC   AAQ75704;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03..
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
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CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTA 18


RESULT 1538
AAQ75708
ID   AAQ75708 standard; DNA; 21 BP.
XX
AC   AAQ75708;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 3 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTA 18


RESULT 1539
AAQ75673
ID   AAQ75673 standard; DNA; 21 BP.
XX
AC   AAQ75673;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTA 18


RESULT 1540
AAQ75768/c
ID   AAQ75768 standard; DNA; 21 BP.
XX
AC   AAQ75768;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
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PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 1541
AAQ75707
ID   AAQ75707 standard; DNA; 21 BP.
XX
AC   AAQ75707;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTA 18


RESULT 1542
AAQ75750/c
ID   AAQ75750 standard; DNA; 21 BP.
XX
AC   AAQ75750;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 3 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 1543
AAQ75710
ID   AAQ75710 standard; DNA; 21 BP.
XX
AC   AAQ75710;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
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XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match              0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTA 18


RESULT 1544
AAQ75745/c
ID   AAQ75745 standard; DNA; 21 BP.
XX
AC   AAQ75745;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;

  Query Match              0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 1545
AAQ75749/c
ID   AAQ75749 standard; DNA; 21 BP.
XX
AC   AAQ75749;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match              0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 1546
AAQ75770/c
ID   AAQ75770 standard; DNA; 21 BP.
XX
AC   AAQ75770;
XX
DT   04-AUG-1995  (first entry)
XX
```

```
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 1547
AAQ75709
ID   AAQ75709 standard; DNA; 21 BP.
XX
AC   AAQ75709;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTA 18


RESULT 1548
AAQ75711
ID   AAQ75711 standard; DNA; 21 BP.
XX
AC   AAQ75711;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTA 18
```

```
RESULT 1549
AAQ75744/c
ID   AAQ75744 standard; DNA; 21 BP.
XX
AC   AAQ75744;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 1550
AAQ75783/c
ID   AAQ75783 standard; DNA; 21 BP.
XX
AC   AAQ75783;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 2 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 1551
AAQ75792/c
ID   AAQ75792 standard; DNA; 21 BP.
XX
AC   AAQ75792;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
```

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XX
SQ   Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 1552
AAQ64706
ID   AAQ64706 standard; cDNA to mRNA; 22 BP.
XX
AC   AAQ64706;
XX
DT   25-MAR-2003  (revised)
DT   04-JAN-1995  (first entry)
XX
DE   2',5'-linked tetraadenylate-antisense oligonucleotide chimeric mol.
XX
KW   antisense; 2',5'-tetraadenylate; 2-5A dependent RNase activator;
KW   RNA cleavage; antiviral therapy; chimeric molecule; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .4
FT                   /*tag=  a
FT                   /label= 2',5'-linked_tetraadenylate
FT                   /note= "nucleotides linked through phosphodiester bonds
FT                   at hydroxyl groups of 2' and 5' carbons"
FT   misc_feature    5. .22
FT                   /*tag=  b
FT                   /note= "antisense region"
XX
PN   WO9409129-A2.
XX
PD   28-APR-1994.
XX
PF   20-OCT-1993;   93WO-US010103.
XX
PR   21-OCT-1992;   92US-00965666.
PR   17-SEP-1993;   93US-00123449.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA   (CLEV-) CLEVELAND CLINIC RES INST.
XX
PI   Torrence P,  Silverman R,  Maitra R,  Lesiak K;
XX
DR   WPI; 1994-151315/18.
XX
PT   Specific cleavage of RNA, useful partic. for treating viral infection,
PT   cancers, etc. - by using anti-sense oligo:nucleotide coupled to activator
PT   of 2-5A dependent RNase.
XX
PS   Example 1; Page 68; 86pp; English.
XX
CC   This sequence is an example of a 2-5A-antisense oligonucleotide chimeric
CC   molecule. The antisense region targets the chimeric molecule to a
CC   particular region of RNA to be specifically cleaved and the 2',5'-linked
CC   tetraadenylate tail activates the 2-5A RNase. Typical applications are
CC   treatment of viral infections (esp. for cleavage of an RNA virus genome),
CC   cancer; leukaemia, cardiovascular disorders (e.g. restenosis after
CC   angioplasty), genetic disorders, osteoarthritis or rheumatoid arthritis.
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 22 BP; 4 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          5 TTTTTTTTTTTTTTTTTT 22


RESULT 1553
AAQ64706/c
ID   AAQ64706 standard; cDNA to mRNA; 22 BP.
XX
AC   AAQ64706;
XX
DT   25-MAR-2003  (revised)
DT   04-JAN-1995  (first entry)
XX
DE   2',5'-linked tetraadenylate-antisense oligonucleotide chimeric mol.
XX
KW   antisense; 2',5'-tetraadenylate; 2-5A dependent RNase activator;
KW   RNA cleavage; antiviral therapy; chimeric molecule; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .4
FT                   /*tag=  a
FT                   /label= 2',5'-linked_tetraadenylate
FT                   /note= "nucleotides linked through phosphodiester bonds
FT                   at hydroxyl groups of 2' and 5' carbons"
FT   misc_feature    5. .22
FT                   /*tag=  b
FT                   /note= "antisense region"
XX
PN   WO9409129-A2.
XX
PD   28-APR-1994.
XX
PF   20-OCT-1993;   93WO-US010103.
XX
PR   21-OCT-1992;   92US-00965666.
PR   17-SEP-1993;   93US-00123449.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA   (CLEV-) CLEVELAND CLINIC RES INST.
XX
PI   Torrence P,  Silverman R,  Maitra R,  Lesiak K;
XX
DR   WPI; 1994-151315/18.
XX
PT   Specific cleavage of RNA, useful partic. for treating viral infection,
PT   cancers, etc. - by using anti-sense oligo:nucleotide coupled to activator
PT   of 2-5A dependent RNase.
XX
PS   Example 1; Page 68; 86pp; English.
XX
CC   This sequence is an example of a 2-5A-antisense oligonucleotide chimeric
CC   molecule. The antisense region targets the chimeric molecule to a
CC   particular region of RNA to be specifically cleaved and the 2',5'-linked
CC   tetraadenylate tail activates the 2-5A RNase. Typical applications are
CC   treatment of viral infections (esp. for cleavage of an RNA virus genome),
CC   cancer; leukaemia, cardiovascular disorders (e.g. restenosis after
CC   angioplasty), genetic disorders, osteoarthritis or rheumatoid arthritis.
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 22 BP; 4 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         22 AAAAAAAAAAAAAAAAAA 5
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RESULT 1554
AAA98276
ID   AAA98276 standard; DNA; 22 BP.
XX
AC   AAA98276;
XX
DT   02-FEB-2001  (first entry)
XX
DE   Human mismatch repair gene hMSH6 intron 9 DNA fragment.
XX
KW   Human mismatch repair gene; hMSH6; disease predisposition; genotype;
KW   mutation; carcinoma; colorectal; endometrial; ovarian; leukemia;
KW   neoplastic disease; drug development; ss.
XX
OS   Homo sapiens.
XX
PN   DE19909878-A1.
XX
PD   07-SEP-2000.
XX
PF   06-MAR-1999;   99DE-01009878.
XX
PR   06-MAR-1999;   99DE-01009878.
XX
PA   (UYDR ) UNIV DRESDEN TECH.
XX
PI   Plaschke J,  Kruppa C,  Schackert H;
XX
DR   WPI; 2000-588378/56.
XX
PT   Novel variants of the human mismatch repair gene, MSH6, useful e.g. for
PT   determining predisposition to cancer and for development of drugs.
XX
PS   Claim 1; Page 4; 14pp; German.
XX
CC   This invention describes a novel method of determining a predisposition
CC   to disease by genotyping a subject's DNA sequence (A) of the human
CC   mismatch repair gene, MSH6 at specified positions and comparing with
CC   reference DNA sequences, optionally taking into account all possible
CC   combinations of variations of the individual mutations, including any
CC   chosen absolute number of variations. (A), and analysis of their
CC   sequences, are useful for the following: (i) determining a predisposition
CC   to disease, especially colorectal, endometrial and ovarian carcinoma and
CC   leukemia; (ii) determining an increased mutation rate (frequency of base
CC   substitutions, insertions and/or deletions) in eukaryotic cells; (iii)
CC   predicting the progression, severity and survival time of patients with
CC   neoplastic disease; (iv) the development of therapeutic and 'life-style'
CC   drugs; (v) predicting individual differences in response to known
CC   chemotherapeutic agents (e.g. cis-platin) or drugs developed from (iv);
CC   (vi) optimizing individual treatments and interventions against neoplasia
CC   ; (vii) controlling the mutation rate in eukaryotic cells, in vitro or in
CC   vivo; (viii) constructing genes and vectors, particularly for development
CC   of pharmaceuticals; (ix) developing diagnostic kits and other systems for
CC   genotyping; and (x) developing in vivo and in vitro test systems for
CC   expressing individual forms of the MSH6 gene, e.g. for studying
CC   pathophysiology of disease or processes in which MSH6 is involved, and
CC   for drug development and testing
XX
SQ   Sequence 22 BP; 4 A; 1 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTT 2182
              ||||||||||||||||||
Db          5 CTTTTTTTTTTTTTTTTT 22


RESULT 1555
AAQ75028
ID   AAQ75028 standard; DNA; 23 BP.
XX
AC   AAQ75028;
XX
DT   25-MAR-2003  (revised)
DT   03-AUG-1995  (first entry)
XX
DE   LCR oligo 2.
XX
KW   Synthetic oligo; solid phase immunoassay; ss.
XX
OS   Synthetic.
XX
PN   WO9426932-A1.
XX
PD   24-NOV-1994.
XX
PF   13-MAY-1994;   94WO-US005407.
XX
PR   13-MAY-1993;   93US-00061694.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Fields HA,  Khudyakov YE;
XX
DR   WPI; 1995-006819/01.
XX
PT   Solid phase immunoassay using oligo:nucleotide as label - also new
PT   conjugates of oligo:nucleotide coupled to antigenic peptide, partic. for
PT   diagnosing hepatitis C or E virus infection.
XX
PS   Example; Page 13; 34pp; English.
XX
CC   AAR62941 and AAR62942 are examples of synthetic immunoreactive peptides.
CC   They are used in a method for detecting an antigen in a subject. The
CC   method involves binding the antigen to a solid support and then reacting
CC   it with an immunoreactive ligand (L) bound to an oligo; removing any
CC   unreacted L, and then detecting the presence of the oligo. A similar
CC   method can be used to detect Abs, in which case the ligand is an oligo-
CC   labelled Ag. The use of an amplifiable oligo as the label allows Ag or Ab
CC   to be detected at very low levels. An exemplary olgi is AAQ75024 which
CC   can be covalently attached by the 5'- terminus to the N- or C-terminal of
CC   a synthetic peptide. For LCR using oligo AAZ75024, oligos 1-4 (see
CC   AAQ75027-Q75030) can be used. (Updated on 25-MAR-2003 to correct PN
CC   field.)
XX
SQ   Sequence 23 BP; 19 A; 4 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db          6 AAAAAAAAAAAAAAAAAA 23


RESULT 1556
AAQ75028/c
ID   AAQ75028 standard; DNA; 23 BP.
XX
AC   AAQ75028;
XX
DT   25-MAR-2003  (revised)
DT   03-AUG-1995  (first entry)
XX
DE   LCR oligo 2.
XX
KW   Synthetic oligo; solid phase immunoassay; ss.
XX
OS   Synthetic.
XX
PN   WO9426932-A1.
```

```
XX
PD   24-NOV-1994.
XX
PF   13-MAY-1994;   94WO-US005407.
XX
PR   13-MAY-1993;   93US-00061694.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Fields HA,  Khudyakov YE;
XX
DR   WPI; 1995-006819/01.
XX
PT   Solid phase immunoassay using oligo:nucleotide as label - also new
PT   conjugates of oligo:nucleotide coupled to antigenic peptide, partic. for
PT   diagnosing hepatitis C or E virus infection.
XX
PS   Example; Page 13; 34pp; English.
XX
CC   AAR62941 and AAR62942 are examples of synthetic immunoreactive peptides.
CC   They are used in a method for detecting an antigen in a subject. The
CC   method involves binding the antigen to a solid support and then reacting
CC   it with an immunoreactive ligand (L) bound to an oligo; removing any
CC   unreacted L, and then detecting the presence of the oligo. A similar
CC   method can be used to detect Abs, in which case the ligand is an oligo-
CC   labelled Ag. The use of an amplifiable oligo as the label allows Ag or Ab
CC   to be detected at very low levels. An exemplary olgi is AAQ75024 which
CC   can be covalently attached by the 5'- terminus to the N- or C-terminal of
CC   a synthetic peptide. For LCR using oligo AAZ75024, oligos 1-4 (see
CC   AAQ75027-Q75030) can be used. (Updated on 25-MAR-2003 to correct PN
CC   field.)
XX
SQ   Sequence 23 BP; 19 A; 4 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db         23 TTTTTTTTTTTTTTTTTT 6


RESULT 1557
AAQ75029
ID   AAQ75029 standard; RNA; 23 BP.
XX
AC   AAQ75029;
XX
DT   25-MAR-2003  (revised)
DT   03-AUG-1995  (first entry)
XX
DE   LCR oligo 3.
XX
KW   Synthetic oligo; solid phase immunoassay; ss.
XX
OS   Synthetic.
XX
PN   WO9426932-A1.
XX
PD   24-NOV-1994.
XX
PF   13-MAY-1994;   94WO-US005407.
XX
PR   13-MAY-1993;   93US-00061694.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Fields HA,  Khudyakov YE;
XX
DR   WPI; 1995-006819/01.
XX
PT   Solid phase immunoassay using oligo:nucleotide as label - also new
PT   conjugates of oligo:nucleotide coupled to antigenic peptide, partic. for
PT   diagnosing hepatitis C or E virus infection.
XX
PS   Example; Page 13; 34pp; English.
XX
CC   AAR62941 and AAR62942 are examples of synthetic immunoreactive peptides.
CC   They are used in a method for detecting an antigen in a subject. The
CC   method involves binding the antigen to a solid support and then reacting
CC   it with an immunoreactive ligand (L) bound to an oligo; removing any
CC   unreacted L, and then detecting the presence of the oligo. A similar
CC   method can be used to detect Abs, in which case the ligand is an oligo-
CC   labelled Ag. The use of an amplifiable oligo as the label allows Ag or Ab
CC   to be detected at very low levels. An exemplary olgi is AAQ75024 which
CC   can be covalently attached by the 5'- terminus to the N- or C-terminal of
CC   a synthetic peptide. For LCR using oligo AAZ75024, oligos 1-4 (see
CC   AAQ75027-Q75030) can be used. (Updated on 25-MAR-2003 to correct PN
CC   field.)
XX
SQ   Sequence 23 BP; 0 A; 0 C; 4 G; 1 T; 18 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 23;
  Best Local Similarity   0.0%;  Pred. No. 1.3e+03;
  Matches    0;  Conservative   18;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ::::::::::::::::::
Db          1 UUUUUUUUUUUUUUUUUU 18


RESULT 1558
AAQ75029/c
ID   AAQ75029 standard; RNA; 23 BP.
XX
AC   AAQ75029;
XX
DT   25-MAR-2003  (revised)
DT   03-AUG-1995  (first entry)
XX
DE   LCR oligo 3.
XX
KW   Synthetic oligo; solid phase immunoassay; ss.
XX
OS   Synthetic.
XX
PN   WO9426932-A1.
XX
PD   24-NOV-1994.
XX
PF   13-MAY-1994;   94WO-US005407.
XX
PR   13-MAY-1993;   93US-00061694.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Fields HA,  Khudyakov YE;
XX
DR   WPI; 1995-006819/01.
XX
PT   Solid phase immunoassay using oligo:nucleotide as label - also new
PT   conjugates of oligo:nucleotide coupled to antigenic peptide, partic. for
PT   diagnosing hepatitis C or E virus infection.
XX
PS   Example; Page 13; 34pp; English.
XX
CC   AAR62941 and AAR62942 are examples of synthetic immunoreactive peptides.
CC   They are used in a method for detecting an antigen in a subject. The
CC   method involves binding the antigen to a solid support and then reacting
CC   it with an immunoreactive ligand (L) bound to an oligo; removing any
CC   unreacted L, and then detecting the presence of the oligo. A similar
CC   method can be used to detect Abs, in which case the ligand is an oligo-
CC   labelled Ag. The use of an amplifiable oligo as the label allows Ag or Ab
CC   to be detected at very low levels. An exemplary olgi is AAQ75024 which
CC   can be covalently attached by the 5'- terminus to the N- or C-terminal of
```

```
CC   a synthetic peptide. For LCR using oligo AAZ75024, oligos 1-4 (see
CC   AAQ75027-Q75030) can be used. (Updated on 25-MAR-2003 to correct PN
CC   field.)
XX
SQ   Sequence 23 BP; 0 A; 0 C; 4 G; 1 T; 18 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1559
AAF85497
ID   AAF85497 standard; DNA; 23 BP.
XX
AC   AAF85497;
XX
DT   23-JUL-2001  (first entry)
XX
DE   PCR primer for DNA encoding Kalata B1 polypeptide fragments.
XX
KW   Kalata B2; transgenic plant; cotton; calcium channel binding; pain;
KW   stroke; C5a binding; antiinflammatory; PCR primer; ss.
XX
OS   Oldenlandia affinis.
XX
PN   WO200134829-A2.
XX
PD   17-MAY-2001.
XX
PF   03-NOV-2000; 2000WO-AU001352.
XX
PR   05-NOV-1999;   99AU-00003884.
PR   25-NOV-1999;   99AU-00004235.
XX
PA   (UYQU ) UNIV QUEENSLAND.
PA   (UYLA-) UNIV LATROBE.
XX
PI   Craik DJ,  Anderson MA,  Jennings CV;
XX
DR   WPI; 2001-343607/36.
XX
PT   Novel nucleic acid molecule encoding amino acid sequence capable of
PT   forming cyclic structure, for generating transgenic plants capable of
PT   producing cyclic knotted protein and resistant to pathogens such as
PT   insects.
XX
PS   Example 10; Fig 1B; 112pp; English.
XX
CC   PCR primers AAF85495-97 were used to amplify a DNA fragment encoding
CC   Kalata B1. Kalata B1 is a macrocyclic peptide with diverse biological
CC   activities. The Kalata B1 polynucleotide represents a nucleic acid
CC   molecule of the invention. The specification describes nucleic acid
CC   molecules which encode an amino acid sequence which is capable of being
CC   cyclised within a cell or a membrane of a cell to form a cyclic backbone.
CC   The amino acid sequence comprises sufficient disulfide bonds to confer a
CC   stabilized folded structure on the three-dimensional structure of the
CC   backbone. The nucleic acid molecules of the invention are useful for
CC   producing transgenic genetically modified food or non-food crop plants,
CC   in particular cotton. The peptides or proteins can be manipulated to
CC   introduce modulating activity, for modulating activity of calcium channel
CC   binding is useful in treatment of pain or stroke and C5a binding activity
CC   useful as an antiinflammatory agent. The nucleic acid molecules are
CC   useful in the generation of molecules having animal or plant therapeutic
CC   properties as well as in a range of diagnostic, industrial and
CC   agricultural including horticultural applications and for protecting
CC   plants such as crop plants from pest and/or pathogen infestation
XX
SQ   Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTT 2182
              ||||||||||||||||||
Db          6 CTTTTTTTTTTTTTTTTT 23


RESULT 1560
AAD33503
ID   AAD33503 standard; DNA; 23 BP.
XX
AC   AAD33503;
XX
DT   01-JUL-2002  (first entry)
XX
DE   T7T18Apad_PS13-23-0001 probe for calibration of molecular array data.
XX
KW   Molecular array; probe; ss.
XX
OS   Unidentified.
XX
PN   EP1186673-A2.
XX
PD   13-MAR-2002.
XX
PF   10-SEP-2001; 2001EP-00307665.
XX
PR   11-SEP-2000; 2000US-00659173.
XX
PA   (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI   Wobler PK,  Delenstarr GC;
XX
DR   WPI; 2002-282886/33.
XX
PT   Calibration of molecular array data by employing calibration probes that
PT   generate signals proportional to total concentrations of labeled target
PT   molecules, and molecular arrays incorporating sets of calibration probes.
XX
PS   Disclosure; Page 14; 32pp; English.
XX
CC   The invention relates to a method for calibrating data scanned from a
CC   molecular array. The method involves employing calibration probes that
CC   generate signals proportional to the total concentrations of labelled
CC   target molecules to which the molecular array probes are directed over an
CC   entire range of sample solutions and molecular arrays incorporating sets
CC   of calibration probes. Method is useful for calibrating different types
CC   of signals scanned from a molecular array, or calibrating signals scanned
CC   from different molecular arrays. The present sequence is poly (A)
CC   normalisation probe used in calibration of molecular array data
XX
SQ   Sequence 23 BP; 18 A; 3 C; 0 G; 2 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 1561
AAD33503/c
ID   AAD33503 standard; DNA; 23 BP.
XX
AC   AAD33503;
XX
DT   01-JUL-2002  (first entry)
XX
```

DE T7T18Apad_PS13-23-0001 probe for calibration of molecular array data.
XX
KW Molecular array; probe; ss.
XX
OS Unidentified.
XX
PN EP1186673-A2.
XX
PD 13-MAR-2002.
XX
PF 10-SEP-2001; 2001EP-00307665.
XX
PR 11-SEP-2000; 2000US-00659173.
XX
PA (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI Wobler PK, Delenstarr GC;
XX
DR WPI; 2002-282886/33.
XX
PT Calibration of molecular array data by employing calibration probes that
PT generate signals proportional to total concentrations of labeled target
PT molecules, and molecular arrays incorporating sets of calibration probes.
XX
PS Disclosure; Page 14; 32pp; English.
XX
CC The invention relates to a method for calibrating data scanned from a
CC molecular array. The method involves employing calibration probes that
CC generate signals proportional to the total concentrations of labelled
CC target molecules to which the molecular array probes are directed over an
CC entire range of sample solutions and molecular arrays incorporating sets
CC of calibration probes. Method is useful for calibrating different types
CC of signals scanned from a molecular array, or calibrating signals scanned
CC from different molecular arrays. The present sequence is poly (A)
CC normalisation probe used in calibration of molecular array data
XX
SQ Sequence 23 BP; 18 A; 3 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTT 2183
||||||||||||||||||
Db 18 TTTTTTTTTTTTTTTTTT 1

RESULT 1562
ABL95973/c
ID ABL95973 standard; DNA; 23 BP.
XX
AC ABL95973;
XX
DT 19-JUN-2002 (first entry)
XX
DE Probe #48 for assaying nucleic acids.
XX
KW Probe; polymorphism detection; mutation detection; disease diagnosis;
KW microbial identification; ss.
XX
OS Unidentified.
XX
PN WO200208414-A1.
XX
PD 31-JAN-2002.
XX
PF 27-JUN-2001; 2001WO-IB001147.
XX
PR 27-JUN-2000; 2000JP-00193133.
PR 03-AUG-2000; 2000JP-00236115.
PR 26-SEP-2000; 2000JP-00292483.
XX
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (KANK-) KANKYO ENG CO LTD.
XX
PI Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;
PI Yokomaku T;
XX
DR WPI; 2002-195876/25.
XX
PT Fluorescently-labeled nucleic acid probes for assaying nucleic acids and
PT their polymorphism and mutation, particularly useful in science and
PT medicine for e.g. analytical applications, disease diagnosis and
PT microbial identification.
XX
PS Disclosure; Fig 3; 152pp; Japanese.
XX
CC The present invention relates to nucleic acid probes, which are useful
CC for assaying nucleic acids by hybridising with a target nucleic acid, in
CC which a single-stranded oligonucleotide is labelled with a fluorescent
CC substance and a quencher in a manner that the fluorescence intensity of
CC the hybridisation reaction system is increased after completion of the
CC hybridisation but no stem loop structure is formed. The probes are useful
CC for assaying nucleic acids and their polymorphism and mutation,
CC particularly useful for e.g. analytical applications, disease diagnosis
CC and microbial identification. The present sequence was used to illustrate
CC the invention
XX
SQ Sequence 23 BP; 0 A; 6 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAAAAAAAA 2802
||||||||||||||||||
Db 18 GAAAAAAAAAAAAAAAAA 1

RESULT 1563
ABN85073/c
ID ABN85073 standard; DNA; 24 BP.
XX
AC ABN85073;
XX
DT 05-SEP-2002 (first entry)
XX
DE Human S4 ribosomal protein 13.97 PCR primer #2.
XX
KW Human; S4 ribosomal protein 13.97; malignant tumour; haemopathy;
KW HIV infection; immunological disease; inflammation; cytostatic; anti-HIV;
KW PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN CN1333268-A.
XX
PD 30-JAN-2002.
XX
PF 07-JUL-2000; 2000CN-00117077.
XX
PR 07-JUL-2000; 2000CN-00117077.
XX
PA (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-292916/34.
XX
PT Human S4 ribosomal protein 13.97 polypeptide and encoding polynucleotide,
PT useful for treating malignant tumor, inflammation, hemopathy, human
PT immunodeficiency virus infection, immunological disease and inflammation.
XX
PS Example 2; Page 16 (Disclosure); 33pp; Chinese.
XX
CC The present invention relates to human S4 ribosomal protein 13.97 (see

```
CC   ABB83379). The ribosomal protein and its coding sequence are useful for
CC   treating malignant tumours, haemopathy, HIV infection, immunological
CC   diseases and various inflammations. The present sequence is a PCR primer,
CC   which was used in an example from the invention
XX
SQ   Sequence 24 BP; 1 A; 2 C; 1 G; 20 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         24 AAAAAAAAAAAAAAAAAA 7


RESULT 1564
AAH76998
ID   AAH76998 standard; DNA; 24 BP.
XX
AC   AAH76998;
XX
DT   15-DEC-2001  (first entry)
XX
DE   Human amyloid precursor protein 9 RT-PCR primer, SEQ ID NO:4.
XX
KW   Human; amyloid precursor protein 9; recombinant production;
KW   malignant tumour; cancer; blood disease; HIV infection;
KW   human immunodeficiency virus; immune disorder; inflammatory condition;
KW   cytostatic; anti-HIV; antiinflammatory; immunomodulator;
KW   reverse transcription-PCR; RT-PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200174878-A1.
XX
PD   11-OCT-2001.
XX
PF   23-MAR-2001; 2001WO-CN000391.
XX
PR   24-MAR-2000; 2000CN-00115106.
XX
PA   (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2001-626386/72.
XX
PT   New human amyloid precursor protein 9 and encoded polynucleotide,
PT   applicable in diagnosis and treatment of cancer, hemopathy, human
PT   immunodeficiency virus infection, immunological diseases and various
PT   inflammations.
XX
PS   Example 2; Page 16; 37pp; Chinese.
XX
CC   The invention relates to human amyloid precursor protein 9 (AAG66809),
CC   nucleic acids encoding it (AAH76996), and a method for the recombinant
CC   production of amyloid precursor protein 9. The protein has a molecular
CC   weight of 9 kD. The present invention additionally discloses an
CC   antagonist of amyloid precursor protein 9 for therapeutic use, and an
CC   antibody which specifically binds to amyloid precursor protein 9. Amyloid
CC   precursor protein 9, and nucleotides which encode it may be used for
CC   treating a variety of diseases, such as malignant tumours, blood
CC   diseases, HIV (human immunodeficiency virus) infection, immune disorders
CC   and inflammatory conditions. The protein may also be used to screen for
CC   modulators of its activity or for peptide fingerprinting identification.
CC   The polynucleotide can be used as a primer for nucleic acid amplification
CC   reactions or as a probe for hybridisation reactions, or in producing gene
CC   chips or microarrays. Sequences AAH75997-AAH76998 represent reverse
CC   transcription-PCR (RT-PCR) primers used in an exemplification of the
CC   invention to isolate human amyloid precursor protein 9 cDNA
XX
SQ   Sequence 24 BP; 1 A; 1 C; 4 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTA 18


RESULT 1565
AAH43079
ID   AAH43079 standard; DNA; 24 BP.
XX
AC   AAH43079;
XX
DT   15-OCT-2001  (first entry)
XX
DE   Nucleotide sequence of a synthetic oligonucleotide.
XX
KW   Nucleic acid immobilisation; ss.
XX
OS   Synthetic.
XX
PN   WO200155365-A1.
XX
PD   02-AUG-2001.
XX
PF   24-JAN-2001; 2001WO-JP000443.
XX
PR   27-JAN-2000; 2000JP-00019301.
XX
PA   (TOJO ) TOYO KOHAN CO LTD.
XX
PI   Tanga M,  Okamura H,  Takagi K,  Takahashi K;
XX
DR   WPI; 2001-488794/53.
XX
PT   Support for immobilizing nucleotides.
XX
PS   Example 1; Page 8; 18pp; Japanese.
XX
CC   The specification describes a support for immobilizing nucleotides which
CC   contributes to the efficient clarification of DNA without damaging the
CC   terminal parts of the DNA. The support is a chemically treated modified
CC   substrate on which oligonucleotides with restriction enzyme cleavage
CC   sites are immobilised. The support is useful for immobilizing nucleic
CC   acids such as DNA. The present sequence represents a synthetic
CC   oligonucleotide used in the course of the invention
XX
SQ   Sequence 24 BP; 3 A; 0 C; 3 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          6 TTTTTTTTTTTTTTTTTT 23


RESULT 1566
AAH43079/c
ID   AAH43079 standard; DNA; 24 BP.
XX
AC   AAH43079;
XX
DT   15-OCT-2001  (first entry)
XX
DE   Nucleotide sequence of a synthetic oligonucleotide.
XX
KW   Nucleic acid immobilisation; ss.
XX
```

OS Synthetic.
XX
PN WO200155365-A1.
XX
PD 02-AUG-2001.
XX
PF 24-JAN-2001; 2001WO-JP000443.
XX
PR 27-JAN-2000; 2000JP-00019301.
XX
PA (TOJO) TOYO KOHAN CO LTD.
XX
PI Tanga M, Okamura H, Takagi K, Takahashi K;
XX
DR WPI; 2001-488794/53.
XX
PT Support for immobilizing nucleotides.
XX
PS Example 1; Page 8; 18pp; Japanese.
XX
CC The specification describes a support for immobilizing nucleotides which
CC contributes to the efficient clarification of DNA without damaging the
CC terminal parts of the DNA. The support is a chemically treated modified
CC substrate on which oligonucleotides with restriction enzyme cleavage
CC sites are immobilised. The support is useful for immobilizing nucleic
CC acids such as DNA. The present sequence represents a synthetic
CC oligonucleotide used in the course of the invention
XX
SQ Sequence 24 BP; 3 A; 0 C; 3 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2803
||||||||||||||||||
Db 23 AAAAAAAAAAAAAAAAAA 6

RESULT 1567
ABQ79878
ID ABQ79878 standard; DNA; 24 BP.
XX
AC ABQ79878;
XX
DT 23-DEC-2002 (first entry)
XX
DE Nucleotide sequence of a PCR primer #8.
XX
KW Polymerase chain reaction; thermal cycle; immobilisation;
KW genetic engineering; PCR; primer; ss.
XX
OS Synthetic.
XX
PN JP2002191369-A.
XX
PD 09-JUL-2002.
XX
PF 27-DEC-2000; 2000JP-00399573.
XX
PR 27-DEC-2000; 2000JP-00399573.
XX
PA (TOJO) TOYO KOHAN CO LTD.
PA (TAKA/) TAKAHASHI K.
XX
DR WPI; 2002-630904/68.
XX
PT Carrying out a thermal cycle of polymerase chain reaction (PCR) by using
PT a substrate on which a DNA is immobilized used in medical, biochemical,
PT molecular biological and gene engineering fields.
XX
PS Example; Page 10; 13pp; Japanese.
XX
CC The invention relates to performing a thermal cycle of PCR by using a
CC substrate on which a deoxyribonucleic acid (DNA) is immobilized. The
CC method is useful in the medical, biochemical, molecular biological and
CC genetic engineering fields. Sequences ABQ79871-881 represent PCR primers
CC used in the method of the invention
XX
SQ Sequence 24 BP; 3 A; 0 C; 3 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTT 2183
||||||||||||||||||
Db 6 TTTTTTTTTTTTTTTTTT 23

RESULT 1568
ABQ79878/c
ID ABQ79878 standard; DNA; 24 BP.
XX
AC ABQ79878;
XX
DT 23-DEC-2002 (first entry)
XX
DE Nucleotide sequence of a PCR primer #8.
XX
KW Polymerase chain reaction; thermal cycle; immobilisation;
KW genetic engineering; PCR; primer; ss.
XX
OS Synthetic.
XX
PN JP2002191369-A.
XX
PD 09-JUL-2002.
XX
PF 27-DEC-2000; 2000JP-00399573.
XX
PR 27-DEC-2000; 2000JP-00399573.
XX
PA (TOJO) TOYO KOHAN CO LTD.
PA (TAKA/) TAKAHASHI K.
XX
DR WPI; 2002-630904/68.
XX
PT Carrying out a thermal cycle of polymerase chain reaction (PCR) by using
PT a substrate on which a DNA is immobilized used in medical, biochemical,
PT molecular biological and gene engineering fields.
XX
PS Example; Page 10; 13pp; Japanese.
XX
CC The invention relates to performing a thermal cycle of PCR by using a
CC substrate on which a deoxyribonucleic acid (DNA) is immobilized. The
CC method is useful in the medical, biochemical, molecular biological and
CC genetic engineering fields. Sequences ABQ79871-881 represent PCR primers
CC used in the method of the invention
XX
SQ Sequence 24 BP; 3 A; 0 C; 3 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2803
||||||||||||||||||
Db 23 AAAAAAAAAAAAAAAAAA 6

RESULT 1569
AAD33505
ID AAD33505 standard; DNA; 24 BP.
XX
AC AAD33505;

XX
DT 01-JUL-2002 (first entry)
XX
DE T7T18Apad_PS12-24-0001 probe for calibration of molecular array data.
XX
KW Molecular array; probe; ss.
XX
OS Unidentified.
XX
PN EP1186673-A2.
XX
PD 13-MAR-2002.
XX
PF 10-SEP-2001; 2001EP-00307665.
XX
PR 11-SEP-2000; 2000US-00659173.
XX
PA (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI Wobler PK, Delenstarr GC;
XX
DR WPI; 2002-282886/33.
XX
PT Calibration of molecular array data by employing calibration probes that
PT generate signals proportional to total concentrations of labeled target
PT molecules, and molecular arrays incorporating sets of calibration probes.
XX
PS Disclosure; Page 14; 32pp; English.
XX
CC The invention relates to a method for calibrating data scanned from a
CC molecular array. The method involves employing calibration probes that
CC generate signals proportional to the total concentrations of labelled
CC target molecules to which the molecular array probes are directed over an
CC entire range of sample solutions and molecular arrays incorporating sets
CC of calibration probes. Method is useful for calibrating different types
CC of signals scanned from a molecular array, or calibrating signals scanned
CC from different molecular arrays. The present sequence is poly (A)
CC normalisation probe used in calibration of molecular array data
XX
SQ Sequence 24 BP; 18 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2803
||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 1570
AAD33505/c
ID AAD33505 standard; DNA; 24 BP.
XX
AC AAD33505;
XX
DT 01-JUL-2002 (first entry)
XX
DE T7T18Apad_PS12-24-0001 probe for calibration of molecular array data.
XX
KW Molecular array; probe; ss.
XX
OS Unidentified.
XX
PN EP1186673-A2.
XX
PD 13-MAR-2002.
XX
PF 10-SEP-2001; 2001EP-00307665.
XX
PR 11-SEP-2000; 2000US-00659173.
XX
PA (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI Wobler PK, Delenstarr GC;
XX
DR WPI; 2002-282886/33.
XX
PT Calibration of molecular array data by employing calibration probes that
PT generate signals proportional to total concentrations of labeled target
PT molecules, and molecular arrays incorporating sets of calibration probes.
XX
PS Disclosure; Page 14; 32pp; English.
XX
CC The invention relates to a method for calibrating data scanned from a
CC molecular array. The method involves employing calibration probes that
CC generate signals proportional to the total concentrations of labelled
CC target molecules to which the molecular array probes are directed over an
CC entire range of sample solutions and molecular arrays incorporating sets
CC of calibration probes. Method is useful for calibrating different types
CC of signals scanned from a molecular array, or calibrating signals scanned
CC from different molecular arrays. The present sequence is poly (A)
CC normalisation probe used in calibration of molecular array data
XX
SQ Sequence 24 BP; 18 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTT 2183
||||||||||||||||||
Db 18 TTTTTTTTTTTTTTTTTT 1

RESULT 1571
ADC75073
ID ADC75073 standard; DNA; 24 BP.
XX
AC ADC75073;
XX
DT 01-JAN-2004 (first entry)
XX
DE Biosensor related oligonucleotide of the invention SEQ ID NO:1.
XX
KW ss; biosensor; hybridisation.
XX
OS Synthetic.
XX
PN JP2003172737-A.
XX
PD 20-JUN-2003.
XX
PF 07-DEC-2001; 2001JP-00374764.
XX
PR 07-DEC-2001; 2001JP-00374764.
XX
PA (TOJO) TOYO KOHAN CO LTD.
XX
DR WPI; 2003-819164/77.
XX
PT Solid support body comprising crystal resonator on which a surface
PT treatment layer is formed, and a substrate whose surface treatment layer
PT is chemically modified, useful as biosensor.
XX
PS Disclosure; SEQ ID NO 1; 7pp; Japanese.
XX
CC The invention relates to a novel solid support body comprising a crystal
CC resonator on which a surface treatment layer is formed. The biosensor is
CC useful for analysing biological samples e.g., gene, a protein, and a
CC peptide, and for analysing bioactive substances. Preferably, the
CC biosensor is useful for analysing base sequences by carrying out
CC hybridisation. The present sequence is used in the exemplification of the
CC invention.
XX
SQ Sequence 24 BP; 3 A; 0 C; 3 G; 18 T; 0 U; 0 Other;

```
  Query Match             0.6%;  Score 18;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          6 TTTTTTTTTTTTTTTTTT 23


RESULT 1572
ADC75073/c
ID   ADC75073 standard; DNA; 24 BP.
XX
AC   ADC75073;
XX
DT   01-JAN-2004  (first entry)
XX
DE   Biosensor related oligonucleotide of the invention SEQ ID NO:1.
XX
KW   ss; biosensor; hybridisation.
XX
OS   Synthetic.
XX
PN   JP2003172737-A.
XX
PD   20-JUN-2003.
XX
PF   07-DEC-2001; 2001JP-00374764.
XX
PR   07-DEC-2001; 2001JP-00374764.
XX
PA   (TOJO ) TOYO KOHAN CO LTD.
XX
DR   WPI; 2003-819164/77.
XX
PT   Solid support body comprising crystal resonator on which a surface
PT   treatment layer is formed, and a substrate whose surface treatment layer
PT   is chemically modified, useful as biosensor.
XX
PS   Disclosure; SEQ ID NO 1; 7pp; Japanese.
XX
CC   The invention relates to a novel solid support body comprising a crystal
CC   resonator on which a surface treatment layer is formed. The biosensor is
CC   useful for analysing biological samples e.g., gene, a protein, and a
CC   peptide, and for analysing bioactive substances. Preferably, the
CC   biosensor is useful for analysing base sequences by carrying out
CC   hybridisation. The present sequence is used in the exemplification of the
CC   invention.
XX
SQ   Sequence 24 BP; 3 A; 0 C; 3 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         23 AAAAAAAAAAAAAAAAAA 6


RESULT 1573
AAA47833/c
ID   AAA47833 standard; DNA; 25 BP.
XX
AC   AAA47833;
XX
DT   16-NOV-2000  (first entry)
XX
DE   Adapter sequence for 3' end of lectin cDNA.
XX
KW   Lectin; mannose; sugar; trangenic plant; crop protection; resistance;
KW   bacteria; virus; fungus; insect; targetting; neutrophil glycoprotein;
KW   polymorphonuclear cell; blood typing; primer; ss.
XX
OS   Hernandia moerenhoutiana.
XX
PN   WO200044780-A1.
XX
PD   03-AUG-2000.
XX
PF   28-JAN-2000; 2000WO-AU000039.
XX
PR   29-JAN-1999;   99AU-00008395.
XX
PA   (AURE-) AUSTRALIAN RED CROSS BLOOD SERVICE.
XX
PI   Clark TR,  Minchinton RM;
XX
DR   WPI; 2000-532807/48.
XX
PT   New polypeptide, capable of binding to mannose, isolated from the plant
PT   Hernandia is useful for the generation of transgenic plants which exhibit
PT   enhanced resistance to micro-organisms, fungi, viruses and insects.
XX
PS   Example 8; Page 35; 63pp; English.
XX
CC   The Hernandia lectin is capable of binding and/or interacting with
CC   mannose or a sugar chemically related to mannose. The genetic sequence
CC   encoding lectin can be used for the generation of transgenic plants which
CC   exhibit enhanced resistance to micro-organisms, fungi, viruses and
CC   insects. The lectin polypeptide is also useful for targetting neutrophil
CC   glycoproteins for diagnostic and therapeutic applications, including
CC   evaluating the nature of immune cells and can also be used in typing,
CC   e.g. blood group typing of polymorphonuclear cells
XX
SQ   Sequence 25 BP; 1 A; 3 C; 2 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         25 AAAAAAAAAAAAAAAAAA 8


RESULT 1574
ABK87633
ID   ABK87633 standard; DNA; 25 BP.
XX
AC   ABK87633;
XX
DT   24-SEP-2002  (first entry)
XX
DE   BamT15G PCR primer.
XX
KW   Atopic dermatitis-associated; asthma; psoriasis; pancreatitis; PCR; ss;
KW   rheumatoid arthritis; nephritis; arteriosclerosis; allergic disease;
KW   viral disease; inflammatory colitis; bronchitis; skin disease; primer.
XX
OS   Unidentified.
XX
PN   WO200251999-A1.
XX
PD   04-JUL-2002.
XX
PF   21-DEC-2001; 2001WO-JP011293.
XX
PR   21-DEC-2000; 2000JP-00388739.
XX
PA   (MOCH ) MOCHIDA PHARM CO LTD.
PA   (KAZU-) KAZUSA DNA RES INST.
XX
PI   Ohara O,  Nagase T,  Negishi T,  Mizushima S,  Furusako S;
XX
```

```
DR   WPI; 2002-519957/55.
XX
PT   Human spleen-originated cDNA library-isolated atopic dermatitis-
PT   associated gene, which encodes a protein, useful in diagnosis and
PT   screening of preventives or remedies for e.g. atopic dermatitis.
XX
PS   Example 1; Page 46; 88pp; Japanese.
XX
CC   The present invention relates to a new DNA containing a fully defined 568
CC   base sequence given in the specification. The polynucleotides and
CC   proteins of the invention are useful in diagnosis and screening of
CC   preventives or remedies for atopic dermatitis. The invention can also be
CC   used in treating asthma, psoriasis, pancreatitis, rheumatoid arthritis,
CC   nephritis, arteriosclerosis, allergic diseases, viral diseases,
CC   inflammatory colitis, bronchitis and skin diseases. The present nucleic
CC   acid sequence represents a PCR primer used in the methods of the
CC   invention
XX
SQ   Sequence 25 BP; 1 A; 5 C; 3 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTT 2180
             ||||||||||||||||||
Db          7 TCCTTTTTTTTTTTTTTT 24


RESULT 1575
ABK87631
ID   ABK87631 standard; DNA; 25 BP.
XX
AC   ABK87631;
XX
DT   24-SEP-2002  (first entry)
XX
DE   BamT15A PCR primer.
XX
KW   Atopic dermatitis-associated; asthma; psoriasis; pancreatitis; PCR; ss;
KW   rheumatoid arthritis; nephritis; arteriosclerosis; allergic disease;
KW   viral disease; inflammatory colitis; bronchitis; skin disease; primer.
XX
OS   Unidentified.
XX
PN   WO200251999-A1.
XX
PD   04-JUL-2002.
XX
PF   21-DEC-2001; 2001WO-JP011293.
XX
PR   21-DEC-2000; 2000JP-00388739.
XX
PA   (MOCH ) MOCHIDA PHARM CO LTD.
PA   (KAZU-) KAZUSA DNA RES INST.
XX
PI   Ohara O,  Nagase T,  Negishi T,  Mizushima S,  Furusako S;
XX
DR   WPI; 2002-519957/55.
XX
PT   Human spleen-originated cDNA library-isolated atopic dermatitis-
PT   associated gene, which encodes a protein, useful in diagnosis and
PT   screening of preventives or remedies for e.g. atopic dermatitis.
XX
PS   Example 1; Page 45; 88pp; Japanese.
XX
CC   The present invention relates to a new DNA containing a fully defined 568
CC   base sequence given in the specification. The polynucleotides and
CC   proteins of the invention are useful in diagnosis and screening of
CC   preventives or remedies for atopic dermatitis. The invention can also be
CC   used in treating asthma, psoriasis, pancreatitis, rheumatoid arthritis,
CC   nephritis, arteriosclerosis, allergic diseases, viral diseases,
CC   inflammatory colitis, bronchitis and skin diseases. The present nucleic
CC   acid sequence represents a PCR primer used in the methods of the
CC   invention
XX
SQ   Sequence 25 BP; 2 A; 5 C; 2 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTT 2180
             ||||||||||||||||||
Db          7 TCCTTTTTTTTTTTTTTT 24


RESULT 1576
ABK87632
ID   ABK87632 standard; DNA; 25 BP.
XX
AC   ABK87632;
XX
DT   24-SEP-2002  (first entry)
XX
DE   BamT15C PCR primer.
XX
KW   Atopic dermatitis-associated; asthma; psoriasis; pancreatitis; PCR; ss;
KW   rheumatoid arthritis; nephritis; arteriosclerosis; allergic disease;
KW   viral disease; inflammatory colitis; bronchitis; skin disease; primer.
XX
OS   Unidentified.
XX
PN   WO200251999-A1.
XX
PD   04-JUL-2002.
XX
PF   21-DEC-2001; 2001WO-JP011293.
XX
PR   21-DEC-2000; 2000JP-00388739.
XX
PA   (MOCH ) MOCHIDA PHARM CO LTD.
PA   (KAZU-) KAZUSA DNA RES INST.
XX
PI   Ohara O,  Nagase T,  Negishi T,  Mizushima S,  Furusako S;
XX
DR   WPI; 2002-519957/55.
XX
PT   Human spleen-originated cDNA library-isolated atopic dermatitis-
PT   associated gene, which encodes a protein, useful in diagnosis and
PT   screening of preventives or remedies for e.g. atopic dermatitis.
XX
PS   Example 1; Page 45; 88pp; Japanese.
XX
CC   The present invention relates to a new DNA containing a fully defined 568
CC   base sequence given in the specification. The polynucleotides and
CC   proteins of the invention are useful in diagnosis and screening of
CC   preventives or remedies for atopic dermatitis. The invention can also be
CC   used in treating asthma, psoriasis, pancreatitis, rheumatoid arthritis,
CC   nephritis, arteriosclerosis, allergic diseases, viral diseases,
CC   inflammatory colitis, bronchitis and skin diseases. The present nucleic
CC   acid sequence represents a PCR primer used in the methods of the
CC   invention
XX
SQ   Sequence 25 BP; 1 A; 6 C; 2 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTT 2180
             ||||||||||||||||||
Db          7 TCCTTTTTTTTTTTTTTT 24


RESULT 1577
```

```
AAD33507
ID   AAD33507 standard; DNA; 25 BP.
XX
AC   AAD33507;
XX
DT   01-JUL-2002  (first entry)
XX
DE   T7T18Apad_PS11-25-0001 probe for calibration of molecular array data.
XX
KW   Molecular array; probe; ss.
XX
OS   Unidentified.
XX
PN   EP1186673-A2.
XX
PD   13-MAR-2002.
XX
PF   10-SEP-2001; 2001EP-00307665.
XX
PR   11-SEP-2000; 2000US-00659173.
XX
PA   (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI   Wobler PK,  Delenstarr GC;
XX
DR   WPI; 2002-282886/33.
XX
PT   Calibration of molecular array data by employing calibration probes that
PT   generate signals proportional to total concentrations of labeled target
PT   molecules, and molecular arrays incorporating sets of calibration probes.
XX
PS   Disclosure; Page 14; 32pp; English.
XX
CC   The invention relates to a method for calibrating data scanned from a
CC   molecular array. The method involves employing calibration probes that
CC   generate signals proportional to the total concentrations of labelled
CC   target molecules to which the molecular array probes are directed over an
CC   entire range of sample solutions and molecular arrays incorporating sets
CC   of calibration probes. Method is useful for calibrating different types
CC   of signals scanned from a molecular array, or calibrating signals scanned
CC   from different molecular arrays. The present sequence is poly (A)
CC   normalisation probe used in calibration of molecular array data
XX
SQ   Sequence 25 BP; 19 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 1578
AAD33507/c
ID   AAD33507 standard; DNA; 25 BP.
XX
AC   AAD33507;
XX
DT   01-JUL-2002  (first entry)
XX
DE   T7T18Apad_PS11-25-0001 probe for calibration of molecular array data.
XX
KW   Molecular array; probe; ss.
XX
OS   Unidentified.
XX
PN   EP1186673-A2.
XX
PD   13-MAR-2002.
XX
PF   10-SEP-2001; 2001EP-00307665.
XX
PR   11-SEP-2000; 2000US-00659173.
XX
PA   (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI   Wobler PK,  Delenstarr GC;
XX
DR   WPI; 2002-282886/33.
XX
PT   Calibration of molecular array data by employing calibration probes that
PT   generate signals proportional to total concentrations of labeled target
PT   molecules, and molecular arrays incorporating sets of calibration probes.
XX
PS   Disclosure; Page 14; 32pp; English.
XX
CC   The invention relates to a method for calibrating data scanned from a
CC   molecular array. The method involves employing calibration probes that
CC   generate signals proportional to the total concentrations of labelled
CC   target molecules to which the molecular array probes are directed over an
CC   entire range of sample solutions and molecular arrays incorporating sets
CC   of calibration probes. Method is useful for calibrating different types
CC   of signals scanned from a molecular array, or calibrating signals scanned
CC   from different molecular arrays. The present sequence is poly (A)
CC   normalisation probe used in calibration of molecular array data
XX
SQ   Sequence 25 BP; 19 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db         18 TTTTTTTTTTTTTTTTTT 1


RESULT 1579
AAD12516/c
ID   AAD12516 standard; DNA; 26 BP.
XX
AC   AAD12516;
XX
DT   25-SEP-2001  (first entry)
XX
DE   Thuja sp. pinoresinol/lariciresinol reductase cDNA cloning linker primer.
XX
KW   Dirigent protein; pinoresinol/lariciresinol reductase; stereospecificity;
KW   lignan biosynthetic pathway; secoisolariciresinol; western red cedar;
KW   PCR primer; ss.
XX
OS   Thuja plicata.
XX
PN   WO200149833-A2.
XX
PD   12-JUL-2001.
XX
PF   22-DEC-2000; 2000WO-US035265.
XX
PR   30-DEC-1999;   99US-00475316.
XX
PA   (UNIW ) UNIV WASHINGTON STATE RES FOUND.
PA   (MINU ) UNIV MINNESOTA.
XX
PI   Lewis NG,  Davin LB,  Dinkova-Kostova AT,  Fujita M,  Gang DR;
PI   Ford JD,  Sarkanen S;
XX
DR   WPI; 2001-465260/50.
XX
PT   Dirigent and/or pinoresinol/lariciresinol reductase proteins useful for
PT   producing optically-pure lignans.
XX
PS   Example 14; Page 56; 183pp; English.
XX
```

CC The present invention relates to an isolated dirigent and/or pinoresinol
CC /lariciresinol reductase protein from a lignan biosynthetic pathway.
CC Dirigent and/or pinoresinol/lariciresinol reductase protein and the
CC nucleic acids that encode it may be expressed either in vivo or in vitro
CC to produce enzymes involved in the biosynthesis of lignans. The 78-kD
CC dirigent protein confers stereospecificity in 8,8'-linked lignan
CC formation and binds to and orients coniferyl alcohol-derived free
CC radicals, which then under go stereospecific coupling to form (+)-
CC pinoresinol. Pinoresinol/lariciresinol reductase catalyses the conversion
CC of pinoresinol to lariciresinol and then to secoisolariciresinol. The
CC present sequence is 3' linker PCR primer, XhoI-poly(dT) used in the
CC cloning of Thuja plicata pinoresinol/ lariciresinol reductase cDNA
XX
SQ Sequence 26 BP; 1 A; 2 C; 3 G; 20 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2803
||||||||||||||||||
Db 26 AAAAAAAAAAAAAAAAAA 9

RESULT 1580
AAV35002/c
ID AAV35002 standard; DNA; 26 BP.
XX
AC AAV35002;
XX
DT 27-AUG-1998 (first entry)
XX
DE Human endothelin-beta 1 receptor PCR primer Vet119.
XX
KW Endothelin beta-1 receptor; ETB-1; screening; signal transduction;
KW agonist; antagonist; vasoconstrictor; vasopressor; cardiogenic shock;
KW pulmonary hypertension; acute myocardial infarct; uraemia; vasculitis;
KW Crohn's disease; ulcerative colitis; sepsis; congestive heart failure;
KW coronary spasm; cyclosporin nephrotoxicity; toxaemia; PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US5773223-A.
XX
PD 30-JUN-1998.
XX
PF 02-SEP-1993; 93US-00117361.
XX
PR 02-SEP-1993; 93US-00117361.
XX
PA (CHIR) CHIRON CORP.
XX
PI Shyamala V, Olson PT;
XX
DR WPI; 1998-386992/33.
XX
PT Screening for modulators of the endothelin B1 receptor - by measuring
PT effect on signal transduction in cells engineered to express the
PT receptor, potentially useful as agonists and antagonists of endothelin.
XX
PS Example 1; Col 18; 23pp; English.
XX
CC AAV35002-V35021 are primers used to amplify and isolate a novel human
CC endothelin-beta1 receptor (ETB-1) which corresponds to a decapeptide
CC insert. This sequence is used in a method involving the screening of
CC compounds for their ability to bind to endothelin B1 (ETB1) receptor
CC polypeptide and to modulate its signal transduction activity by applying
CC test compound to host cells transformed with DNA encoding ETB-1 and
CC optionally lysing the cells and then measuring signal transduction
CC activity. The method is used to identify agonists and antagonists of
CC endothelin (ET), a known vasoconstrictor/vasopressor agent, associated
CC with cardiogenic shock, pulmonary hypertension, acute myocardial infarct,
CC uraemia, Crohn's disease, ulcerative colitis, sepsis, congestive heart
CC failure, coronary spasm, cyclosporin nephrotoxicity, vasculitis and
CC toxaemia in pregnancy, and is also present at elevated levels after
CC orthotopic liver transplantation and major abdominal surgery
XX
SQ Sequence 26 BP; 3 A; 2 C; 1 G; 20 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2803
||||||||||||||||||
Db 26 AAAAAAAAAAAAAAAAAA 9

RESULT 1581
AAA88688/c
ID AAA88688 standard; DNA; 26 BP.
XX
AC AAA88688;
XX
DT 05-FEB-2001 (first entry)
XX
DE Oligo-dT-XhoI primer.
XX
KW Sweetgum; angiosperm; cytochrome P450-1; conifer; loblolly pine;
KW transgenic plant; lignin; paper; pulping; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200058489-A2.
XX
PD 05-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US008083.
XX
PR 26-MAR-1999; 99US-00277248.
XX
PA (INTO) INT PAPER CO.
XX
PI Chiang VL, Carraway DT;
XX
DR WPI; 2000-647240/62.
XX
PT Use of angiosperm coniferyl aldehyde 5-hydroxylase which catalyzes 5-
PT hydroxylation of coniferyl aldehyde, for modifying lignin biosynthesis in
PT gymnosperms, involves expressing the enzyme in a gymnosperm plant.
XX
PS Example 3; Page 23; 123pp; English.
XX
CC The present sequence is that of an oligo-dT primer including a 5' XboI
CC site. The primer was used with a gene-specific primer to amplify sweetgum
CC cytochrome P450-1 cDNA (see AAA88681). An aim of the invention is to
CC identify, sequence and clone specific genes such as P450-1 from an
CC angiosperm that are involved in production of syringyl lignin, and to
CC then introduce such genes into the genome of a gymnosperm, such as
CC loblolly pine, to induce production of syringyl lignin and thereby
CC provide enhanced pulpability to the wood structure
XX
SQ Sequence 26 BP; 2 A; 1 C; 3 G; 20 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2803
||||||||||||||||||
Db 26 AAAAAAAAAAAAAAAAAA 9

RESULT 1582
AAC93128/c

ID AAC93128 standard; DNA; 26 BP.
XX
AC AAC93128;
XX
DT 21-MAR-2001 (first entry)
XX
DE Stephania tetrandra S. moore RNA reverse transcriptase primer NotI-dT.
XX
KW Stephania tetrandra S. Moore; IL-6; interleukin-6; hepatotropic;
KW antiinflammatory; hepatocirrhosis; hepatitis; alcoholism; primer; ss.
XX
OS Unidentified.
XX
PN US6162437-A.
XX
PD 19-DEC-2000.
XX
PF 25-NOV-1997; 97US-00978321.
XX
PR 05-JUN-1995; 95WO-KR000073.
PR 06-DEC-1996; 96US-00750462.
XX
PA (KOAD) KOREA ADV INST SCI & TECHNOLOGY.
XX
PI Lee J, Kim Y, Kang H, Pyun K, Choi I;
XX
DR WPI; 2001-146043/15.
XX
PT Treatment of hepatocirrhosis comprises administering an extract of the
PT root of Stephania tetrandra in an amount effective to inhibit production
PT of interleukin-6.
XX
PS Example 4; Col 9; 27pp; English.
XX
CC The present sequence was used in an example to illustrate a method for
CC treating hepatocirrhosis. The method comprises administering an extract
CC of the root of Stephania tetrandra in an amount effective to inhibit
CC production of interleukin-6 (IL-6). Hepatocirrhosis is often associated
CC with chronic hepatitis or chronic alcoholism
XX
SQ Sequence 26 BP; 0 A; 4 C; 4 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2803
||||||||||||||||||
Db 26 AAAAAAAAAAAAAAAAAA 9

RESULT 1583
AAQ47178
ID AAQ47178 standard; DNA; 26 BP.
XX
AC AAQ47178;
XX
DT 25-MAR-2003 (revised)
DT 25-JAN-1994 (first entry)
XX
DE MHC DR A intron binding oligomer Tcon.
XX
KW MHC; major histocompatability complex; class II; control oligomers; DR A;
KW transplantation; antigen; autoimmune disease; ss.
XX
OS Synthetic.
XX
PN WO9314769-A1.
XX
PD 05-AUG-1993.
XX
PF 29-JAN-1993; 93WO-US000797.
XX
PR 31-JAN-1992; 92US-00830427.
PR 14-SEP-1992; 92US-00944868.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Weiss TL, Garovoy MR, Hunt A, Huey B, Tam S;
XX
DR WPI; 1993-258367/32.
XX
PT Depletion of transplantation antigens in donor cells - using anti-sense
PT or triplex-forming oligonucleotide(s), used for treating auto-immune
PT disease and in transplants.
XX
PS Example; Page 22; 71pp; English.
XX
CC The sequences given in AAQ47176-77 represent triplex forming oligo-
CC nucleotides which bind to the mRNA sequence of the MHC class II locus DR
CC A structural gene at positions 851-876. The sequences given in AAQ47178-
CC 80 represent control oligomers which contain base compositions similar to
CC that around this DR A region but not containing the correct sequences. DR
CC A is a transplantation antigen. Binding of this sequence to the DR A gene
CC inhibits antigen production. This method may be used for treating
CC individuals with autoimmune disease, characterised by dysfunctional
CC expression of a transplantation antigen. It may also be used to produce
CC cells which are more easily transplanted into a recipient. (Updated on 25
CC -MAR-2003 to correct PN field.)
XX
SQ Sequence 26 BP; 0 A; 0 C; 4 G; 22 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 26;
Best Local Similarity 80.8%; Pred. No. 1.7e+03;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2159 TTTCTCCTTTTTTTTTTTTTTTTT 2184
||| | ||| ||||||| |||||||
Db 1 TTTGTGTTTTGTTTTTTTGTTTTTTT 26

RESULT 1584
AAZ25387
ID AAZ25387 standard; DNA; 26 BP.
XX
AC AAZ25387;
XX
DT 16-DEC-1999 (first entry)
XX
DE Infectious pancreatic necrosis virus PCR primer #1.
XX
KW Infectious pancreatic necrosis virus; IPNV; strain West Buxton;
KW strain SP; segment A; segment B; nonpathogenic; Birnavirdae family;
KW infection; live attenuated vaccine; aquaculture industry; Rainbow trout;
KW Brook trout; Atlantic salmon; PCR primer; ss.
XX
OS Synthetic.
OS Infectious pancreatic necrosis virus.
XX
PN WO9950419-A2.
XX
PD 07-OCT-1999.
XX
PF 31-MAR-1999; 99WO-US004285.
XX
PR 31-MAR-1998; 98US-0080178P.
XX
PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
XX
PI Vakharia VN, Yao K;
XX
DR WPI; 1999-591321/50.
XX
PT Preparing nonpathogenic infectious pancreatic necrosis virus, IPNV,
PT useful for producing attenuated virus for vaccines useful in the
PT aquaculture industry.

```
XX
PS   Example 1; Page 21; 63pp; English.
XX
CC   A method has been developed for preparing nonpathogenic, infectious
CC   pancreatic necrosis virus (IPNV). The method comprises: 1) preparing cDNA
CC   containing the IPNV genome segments A and B where A is modified to
CC   prevent expression of an arginine-rich non-structural (NS) protein; 2)
CC   transcribing the cDNA to produce RNA; 3) incubating the host cells in a
CC   culture medium; and 4) isolating live IPNV from the culture medium. The
CC   method is useful to produce live nonpathogenic IPNV, useful to study
CC   viral pathogenesis and for the production of live, nonpathogenic IPNV
CC   vaccines, since it was demonstrated that the NS protein-deficient virus
CC   could replicate but did not invoke a pathological response in hosts.
CC   Combination vaccines may also be produced by combining the IPNV with
CC   bacterial antigens (especially from gram negative bacteria e.g. Aeromonas
CC   salmonicida) and/or antigens from aquatic viruses other than Birnaviruses
CC   (the family to which IPNV belongs) e.g. infectious haematopoietic
CC   necrosis virus. The method may also be used to generate a nonpathogenic
CC   chimeric virus when the cDNA of segment A encodes epitopic determinants
CC   from at least two different IPNV strains. IPNV causes a highly contagious
CC   and destructive disease of juvenile Rainbow and Brook trout and Atlantic
CC   salmon (e.g. highly virulent strains can cause more than 90 % mortality
CC   in hatchery stocks less than 4 months old and survivors can remain
CC   lifelong carriers and reservoirs of infection); IPNV is therefore a
CC   pathogen of major economic importance to the aquaculture industry. The
CC   present sequence represents an IPNV PCR primer used in an example from
CC   the present invention
XX
SQ   Sequence 26 BP; 0 A; 6 C; 4 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTTTT 2181
              ||||||||||||||||||
Db          9 CCTTTTTTTTTTTTTTTT 26


RESULT 1585
AAA91664/c
ID   AAA91664 standard; RNA; 26 BP.
XX
AC   AAA91664;
XX
DT   03-JAN-2001  (first entry)
XX
DE   HCV(+)RNA oligonucleotide.
XX
KW   Hepatitis C virus; HCV; HCV RNA replication inhibitor; ribozyme;
KW   antiviral; ss.
XX
OS   Hepatitis C virus.
XX
PN   US6107028-A.
XX
PD   22-AUG-2000.
XX
PF   15-MAY-1996;   96US-00648272.
XX
PR   14-DEC-1994;   94US-00357508.
PR   07-JUN-1995;   95US-00476257.
PR   11-SEP-1995;   95US-00534220.
XX
PA   (UNIW ) UNIV WASHINGTON.
XX
PI   Lieber A,  Kay MA;
XX
DR   WPI; 2000-578530/54.
XX
PT   Inhibiting hepatitis C viral RNA replication in an infected cell for
PT   treating or preventing viral infection, comprises introducing ribozymes
PT   specific for a minus strand of the viral 5' non-coding sequence.
XX
PS   Example 2; Col 17; 28pp; English.
XX
CC   The present sequence is an oligonucleotide which was used for in solution
CC   hybridisation to quantitate hepatitis C virus (HCV) RNA following
CC   ribozyme expression. Ribozymes were identified that can specifically
CC   cleave HCV RNA in a HCV 5' non-coding sequence, the capsid sequence, the
CC   NS-5 sequence or any other conserved region of the hepatitis C RNA.
CC   Ribozymes may be introduced into a cell infected with HCV in order to
CC   inhibit HCV RNA replication or expression. Unlike prior art compositions
CC   and methods, compositions comprising these ribozymes effectively reduce
CC   and eradicate HCV from the infected cells and significantly impair the
CC   ability of the virus to replicate, thus preventing further dissemination
CC   of the disease. The composition is inherently specific for HCV and has
CC   negligible toxicity
XX
SQ   Sequence 26 BP; 2 A; 5 C; 12 G; 7 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 26;
  Best Local Similarity   80.8%;  Pred. No. 1.7e+03;
  Matches   21;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        437 CACCAGCCGGCGCCCACAGGCAGCCA 462
              ||||| ||| ||||||||||  | ||
Db         26 CACCAACCGTCGCCCACAGGACGTCA 1


RESULT 1586
AAS01617/c
ID   AAS01617 standard; DNA; 26 BP.
XX
AC   AAS01617;
XX
DT   18-JUL-2001  (first entry)
XX
DE   Human MINT31/CACNA1G region 6 bisulfite GM6 reverse PCR primer.
XX
KW   Human; T-type calcium channel; CACNA1G; cytosine methylation; CpG island;
KW   cellular proliferative disorder; colorectal cancer; age related disease;
KW   apolipoprotein B; APOB; caudal type homeobox transcription factor 2;
KW   CDX2; epidermal growth factor receptor; EGFR; fibrillin-1; FBN1;
KW   G protein-coupled receptor 37; GPR37; heat shock 70kD protein 6; HSP70B';
KW   HSPA6; RasGAP-related protein; IQGAP2; proteinase-activated receptor 2;
KW   PAR2; paired-like homeodomain transcription factor 2; PITX2; klotho; KL;
KW   patched A; patched B; PTCHA; PTCHB; syndecan 1; syndecan 4; SDC1; SDC4;
KW   chromosome 17; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200119845-A1.
XX
PD   22-MAR-2001.
XX
PF   14-SEP-2000; 2000WO-US025479.
XX
PR   15-SEP-1999;   99US-00398522.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI   Issa J;
XX
DR   WPI; 2001-244777/25.
XX
PT   New nucleic acid molecule for use as a marker for screening cancer,
PT   comprises the coding region for a T-type calcium channel and regulatory
PT   sequences associated with the channel.
XX
PS   Claim 21; Page 35; 125pp; English.
XX
CC   The present sequence for bisulfite GM6 reverse PCR primer is used to
CC   study the methylation state of region 6 in human MINT31/T-type calcium
CC   channel CACNA1G which map to chromosome 17. The methylation state of
CC   specific regions within CpG islands associated with the CACNA1G gene
```

```
CC   correlate with several cancerous phenotypes involving various tissue and
CC   cell types. Since aberrant methylation of normally unmethylated CpG
CC   islands is often observed in immortalised and transformed cells, CACNA1G
CC   is implicated in cellular proliferative disorders e.g. leukaemia,
CC   colorectal, lung, breast and other cancers. The nucleic acid coding for
CC   CACNA1G is useful as a marker for screening cancer and age related
CC   diseases. A diagnostic kit containing primers (AAS01574-AAS01623) for
CC   amplification of a CpG-containing nucleic acid, where the primer
CC   hybridises with a target polynucleotide sequence (AAS01627-AAS01676), can
CC   be used for detecting aberrant methylation. The CpG island sequences
CC   (AAS01677-AAS01692) are selected from genes encoding CACNA1G,
CC   apolipoprotein B (APOB), caudal type homeobox transcription factor 2
CC   (CDX2), epidermal growth factor receptor (EGFR), fibrillin-1 (FBN1), G
CC   protein-coupled receptor 37 (GPR37), heat shock 70kD protein 6 (HSP70B';
CC   HSPA6), RasGAP-related protein (IQGAP2), klotho (KL), proteinase-
CC   activated receptor 2 (PAR2), paired-like homeodomain transcription factor
CC   2 (PITX2), patched A and B (PTCHA; PTCHB) and syndecan 1 and 4 (SDC1;
CC   SDC4) or a MINT31 sequence
XX
SQ   Sequence 26 BP; 18 A; 3 C; 0 G; 4 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 26;
  Best Local Similarity   90.0%;  Pred. No. 1.7e+03;
  Matches   18;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||: |
Db         20 TTTTTTTTTTTTTTTTTYGT 1


RESULT 1587
AAS01577/c
ID   AAS01577 standard; DNA; 26 BP.
XX
AC   AAS01577;
XX
DT   18-JUL-2001  (first entry)
XX
DE   Human T-type calcium channel CACNA1G R6 3'-bisulfite PCR primer.
XX
KW   Human; T-type calcium channel; CACNA1G; cytosine methylation; CpG island;
KW   cellular proliferative disorder; colorectal cancer; age related disease;
KW   apolipoprotein B; APOB; caudal type homeobox transcription factor 2;
KW   CDX2; epidermal growth factor receptor; EGFR; fibrillin-1; FBN1;
KW   G protein-coupled receptor 37; GPR37; heat shock 70kD protein 6; HSP70B';
KW   HSPA6; RasGAP-related protein; IQGAP2; proteinase-activated receptor 2;
KW   PAR2; paired-like homeodomain transcription factor 2; PITX2; klotho; KL;
KW   patched A; patched B; PTCHA; PTCHB; syndecan 1; syndecan 4; SDC1; SDC4;
KW   chromosome 17; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200119845-A1.
XX
PD   22-MAR-2001.
XX
PF   14-SEP-2000; 2000WO-US025479.
XX
PR   15-SEP-1999;   99US-00398522.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI   Issa J;
XX
DR   WPI; 2001-244777/25.
XX
PT   New nucleic acid molecule for use as a marker for screening cancer,
PT   comprises the coding region for a T-type calcium channel and regulatory
PT   sequences associated with the channel.
XX
PS   Claim 21; Page 34; 125pp; English.
XX
CC   The present sequence for 3'-bisulfite PCR primer is used to study the
CC   methylation state of region R6 in a novel human T-type calcium channel
CC   CACNA1G which maps to chromosome 17. The methylation state of specific
CC   regions within CpG islands associated with the CACNA1G gene correlate
CC   with several cancerous phenotypes involving various tissue and cell
CC   types. Since aberrant methylation of normally unmethylated CpG islands is
CC   often observed in immortalised and transformed cells, CACNA1G is
CC   implicated in cellular proliferative disorders e.g. leukaemia,
CC   colorectal, lung, breast and other cancers. The nucleic acid coding for
CC   CACNA1G is useful as a marker for screening cancer and age related
CC   diseases. A diagnostic kit containing primers (AAS01574-AAS01623) for
CC   amplification of a CpG-containing nucleic acid, where the primer
CC   hybridises with a target polynucleotide sequence (AAS01627-AAS01676), can
CC   be used for detecting aberrant methylation. The CpG island sequences
CC   (AAS01677-AAS01692) are selected from genes encoding CACNA1G,
CC   apolipoprotein B (APOB), caudal type homeobox transcription factor 2
CC   (CDX2), epidermal growth factor receptor (EGFR), fibrillin-1 (FBN1), G
CC   protein-coupled receptor 37 (GPR37), heat shock 70kD protein 6 (HSP70B';
CC   HSPA6), RasGAP-related protein (IQGAP2), klotho (KL), proteinase-
CC   activated receptor 2 (PAR2), paired-like homeodomain transcription factor
CC   2 (PITX2), patched A and B (PTCHA; PTCHB) and syndecan 1 and 4 (SDC1;
CC   SDC4) or a MINT31 sequence
XX
SQ   Sequence 26 BP; 18 A; 3 C; 0 G; 4 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 26;
  Best Local Similarity   90.0%;  Pred. No. 1.7e+03;
  Matches   18;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||: |
Db         20 TTTTTTTTTTTTTTTTTYGT 1


RESULT 1588
AAS01670
ID   AAS01670 standard; DNA; 26 BP.
XX
AC   AAS01670;
XX
DT   18-JUL-2001  (first entry)
XX
DE   Human MINT31/CACNA1G region 6 reverse target sequence for bisulfite PCR.
XX
KW   Human; T-type calcium channel; CACNA1G; cytosine methylation; CpG island;
KW   cellular proliferative disorder; colorectal cancer; age related disease;
KW   apolipoprotein B; APOB; caudal type homeobox transcription factor 2;
KW   CDX2; epidermal growth factor receptor; EGFR; fibrillin-1; FBN1;
KW   G protein-coupled receptor 37; GPR37; heat shock 70kD protein 6; HSP70B';
KW   HSPA6; RasGAP-related protein; IQGAP2; proteinase-activated receptor 2;
KW   PAR2; paired-like homeodomain transcription factor 2; PITX2; klotho; KL;
KW   patched A; patched B; PTCHA; PTCHB; syndecan 1; syndecan 4; SDC1; SDC4;
KW   chromosome 17; ds.
XX
OS   Homo sapiens.
XX
PN   WO200119845-A1.
XX
PD   22-MAR-2001.
XX
PF   14-SEP-2000; 2000WO-US025479.
XX
PR   15-SEP-1999;   99US-00398522.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI   Issa J;
XX
DR   WPI; 2001-244777/25.
XX
PT   New nucleic acid molecule for use as a marker for screening cancer,
PT   comprises the coding region for a T-type calcium channel and regulatory
PT   sequences associated with the channel.
XX
```

```
PS   Claim 20; Page 36; 125pp; English.
XX
CC   The present sequence for human MINT31/T-type calcium channel CACNA1G
CC   region 6 reverse target sequence is used to study the methylation state
CC   of region 6 in MINT31/CACNA1G which map to chromosome 17. The methylation
CC   state of specific regions within CpG islands associated with the CACNA1G
CC   gene correlate with several cancerous phenotypes involving various tissue
CC   and cell types. Since aberrant methylation of normally unmethylated CpG
CC   islands is often observed in immortalised and transformed cells, CACNA1G
CC   is implicated in cellular proliferative disorders e.g. leukaemia,
CC   colorectal, lung, breast and other cancers. The nucleic acid coding for
CC   CACNA1G is useful as a marker for screening cancer and age related
CC   diseases. A diagnostic kit containing primers (AAS01574-AAS01623) for
CC   amplification of a CpG-containing nucleic acid, where the primer
CC   hybridises with a target polynucleotide sequence (AAS01627-AAS01676), can
CC   be used for detecting aberrant methylation. The CpG island sequences
CC   (AAS01677-AAS01692) are selected from genes encoding CACNA1G,
CC   apolipoprotein B (APOB), caudal type homeobox transcription factor 2
CC   (CDX2), epidermal growth factor receptor (EGFR), fibrillin-1 (FBN1), G
CC   protein-coupled receptor 37 (GPR37), heat shock 70kD protein 6 (HSP70B';
CC   HSPA6), RasGAP-related protein (IQGAP2), klotho (KL), proteinase-
CC   activated receptor 2 (PAR2), paired-like homeodomain transcription factor
CC   2 (PITX2), patched A and B (PTCHA; PTCHB) and syndecan 1 and 4 (SDC1;
CC   SDC4) or a MINT31 sequence
XX
SQ   Sequence 26 BP; 4 A; 0 C; 3 G; 18 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 26;
  Best Local Similarity   90.0%;  Pred. No. 1.7e+03;
  Matches   18;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||: |
Db          7 TTTTTTTTTTTTTTTTTYGT 26


RESULT 1589
ABK66615
ID   ABK66615 standard; DNA; 26 BP.
XX
AC   ABK66615;
XX
DT   02-JUL-2002  (first entry)
XX
DE   Human gene specific PCR primer #703.
XX
KW   Primer; ss; DNA microarray; differential expression analysis; human.
XX
OS   Homo sapiens.
XX
PN   US6352829-B1.
XX
PD   05-MAR-2002.
XX
PF   05-JAN-1999;   99US-00225928.
XX
PR   21-MAY-1997;   97US-00859998.
XX
PA   (CLON-) CLONTECH LAB INC.
XX
PI   Chenchik A,  Jokhadze G,  Bibilashvilli R;
XX
DR   WPI; 2002-314699/35.
XX
PT   Producing sub-population of labeled nucleic acids, useful for analyzing
PT   differences in RNA profiles between several different physiological
PT   sources, using set of distinct gene specific primers.
XX
PS   Example 3; SEQ ID NO 703; 11pp; English.
XX
CC   The invention relates to producing a sub-population of labeled nucleic
CC   acids (NAs) comprising contacting a NA sample from a physiological
CC   source, with a pool of 50 distinct gene specific primers under suitable
CC   conditions to enzymatically generate sub-population of NAs, where each
CC   gene specific primer has a sequence complementary to a distinct mRNA, and
CC   each labeled NA is generated using a single gene specific primer. The
CC   method is useful for producing a sub-population of labeled NAs which is
CC   useful for analysing the differences in the RNA profiles between several
CC   different physiological sources, where the method comprises producing
CC   subpopulation of labeled NAs for the different physiological sources,
CC   comprising the populations for each physiological source to identify
CC   differences in the population, where the comparison is preferably
CC   performed by hybridising the labeled NAs for each of the distinct
CC   physiological sources to an array of probe NAs stably associated with the
CC   surface of a substrate to produce a hybridisation pattern for each of the
CC   sources, and comparing the patterns for each of the sources, where
CC   differential gene expression assays are utilised in differential
CC   expression analysis of diseased a normal tissue e.g. neoplastic a normal
CC   tissue, or different tissue or subtissue types. The present sequence is a
CC   human gene specific PCR primer used in the method of the invention. Note:
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from USPTO
CC   at http.wipo.seqdata.uspto.gov/sequence.html?DocID=6352829B1
XX
SQ   Sequence 26 BP; 5 A; 8 C; 7 G; 6 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 26;
  Best Local Similarity   80.8%;  Pred. No. 1.7e+03;
  Matches   21;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1093 AGCTGTTCATTTGGCTAGGGACTTTG 1118
              |||||| ||  | || ||||||||||
Db          1 AGCTGTCCACCTAGCCAGGGACTTTG 26


RESULT 1590
AAD33509
ID   AAD33509 standard; DNA; 26 BP.
XX
AC   AAD33509;
XX
DT   01-JUL-2002  (first entry)
XX
DE   T7T18Apad_PS10-26-0001 probe for calibration of molecular array data.
XX
KW   Molecular array; probe; ss.
XX
OS   Unidentified.
XX
PN   EP1186673-A2.
XX
PD   13-MAR-2002.
XX
PF   10-SEP-2001; 2001EP-00307665.
XX
PR   11-SEP-2000; 2000US-00659173.
XX
PA   (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI   Wobler PK,  Delenstarr GC;
XX
DR   WPI; 2002-282886/33.
XX
PT   Calibration of molecular array data by employing calibration probes that
PT   generate signals proportional to total concentrations of labeled target
PT   molecules, and molecular arrays incorporating sets of calibration probes.
XX
PS   Disclosure; Page 14; 32pp; English.
XX
CC   The invention relates to a method for calibrating data scanned from a
CC   molecular array. The method involves employing calibration probes that
CC   generate signals proportional to the total concentrations of labelled
CC   target molecules to which the molecular array probes are directed over an
CC   entire range of sample solutions and molecular arrays incorporating sets
CC   of calibration probes. Method is useful for calibrating different types
CC   of signals scanned from a molecular array, or calibrating signals scanned
```

```
CC   from different molecular arrays. The present sequence is poly (A)
CC   normalisation probe used in calibration of molecular array data
XX
SQ   Sequence 26 BP; 20 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 1591
AAD33509/c
ID   AAD33509 standard; DNA; 26 BP.
XX
AC   AAD33509;
XX
DT   01-JUL-2002  (first entry)
XX
DE   T7T18Apad_PS10-26-0001 probe for calibration of molecular array data.
XX
KW   Molecular array; probe; ss.
XX
OS   Unidentified.
XX
PN   EP1186673-A2.
XX
PD   13-MAR-2002.
XX
PF   10-SEP-2001; 2001EP-00307665.
XX
PR   11-SEP-2000; 2000US-00659173.
XX
PA   (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI   Wobler PK,  Delenstarr GC;
XX
DR   WPI; 2002-282886/33.
XX
PT   Calibration of molecular array data by employing calibration probes that
PT   generate signals proportional to total concentrations of labeled target
PT   molecules, and molecular arrays incorporating sets of calibration probes.
XX
PS   Disclosure; Page 14; 32pp; English.
XX
CC   The invention relates to a method for calibrating data scanned from a
CC   molecular array. The method involves employing calibration probes that
CC   generate signals proportional to the total concentrations of labelled
CC   target molecules to which the molecular array probes are directed over an
CC   entire range of sample solutions and molecular arrays incorporating sets
CC   of calibration probes. Method is useful for calibrating different types
CC   of signals scanned from a molecular array, or calibrating signals scanned
CC   from different molecular arrays. The present sequence is poly (A)
CC   normalisation probe used in calibration of molecular array data
XX
SQ   Sequence 26 BP; 20 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db         18 TTTTTTTTTTTTTTTTTT 1


RESULT 1592
AAX15434/c
ID   AAX15434 standard; DNA; 27 BP.
XX
AC   AAX15434;
XX
DT   07-MAY-1999  (first entry)
XX
DE   PCR primer used to amplify DNA encoding trehalose phosphorylase.
XX
KW   Trehalose phosphorylase; trehalose; D-glucose;
KW   alpha-D-glucose-1-phosphate; PCR primer; ss.
XX
OS   Synthetic.
OS   Grifola frondosa.
XX
PN   WO9844116-A1.
XX
PD   08-OCT-1998.
XX
PF   30-MAR-1998;   98WO-JP001423.
XX
PR   31-MAR-1997;   97JP-00098173.
XX
PA   (KURE ) KUREHA CHEM IND CO LTD.
XX
PI   Horinouchi S,  Saitoh K,  Takahashi E;
XX
DR   WPI; 1998-557113/47.
XX
PT   Trehalose phosphorylase from Grifola frondosa and gene encoding it - for
PT   producing enzyme for industrial scale production of trehalose.
XX
PS   Example 5; Page 25; 52pp; Japanese.
XX
CC   The present PCR primer was used to amplify DNA encoding a trehalose
CC   phosphorylase enzyme, and is derived from Grifola frondosa. Vectors and
CC   cells containing the nucleic acid sequence can be used in the large scale
CC   production of trehalose phosphorylase for industrial-scale manufacture of
CC   trehalose from D-glucose and alpha-D-glucose-1-phosphate. Trehalose is
CC   used in the foodstuff and drug industries
XX
SQ   Sequence 27 BP; 1 A; 3 C; 4 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAAA 10


RESULT 1593
AAT94842/c
ID   AAT94842 standard; DNA; 27 BP.
XX
AC   AAT94842;
XX
DT   27-MAR-1998  (first entry)
XX
DE   Human ESF I 3' PCR primer.
XX
KW   Endometrial specific steroid-binding factor I; ESF I; human;
KW   inflammation; asthma; rhinitis; cystic fibrosis; airway disease;
KW   neoplasia; atopy; therapy; diagnosis; primer; PCR; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9734997-A1.
XX
PD   25-SEP-1997.
XX
PF   21-MAR-1996;   96WO-US003857.
XX
PR   21-MAR-1996;   96WO-US003857.
```

XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ni J, Yu G, Gentz RL;
XX
DR WPI; 1997-480206/44.
XX
PT Human endometrial specific steroid-binding factor I, II and III - used to
PT treat inflammation, asthma, rhinitis, cystic fibrosis, airway disease,
PT neoplasia, atopy etc.
XX
PS Example 2; Page 52-53; 92pp; English.
XX
CC This oligonucleotide contains an Asp718 site followed by 18 nucleotides
CC complementary to a polyA tail. It was used with a 5' primer (see
CC AAT94839), containing a BamHI site and 20 bases of the human endometrial
CC specific steroid binding factor I (ESF I) coding sequence (see AAT94830),
CC to amplify ESF I cDNA deposited as ATCC 97401. The PCR product was
CC incorporated into baculovirus vector pRG1 and recombinant ESF I was
CC expressed in Spodoptera frugiperda Sf9 cells. Human ESF I (see AAW35802)
CC can be used to treat inflammation, asthma, rhinitis, cystic fibrosis,
CC airway disease, neoplasia, atopy etc
XX
SQ Sequence 27 BP; 1 A; 5 C; 2 G; 19 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2803
||||||||||||||||||
Db 27 AAAAAAAAAAAAAAAAAA 10

RESULT 1594
AAA59740/c
ID AAA59740 standard; DNA; 27 BP.
XX
AC AAA59740;
XX
DT 06-OCT-2000 (first entry)
XX
DE PCR primer for hESF I cDNA sequence amplification.
XX
KW Endometrial specific steroid-binding factor; human; hESF; inflammation;
KW asthma; rhinitis; cystic fibrosis; air way disease; neoplasia; atopy;
KW eicosanoid level regulator; chemotaxis inhibitor; endometrial cancer;
KW PCR primer; ss.
XX
OS Homo sapiens.
XX
PN US6066724-A.
XX
PD 23-MAY-2000.
XX
PF 21-MAR-1997; 97US-00821451.
XX
PR 21-MAR-1996; 96US-0014724P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Yu G, Gentz R, Ni J;
XX
DR WPI; 2000-375600/32.
XX
PT Novel gene encoding human endometrial specific steroid-binding factor I,
PT II and III which is useful for treating asthma, rhinitis, cystic
PT fibrosis, airway disease and neoplasia.
XX
PS Example 2; Col 34; 36pp; English.
XX
CC This invention relates to nucleic acid molecules encoding portions of the
CC human endometrial specific steroid-binding factors I, II, and III. Also
CC included in the invention are hESF I, II, and III polypeptide sequences.
CC The nucleotide sequence exhibit antiasthmatic, antiinflammatory,
CC antiallergic, and cytostatic properties. The polynucleotides are used in
CC gene therapy to express hESF I, II and III polypeptides in vivo to treat
CC and/or prevent inflammation, asthma, rhinitis, cystic fibrosis, air way
CC disease, neoplasia and atopy. The polynucleotides are also used to
CC inhibit phospholipase A2 activity, bind polychlorinated biphenyls, reduce
CC foreign protein antigenicity, inhibit monocyte and neutrophil chemotaxis
CC and phagocytosis, inhibit platelet aggregation, regulate eicosanoid
CC levels in the human uterus and control the growth of endometrial cells.
CC The polynucleotides are also useful for detecting complementary
CC polynucleotides as a diagnostic reagent. The hESF I, II and III
CC polynucleotides are used to detect complementary polynucleotides such as
CC a diagnostic reagent. Detection of a mutated form of hESF I, II and III
CC associated with a dysfunction will provide a diagnostic tool that can
CC define diagnosis of a disease or susceptibility to a disease which
CC results from under-expression, over-expression or altered expression of
CC hESF I, II and III e.g. a susceptibility to inherited asthma and
CC endometrial cancer. They are also useful for chromosome identification.
CC The present sequence represents a PCR primer used to amplify the hESF I
CC cDNA sequence
XX
SQ Sequence 27 BP; 1 A; 5 C; 2 G; 19 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2803
||||||||||||||||||
Db 27 AAAAAAAAAAAAAAAAAA 10

RESULT 1595
AAF25224/c
ID AAF25224 standard; DNA; 27 BP.
XX
AC AAF25224;
XX
DT 30-APR-2001 (first entry)
XX
DE 3' primer for an endometrial specific steroid binding factor I cDNA.
XX
KW Human; endometrial specific steroid binding factor; hESF; hESFI; hESFII;
KW hESFIII; inflammation; asthma; rhinitis; cystic fibrosis; airway disease;
KW neoplasia; atopy; phospholipase A2; polychlorinated biphenyl; chemotaxis;
KW phagocytosis; platelet aggregation; eicosanoid; endometrial cell;
KW PCR primer; ss.
XX
OS Homo sapiens.
XX
PN US6174992-B1.
XX
PD 16-JAN-2001.
XX
PF 08-MAR-1999; 99US-00263810.
XX
PR 21-MAR-1996; 96US-0014724P.
PR 21-MAR-1997; 97US-00821451.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ni J, Yu G, Gentz R;
XX
DR WPI; 2001-158477/16.
XX
PT New human endometrial specific steroid binding factors, useful for
PT treating and preventing inflammation, asthma, rhinitis, cystic fibrosis,
PT airway disease, neoplasia and atopy.
XX
PS Example 2; Col 33; 36pp; English.
XX
CC PCR primers AAF25221 and AAF25224 were used to amplify cDNA encoding a

```
CC   human endometrial specific steroid binding factor (hESF). The
CC   specification describes hESFI, hESFII, and hESFIII. hESFI, II and III
CC   polypeptides, and polynucleotides encoding them are useful for treating
CC   and preventing inflammation, asthma, rhinitis, cystic fibrosis, airway
CC   disease, neoplasia and atopy, inhibiting phospholipase A2 activity,
CC   binding polychlorinated biphenyls, reducing foreign protein antigenicity,
CC   inhibiting monocyte and neutrophil chemotaxis and phagocytosis,
CC   inhibiting platelet aggregation, regulating eicosanoid levels in the
CC   human uterus, and for controlling the growth of endometrial cells. hESF
CC   polypeptides and nucleotides are also useful for research, biological,
CC   clinical or therapeutic purposes
XX
SQ   Sequence 27 BP; 1 A; 5 C; 2 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAAA 10


RESULT 1596
ABL41793/c
ID   ABL41793 standard; DNA; 27 BP.
XX
AC   ABL41793;
XX
DT   29-MAY-2002  (first entry)
XX
DE   Primer for human endometrial specific steroid-binding factor I cDNA.
XX
KW   Human; endometrial specific steroid-binding factor; ESF;
KW   prostatic steroid-binding protein; hESF I; hESF II; hESF III; asthma;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   US6338948-B1.
XX
PD   15-JAN-2002.
XX
PF   30-MAY-2000; 2000US-00583169.
XX
PR   21-MAR-1996;   96US-0014724P.
PR   21-MAR-1997;   97US-00821451.
PR   08-MAR-1999;   99US-00263810.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ni J,  Yu G,  Gentz R;
XX
DR   WPI; 2002-215019/27.
XX
PT   New antibody specific for human endometrial specific steroid-binding
PT   factor (hESF) III, useful for detecting hESF III protein in biological
PT   sample and to isolate or identify clones expressing the protein.
XX
PS   Example 2; Col 33; 36pp; English.
XX
CC   PCR primers ABL41790 and ABL41793 were used to amplify cDNA encoding
CC   human endometrial specific steroid-binding factor (hESF) I. The primers
CC   were used to introduce restriction sites for cloning. The full length
CC   hESF I protein has a molecular weight of 9.8 kDa. The protein has
CC   homology to rat prostatic steroid-binding protein. Antibodies which bind
CC   hESF proteins, such as hESF I, hESF II, and hESF III are useful for
CC   isolating or to identify clones expressing the polypeptides or to purify
CC   the polypeptides by affinity chromatography. Agonists and antagonists of
CC   hESF proteins are useful for treating and/or preventing susceptibility to
CC   asthma
XX
SQ   Sequence 27 BP; 1 A; 5 C; 2 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAAA 10


RESULT 1597
ABX14927/c
ID   ABX14927 standard; DNA; 27 BP.
XX
AC   ABX14927;
XX
DT   08-APR-2003  (first entry)
XX
DE   hESF I amplifying 3' PCR primer for expression using baculovirus.
XX
KW   Human; PCR; ss; endometrial specific steroid-binding factor; hESF;
KW   Clara cell 10 kDa; CC10; secretory protein; asthma; primer;
KW   prostatic steroid-binding protein; hormone; lung; uterus; gene therapy.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   US2002151012-A1.
XX
PD   17-OCT-2002.
XX
PF   06-NOV-2001; 2001US-00985911.
XX
PR   21-MAR-1996;   96US-0014724P.
PR   21-MAR-1997;   97US-00821451.
PR   08-MAR-1999;   99US-00263810.
PR   30-MAY-2000; 2000US-00583169.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ni J,  Yu G,  Gentz R;
XX
DR   WPI; 2003-182506/18.
XX
PT   New human endometrial specific steroid-binding factor (hESF) proteins and
PT   genes, useful for treating or diagnosing a disease or susceptibility to a
PT   disease, particularly asthma.
XX
PS   Example 2; Page 18; 37pp; English.
XX
CC   The invention discloses isolated polypeptides, which comprise human
CC   endometrial specific steroid-binding factors I, II and III (hESF I, II
CC   and III), and the nucleic acids encoding them. The hESF polypeptide has
CC   homologies to mammalian Clara cell 10 kDa (CC10) secretory protein and
CC   rat prostatic steroid-binding protein which are factors which modulate or
CC   mediate the action of hormones involved in the regulation of functions of
CC   the lung and uterus. The nucleic acids and polypeptides can be used to
CC   identify compounds that bind to and inhibit activation, raise antibodies
CC   or develop antagonists against the isolated hESF polypeptide. The
CC   polypeptides or polynucleotides are useful for treating a patient having
CC   a need of hESF I, hESF II, hESF III or for treating a patient having a
CC   need to inhibit hESF. The polypeptide is administered by providing to the
CC   patient the DNA encoding the hESF polypeptide in vivo (gene therapy). In
CC   particular, the disease is asthma. The hESF polypeptides or
CC   polynucleotides are also useful for diagnosing a disease or a
CC   susceptibility to the disease. The sequence presented is the 3' PCR
CC   primer which was used to amplify hESF I cDNA for expression using
CC   baculovirus expression system T
XX
SQ   Sequence 27 BP; 1 A; 5 C; 2 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 27;
```

```
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAAA 10


RESULT 1598
AAL47309/c
ID   AAL47309 standard; DNA; 27 BP.
XX
AC   AAL47309;
XX
DT   30-AUG-2002  (first entry)
XX
DE   Intracellular target molecule property modulation method oligo #1.
XX
KW   Intracellular target; cellular component; property modulation;
KW   antimicrobial; immunomodulatory; nootropic; neuroprotective; metabolic;
KW   neuroleptic; cytostatic; cardiant; infection; ds; immunological disorder;
KW   neurological disorder; metabolic disorder; psychiatric disorder;
KW   myopathy; cancer; cardiovascular disorder.
XX
OS   Synthetic.
XX
PN   EP1205191-A1.
XX
PD   15-MAY-2002.
XX
PF   13-NOV-2000; 2000EP-00403156.
XX
PR   13-NOV-2000; 2000EP-00403156.
XX
PA   (CNRS ) CENT NAT RECH SCI.
PA   (MASS-) MASSACHUSETTS GEN HOSPITAL.
PA   (MOLE-) MOLECULAR SCI INST.
XX
PI   Colas P,  Brent R,  Cohen BA;
XX
DR   WPI; 2002-418829/45.
XX
PT   Process for specifically modulating the properties of an intracellular
PT   target molecule used for the treatment of various disorders.
XX
PS   Example 4; Page 16; 33pp; English.
XX
CC   The present invention relates to a process for specifically modulating
CC   the properties of an intracellular target molecule T, and/or of a
CC   cellular component C which interacts directly or indirectly in a cell
CC   with the target. The process involves the introduction into the cell of a
CC   chimeric molecule known as a targeted effector, comprising a recognition
CC   moiety capable of recognising T and an effector moiety. The chimeric
CC   protein or nucleic acid can be used in the preparation of a medicament
CC   for the treatment of microbial infections, immunological disorders,
CC   neurological disorders, metabolic disorders, psychiatric disorders,
CC   myopathies, genetic disorders, cancer, cardiovascular disorders and
CC   dental disorders. The present sequence is an oligonucleotide used in the
CC   construction of a fusion protein in the exemplification of the invention
XX
SQ   Sequence 27 BP; 19 A; 1 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 27;
  Best Local Similarity   80.8%;  Pred. No. 1.9e+03;
  Matches   21;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTTTTAACT 2190
              |||||| |||||||| || || || |
Db         26 CTTTTTCTTTTTTTTCTTCTTCAATT 1


RESULT 1599
AAX23568/c
ID   AAX23568 standard; DNA; 27 BP.
XX
AC   AAX23568;
XX
DT   18-JUN-1999  (first entry)
XX
DE   Deletion sequence oligonucleotide 21.
XX
KW   Deletion sequence oligonucleotide; sensor array; eukaryotic pathogen;
KW   probe; cellular adhesion modulator; cellular proliferation modulator;
KW   human retrovirus; human immunodeficiency virus; non-human retrovirus;
KW   HIV; primer; ss.
XX
OS   Synthetic.
XX
PN   WO9911820-A1.
XX
PD   11-MAR-1999.
XX
PF   01-SEP-1998;   98WO-US018084.
XX
PR   02-SEP-1997;   97US-00923771.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Chen D,  Srivatsa GS;
XX
DR   WPI; 1999-205198/17.
XX
PT   New compositions comprising sensor arrays made up of unique probe
PT   oligonucleotides - useful for characterizing a sample of target deletion
PT   oligonucleotides.
XX
PS   Example 1; Page 96; 163pp; English.
XX
CC   This invention describes a novel composition comprising a number of
CC   sensor arrays, where each array comprises a unique probe oligonucleotide,
CC   which is the reverse complement of part of a unique target
CC   oligonucleotide present in a mixture of target deletion sequence
CC   oligonucleotides. The compositions form a method for characterizing a
CC   sample of target deletion oligonucleotides which are labelled and
CC   hybridize with the probe oligonucleotides of the sensor arrays. Such
CC   oligonucleotides and their targets are represented in AAX23548-X23709.
CC   Oligonucleotides characterized by the method form pharmaceutical
CC   compositions that are useful for modulating cellular adhesion or
CC   proliferation, and being active against a eukaryotic pathogen, a human
CC   retrovirus, a human immunodeficiency virus (HIV), or a non-human
CC   retrovirus, including influenza virus, Epstein-Barr virus, Respiratory
CC   Syncytial Virus or cytomegalovirus (CMV). The compositions enable
CC   characterization of deletion sequence oligonucleotides having related,
CC   but different nucleobase sequences, and quantification of different
CC   species of deletion sequence ("target") oligonucleotides in a mixture.
CC   Also, if the specificity of the oligonucleotide's nucleobase sequence for
CC   its reverse complement is not modified, the method may be performed using
CC   oligodeoxynucleotides
XX
SQ   Sequence 27 BP; 7 A; 2 C; 3 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAA 2800
              ||||||||||||||||||
Db         18 TTGAAAAAAAAAAAAAAA 1


RESULT 1600
AAX23572/c
ID   AAX23572 standard; DNA; 27 BP.
XX
AC   AAX23572;
XX
```

```
DT   18-JUN-1999  (first entry)
XX
DE   Deletion sequence oligonucleotide 25.
XX
KW   Deletion sequence oligonucleotide; sensor array; eukaryotic pathogen;
KW   probe; cellular adhesion modulator; cellular proliferation modulator;
KW   human retrovirus; human immunodeficiency virus; non-human retrovirus;
KW   HIV; primer; ss.
XX
OS   Synthetic.
XX
PN   WO9911820-A1.
XX
PD   11-MAR-1999.
XX
PF   01-SEP-1998;   98WO-US018084.
XX
PR   02-SEP-1997;   97US-00923771.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Chen D,  Srivatsa GS;
XX
DR   WPI; 1999-205198/17.
XX
PT   New compositions comprising sensor arrays made up of unique probe
PT   oligonucleotides - useful for characterizing a sample of target deletion
PT   oligonucleotides.
XX
PS   Example 1; Page 98; 163pp; English.
XX
CC   This invention describes a novel composition comprising a number of
CC   sensor arrays, where each array comprises a unique probe oligonucleotide,
CC   which is the reverse complement of part of a unique target
CC   oligonucleotide present in a mixture of target deletion sequence
CC   oligonucleotides. The compositions form a method for characterizing a
CC   sample of target deletion oligonucleotides which are labelled and
CC   hybridize with the probe oligonucleotides of the sensor arrays. Such
CC   oligonucleotides and their targets are represented in AAX23548-X23709.
CC   Oligonucleotides characterized by the method form pharmaceutical
CC   compositions that are useful for modulating cellular adhesion or
CC   proliferation, and being active against a eukaryotic pathogen, a human
CC   retrovirus, a human immunodeficiency virus (HIV), or a non-human
CC   retrovirus, including influenza virus, Epstein-Barr virus, Respiratory
CC   Syncytial Virus or cytomegalovirus (CMV). The compositions enable
CC   characterization of deletion sequence oligonucleotides having related,
CC   but different nucleobase sequences, and quantification of different
CC   species of deletion sequence ("target") oligonucleotides in a mixture.
CC   Also, if the specificity of the oligonucleotide's nucleobase sequence for
CC   its reverse complement is not modified, the method may be performed using
CC   oligodeoxynucleotides
XX
SQ   Sequence 27 BP; 7 A; 2 C; 3 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 27;
  Best Local Similarity   80.8%;  Pred. No. 1.9e+03;
  Matches   21;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2776 GTTAGAATTGAAAAAAAAAAAAAAA 2801
              ||| |  ||  ||||||||||||||
Db         26 GTTTGTCTTCTAAAAAAAAAAAAAAA 1


RESULT 1601
AAD33510
ID   AAD33510 standard; DNA; 27 BP.
XX
AC   AAD33510;
XX
DT   01-JUL-2002  (first entry)
XX
DE   T7T18Apad_PS9-27-0001 probe for calibration of molecular array data.
XX
KW   Molecular array; probe; ss.
XX
OS   Unidentified.
XX
PN   EP1186673-A2.
XX
PD   13-MAR-2002.
XX
PF   10-SEP-2001; 2001EP-00307665.
XX
PR   11-SEP-2000; 2000US-00659173.
XX
PA   (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI   Wobler PK,  Delenstarr GC;
XX
DR   WPI; 2002-282886/33.
XX
PT   Calibration of molecular array data by employing calibration probes that
PT   generate signals proportional to total concentrations of labeled target
PT   molecules, and molecular arrays incorporating sets of calibration probes.
XX
PS   Disclosure; Page 14; 32pp; English.
XX
CC   The invention relates to a method for calibrating data scanned from a
CC   molecular array. The method involves employing calibration probes that
CC   generate signals proportional to the total concentrations of labelled
CC   target molecules to which the molecular array probes are directed over an
CC   entire range of sample solutions and molecular arrays incorporating sets
CC   of calibration probes. Method is useful for calibrating different types
CC   of signals scanned from a molecular array, or calibrating signals scanned
CC   from different molecular arrays. The present sequence is poly (A)
CC   normalisation probe used in calibration of molecular array data
XX
SQ   Sequence 27 BP; 21 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 1602
AAD33510/c
ID   AAD33510 standard; DNA; 27 BP.
XX
AC   AAD33510;
XX
DT   01-JUL-2002  (first entry)
XX
DE   T7T18Apad_PS9-27-0001 probe for calibration of molecular array data.
XX
KW   Molecular array; probe; ss.
XX
OS   Unidentified.
XX
PN   EP1186673-A2.
XX
PD   13-MAR-2002.
XX
PF   10-SEP-2001; 2001EP-00307665.
XX
PR   11-SEP-2000; 2000US-00659173.
XX
PA   (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI   Wobler PK,  Delenstarr GC;
XX
DR   WPI; 2002-282886/33.
XX
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```
PT   Calibration of molecular array data by employing calibration probes that
PT   generate signals proportional to total concentrations of labeled target
PT   molecules, and molecular arrays incorporating sets of calibration probes.
XX
PS   Disclosure; Page 14; 32pp; English.
XX
CC   The invention relates to a method for calibrating data scanned from a
CC   molecular array. The method involves employing calibration probes that
CC   generate signals proportional to the total concentrations of labelled
CC   target molecules to which the molecular array probes are directed over an
CC   entire range of sample solutions and molecular arrays incorporating sets
CC   of calibration probes. Method is useful for calibrating different types
CC   of signals scanned from a molecular array, or calibrating signals scanned
CC   from different molecular arrays. The present sequence is poly (A)
CC   normalisation probe used in calibration of molecular array data
XX
SQ   Sequence 27 BP; 21 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db         18 TTTTTTTTTTTTTTTTTT 1


RESULT 1603
ACC83476/c
ID   ACC83476 standard; DNA; 28 BP.
XX
AC   ACC83476;
XX
DT   08-SEP-2003  (first entry)
XX
DE   Oligo dT primer.
XX
KW   Rat; Czf-1; chondrocyte; zinc finger; osteopathic; antiarthritic;
KW   antirheumatic; PCR; primer; ss.
XX
OS   Synthetic.
XX
PN   WO2003044159-A2.
XX
PD   30-MAY-2003.
XX
PF   20-NOV-2002; 2002WO-IL000925.
XX
PR   20-NOV-2001; 2001US-0331626P.
XX
PA   (PROC-) PROCHON BIOTECH LTD.
XX
PI   Yayon A,  Blumenstein S,  Harari D;
XX
DR   WPI; 2003-457599/43.
XX
PT   New chondrocyte-derived zinc finger polypeptides and encoding
PT   polynucleotides, useful for detecting, diagnosing and treating Czf-1
PT   protein-related diseases, such as osteoarthritis and rheumatoid
PT   arthritis.
XX
PS   Example 1; Page 27; 64pp; English.
XX
CC   The present sequence is that of an oligo-dT primer, which was used in the
CC   PCR amplification of cDNA (see ACC83474) encoding a novel rat zinc finger
CC   protein, designated Czf-1 (see ABR42912). Czf-1 is expressed in
CC   osteoblasts and chondrocytes, and serves as a marker for osteoarthritis.
CC   Czf-1 polynucleotides, polypeptides and antibodies can be used in the
CC   characterisation, diagnosis and treatment of fibroblast growth factor
CC   receptor-related and skeletal diseases and disorders, such as
CC   osteoarthritis, rheumatoid arthritis, and cartilage-related diseases
XX
SQ   Sequence 28 BP; 2 A; 3 C; 3 G; 20 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         28 AAAAAAAAAAAAAAAAAA 11


RESULT 1604
ABZ59816/c
ID   ABZ59816 standard; RNA; 28 BP.
XX
AC   ABZ59816;
XX
DT   01-APR-2003  (first entry)
XX
DE   Potato gene PCR primer DDT18AN.
XX
KW   Potato; plant; mitochondrial carrier protein; elongation factor EF-2;
KW   transferrin binding protein; receptor-like protein kinase; helicase;
KW   non-long terminal repeat retroelement reverse transcriptase;
KW   overwatering; transgenic; reverse transcriptase; PCR; primer; ss.
XX
OS   Synthetic.
XX
PN   DE10114063-A1.
XX
PD   10-OCT-2002.
XX
PF   22-MAR-2001; 2001DE-01014063.
XX
PR   22-MAR-2001; 2001DE-01014063.
XX
PA   (MPBC-) MPB COLOGNE GMBH MOLECULAR PLANT & PROTE.
XX
PI   Buelow L,  Tscharntke M,  Haussuehl K;
XX
DR   WPI; 2003-041808/04.
XX
PT   New DNA sequences from potato, useful for producing plants with altered
PT   properties, e.g. tolerance of flooding, also related proteins, antibodies
PT   and inhibitory sequences.
XX
PS   Example 1; Page 8; 26pp; German.
XX
CC   The invention relates to DNA sequences (I) that encode six specific plant
CC   proteins: (i) a protein (ABP60425) with mitochondrial carrier protein
CC   activity (IIa); (ii) a protein (ABP60426) with transferrin binding
CC   protein activity (IIb); (iii) a protein (ABP60427) with receptor-like
CC   protein kinase activity (IIc); (iv) a protein (ABP60428) with elongation
CC   factor EF-2 activity (IId); (v) a protein (ABP60429) with non-long
CC   terminal repeat retroelement reverse transcriptase activity (IIe); or
CC   (vi) a protein (ABP60430) with helicase activity (IIf). (I), also related
CC   sequences, derived ribozymes and antisense sequences, expression vectors,
CC   encoded proteins and antibodies against the proteins, are used to produce
CC   plants with altered properties, including tolerance of overwatering. The
CC   antibodies are also used for isolation of the proteins and in
CC   immunoassays. Also (I) or their primer or probe fragments are used to
CC   screen for terminators and constitutively, aerobically or anaerobically
CC   inducible plant promoters, specifically for use in potatoes and the
CC   sequence that encodes (IId) is used to alter the translation profile in
CC   plants. Since (I) are derived from potato, their promoters and
CC   terminators provide high level transgene expression in potato, with
CC   improved tissue specificity and inducibility, and can also be used to
CC   control endogenous genes. The present sequence is that of a PCR primer
CC   used in the first strand synthesis of cDNAs derived from Potato
XX
SQ   Sequence 28 BP; 3 A; 2 C; 2 G; 20 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
```

```
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         26 AAAAAAAAAAAAAAAAAA 9


RESULT 1605
ADD35234/c
ID   ADD35234 standard; DNA; 28 BP.
XX
AC   ADD35234;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Mouse mitochondrial DNA sequence SEQ ID NO:3014.
XX
KW   ds; mouse; array; mitochondrial; hybridisation; energy-metabolism;
KW   mitochondrial disease; oxidative phosphorylation dysfunction;
KW   oxidative stress; apoptosis; aging.
XX
OS   Mus musculus.
XX
PN   WO2003020220-A2.
XX
PD   13-MAR-2003.
XX
PF   30-AUG-2002; 2002WO-US027886.
XX
PR   30-AUG-2001; 2001US-0316323P.
PR   31-AUG-2001; 2001CA-02356540.
XX
PA   (UYEM-) UNIV EMORY.
XX
PI   Wallace DC,  Levy S,  Kerstann K,  Procaccio V;
XX
DR   WPI; 2003-300821/29.
XX
PT   Array containing probes for genes involved in mitochondrial biology,
PT   useful for determining mitochondrial biology gene expression profiles for
PT   use in diagnosing pathologies and identifying biochemical pathways.
XX
PS   Claim 2; SEQ ID NO 3014; 201pp; English.
XX
CC   The invention relates to a novel array comprising at least two isolated
CC   nucleotide molecules, each molecule having a sequence capable of uniquely
CC   hybridising to a nucleic acid molecule which is an expression product of
CC   a gene involved in mitochondrial biology. The array comprises two or more
CC   isolated nucleic acid molecules or spots, each molecule having a sequence
CC   chosen from sequence of 994 human probes and 2046 mouse probes. An array
CC   of the invention is useful for determining an expression profile of a
CC   mouse or human sample containing nucleic acid, by contacting the array
CC   with the sample under conditions allowing selective hybridisation, and
CC   measuring hybridisation of nucleic acid in the sample to the array to
CC   produce an expression profile. The array is also useful for determining
CC   an expression profile of a first labelled sample containing nucleic acid
CC   relative to a second, differently labelled sample containing nucleic
CC   acid. The second sample is a reference or a standard. An array is useful
CC   for determining an expression profile diagnostic of an energy-metabolism-
CC   related physiological condition. An array of the invention is useful for
CC   determining mitochondrial biology gene expression profiles of organisms,
CC   such as human, mice and closely related species, tissue and organs of
CC   such organisms, which are useful for determining expression profiles
CC   diagnostic of energy metabolism-related physiological conditions,
CC   diagnosing such physiological conditions, identifying biochemical
CC   pathways, genes, and mutations involved in such physiological conditions,
CC   identifying therapeutic agents useful for preventing and/or treating such
CC   physiological conditions, evaluating and/or monitoring the efficacy of
CC   such therapies, and creating and identifying animal models of human
CC   energy metabolism-related physiological conditions. An array is also
CC   useful for defining expression signatures or profiles for mitochondrial
CC   diseases, as well as distinguishing clinical disorders that result from
CC   oxidative phosphorylation (OXPHOS) dysfunction, oxidative stress,
CC   apoptosis and aging. An array of the invention contains probes of genes
CC   not previously recognised to participate in mitochondrial biology. The
CC   sequences shown in ADD33224-ADD35260 represent murine mitochondrial DNA
CC   clones used to make the probes of the invention. Some sequences are not
CC   present, these are SEQ ID NO's 295, 1174, 1213, 1700, 1728, 1730, 1905,
CC   1906, 2408 and 2643.
XX
SQ   Sequence 28 BP; 0 A; 6 C; 4 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         28 AAAAAAAAAAAAAAAAAA 11


RESULT 1606
AAT70108/c
ID   AAT70108 standard; DNA; 28 BP.
XX
AC   AAT70108;
XX
DT   24-SEP-1997  (first entry)
XX
DE   PolyTV primer 3.
XX
KW   primer; polymerase chain reaction; cDNA library; anchored end; PCSUB;
KW   lock-docking; screening; PCR-based cDNA subtractive cloning; ss.
XX
OS   Synthetic.
XX
PN   WO9640998-A1.
XX
PD   19-DEC-1996.
XX
PF   05-JUN-1996;   96WO-US008582.
XX
PR   07-JUN-1995;   95US-00481687.
XX
PA   (PION-) PIONEER HI-BRED INT INC.
XX
PI   Wang X,  Duvick JP,  Briggs SP;
XX
DR   WPI; 1997-087067/08.
XX
PT   Method for prodn. of cDNA libraries with anchored ends - useful for
PT   subtractive cloning of sequences of interest.
XX
PS   Claim 1; Page 27; 56pp; English.
XX
CC   The invention provides a PCR-based method for generating a full-length
CC   cDNA library with anchored ends. The method uses lock-docking primers
CC   (AAT70106-11), where one primer, poly TV (V = G,C or A) locks over the
CC   polyA tail of eukaryotic mRNA producing first strand synthesis and a
CC   second primer, polyGH (H = A, C or T) locks onto the polyC tail added by
CC   terminal deoxynucleotidyl transferase (TdT). In the final step, AAT70112-
CC   17 (polyAB and polyCD primers; B = G, T or C; D = G, A or T) are used to
CC   amplify the first strand and produce a cDNA library with anchored ends.
CC   cDNA libraries produced may be used to identify new (unique) nucleotide
CC   sequences from PCSUB (PCR-based cDNA subtractive) libraries. The new
CC   method produces discreet sized PCR products which would not necessarily
CC   require further subcloning/screening. The method also produces full-
CC   length cDNA's obtainable from the libraries as opposed to specific cDNA
CC   clones, as produced by previously known methods. Other methods such as
CC   PCR and RACE require a knowledge of the target sequence to be amplified,
CC   by using the PCSUB method no previous knowledge is necessary
XX
SQ   Sequence 28 BP; 1 A; 5 C; 4 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
```

```
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||
Db         28 GAAAAAAAAAAAAAAAA 11


RESULT 1607
AAV61015/c
ID   AAV61015 standard; DNA; 28 BP.
XX
AC   AAV61015;
XX
DT   03-DEC-1998  (first entry)
XX
DE   HS/HIP reverse transcriptase PCR primer #4.
XX
KW   Human; heparan sulfate/heparin interacting protein; HIP; diagnosis;
KW   blood coagulation; antithrombin-3; bleeding; wound; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9838214-A1.
XX
PD   03-SEP-1998.
XX
PF   27-FEB-1998;   98WO-US003788.
XX
PR   28-FEB-1997;   97US-00810609.
XX
PA   (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
PI   Carson DD,  Hoeoek M,  Liu S;
XX
DR   WPI; 1998-495388/42.
XX
PT   Use of heparin sulphate/heparin interacting protein - for modulating
PT   blood coagulation, e.g. for neutralising heparin, treating diseases
PT   involving excessive bleeding or administration to wound sites.
XX
PS   Example 1; Page 78; 148pp; English.
XX
CC   A method has been developed for identifying a heparin (Hp) component that
CC   binds to antithrombin-3 (AT-3). The method comprises:(a) contacting a Hp
CC   sample suspected of containing a Hp component that binds to AT-3 with a
CC   heparan sulphate (HS)/Hp interacting protein (HIP) to allow binding of
CC   the Hp component; and (b) detecting the binding of the Hp component to
CC   the HS/HIP. The present sequence represents a primer for reverse
CC   transcriptase PCR of heparan sulfate/heparin interacting protein
CC   (HS/HIP). Products from the present invention can be used for modulating
CC   blood coagulation. They can be used for neutralising heparin, treating
CC   diseases characterised by excessive bleeding or administration to wound
CC   sites. The HS/HIPs can also be used for the production of antibodies and
CC   in diagnostic applications
XX
SQ   Sequence 28 BP; 0 A; 6 C; 4 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2803
              |||||||||||||||||
Db         28 AAAAAAAAAAAAAAAAA 11


RESULT 1608
AAZ61254/c
ID   AAZ61254 standard; DNA; 28 BP.
XX
AC   AAZ61254;
XX
DT   30-MAY-2000  (first entry)
XX
DE   Oligo dT primer for honey bee venom PX3.101 cDNA.
XX
KW   Protein PX3.101; honey bee; venom; interleukin-8; IL-8; receptor; CXCR1;
KW   CXCR2; cyclooxygenase; lipoxygenase; phospholipase; protease;
KW   inflammatory disease; gene therapy; cancer; autoimmune disease; pain;
KW   chemokine imbalance; rheumatoid arthritis; multiple sclerosis; psoriasis;
KW   systemic lupus erythematosus; Crohn's disease; vasculitis; scleroderma;
KW   metastatic cancer; Alzheimer's disease; wound healing; aging process;
KW   antigen; primer; ss.
XX
OS   Apis mellifera.
XX
PN   GB2341389-A.
XX
PD   15-MAR-2000.
XX
PF   13-SEP-1999;   99GB-00021605.
XX
PR   14-SEP-1998;   98US-0100172P.
XX
PA   (PANP-) PAN PACIFIC PHARM INC.
XX
PI   Chi X,  Lu Y;
XX
DR   WPI; 2000-185368/17.
XX
PT   Isolated nucleic acids encoding the bee venom protein PX3.101 useful for
PT   treating autoimmune and inflammatory disorders such as rheumatoid
PT   arthritis.
XX
PS   Example 3; Page 43; 83pp; English.
XX
CC   The present primer was used for cDNA encoding the protein PX3.101, which
CC   is a honey bee venom isolated Apis mellifera. PX3.101 inhibits the
CC   binding of interleukin-8 (IL-8) to its receptor (e.g. CXCR1 and CXCR2)
CC   and inhibits a variety of enzymes (e.g. cyclooxygenases, lipoxygenases,
CC   phospholipases and proteases) associated with inflammatory diseases. The
CC   nucleic acids may be used for the recombinant production of PX3.101
CC   proteins either in vivo (as part of a gene therapy protocol) or in vitro
CC   (as a fermentation culture). The nucleic acids may also be used as probes
CC   to identify similar sequences in samples. The PX3.101 protein may be used
CC   for the treatment of inflammatory diseases, cancers, autoimmune diseases,
CC   pain and/or diseases associated with chemokine (especially IL-8)
CC   imbalances such as rheumatoid arthritis, multiple sclerosis, psoriasis,
CC   systemic lupus erythematosus (SLE), Crohn's disease, vasculitis,
CC   scleroderma, metastatic cancer and Alzheimer's disease in humans. It is
CC   also disclosed that the proteins may be used to accelerate wound healing,
CC   reduce several aging processes and protect against ultraviolet light. The
CC   proteins may also be used as antigens in the production of antibodies
CC   specific for PX3.101. The antibodies may be used as diagnostic agents to
CC   detect PX3.101 protein in samples and to down regulate PX3.101 activity
XX
SQ   Sequence 28 BP; 0 A; 4 C; 4 G; 20 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2803
              |||||||||||||||||
Db         28 AAAAAAAAAAAAAAAAA 11


RESULT 1609
AAI71210/c
ID   AAI71210 standard; DNA; 28 BP.
XX
AC   AAI71210;
XX
DT   22-JAN-2002  (first entry)
XX
```

DE Single stranded DNA PCR primer SEQ ID NO:5.
XX
KW Single stranded DNA primer; PCR primer; amplification; ss.
XX
OS Synthetic.
XX
PN JP2001204472-A.
XX
PD 31-JUL-2001.
XX
PF 21-JAN-2000; 2000JP-00012535.
XX
PR 21-JAN-2000; 2000JP-00012535.
XX
PA (SUME) SUMITOMO ELECTRIC IND CO.
XX
DR WPI; 2001-609513/70.
XX
PT New polynucleotide for the amplification of a one-side single-stranded
PT DNA and the production of a double-stranded cDNA comprises a single-
PT stranded DNA primer.
XX
PS Disclosure; Page 11; 13pp; Japanese.
XX
CC The present invention describes a single-stranded DNA primer comprising a
CC single-stranded DNA having a dTn sequence, which hybridises with the
CC polyA site of an mRNA at the 3'-terminal, and has a blocking group at the
CC 5'-terminal in which the other part constitutes an adapter double-
CC stranded DNA connected to the double-stranded cDNA. The terminal of the
CC side of the DNA is not connected to the double-stranded cDNA, which
CC consists of a base sequence having full homology to the single-stranded
CC DNA corresponding to the 5'-terminal. A method is also described for the
CC preparation of a double-stranded cDNA in which the above single-stranded
CC DNA primer is hybridised with the polyA site of an mRNA and said single-
CC stranded DNA primer is used as the primer to reverse-transcribe said mRNA
CC and further it is converted to a double-stranded cDNA by a DNA
CC polymerase. The primer is used for the uniform amplification of DNAs. The
CC present sequence represents a PCR primer which is given in the
CC exemplification of the present invention
XX
SQ Sequence 28 BP; 3 A; 3 C; 2 G; 20 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2803
||||||||||||||||||
Db 28 AAAAAAAAAAAAAAAAAA 11

RESULT 1610
AAD33512
ID AAD33512 standard; DNA; 28 BP.
XX
AC AAD33512;
XX
DT 01-JUL-2002 (first entry)
XX
DE T7T18Apad_PS8-28-0001 probe for calibration of molecular array data.
XX
KW Molecular array; probe; ss.
XX
OS Unidentified.
XX
PN EP1186673-A2.
XX
PD 13-MAR-2002.
XX
PF 10-SEP-2001; 2001EP-00307665.
XX
PR 11-SEP-2000; 2000US-00659173.
XX
PA (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI Wobler PK, Delenstarr GC;
XX
DR WPI; 2002-282886/33.
XX
PT Calibration of molecular array data by employing calibration probes that
PT generate signals proportional to total concentrations of labeled target
PT molecules, and molecular arrays incorporating sets of calibration probes.
XX
PS Disclosure; Page 14; 32pp; English.
XX
CC The invention relates to a method for calibrating data scanned from a
CC molecular array. The method involves employing calibration probes that
CC generate signals proportional to the total concentrations of labelled
CC target molecules to which the molecular array probes are directed over an
CC entire range of sample solutions and molecular arrays incorporating sets
CC of calibration probes. Method is useful for calibrating different types
CC of signals scanned from a molecular array, or calibrating signals scanned
CC from different molecular arrays. The present sequence is poly (A)
CC normalisation probe used in calibration of molecular array data
XX .
SQ Sequence 28 BP; 22 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2803
||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 1611
AAA90025/c
ID AAA90025 standard; DNA; 29 BP.
XX
AC AAA90025;
XX
DT 20-DEC-2000 (first entry)
XX
DE PCR primer for fatty acid binding protein (FABP) DNA amplification.
XX
KW Vaccine; Japanese schistosomiasis; fatty acid binding protein; FABP;
KW PCR primer; ss.
XX
OS Unidentified.
XX
PN CN1255548-A.
XX
PD 07-JUN-2000.
XX
PF 27-NOV-1998; 98CN-00122043.
XX
PR 27-NOV-1998; 98CN-00122043.
XX
PA (SHAN-) SHANGHAI DOMESTIC ANIMAL PARASITOSIS INS.
XX
PI Lin J, Wu X, Liu J;
XX
DR WPI; 2000-524988/48.
XX
PT Clone of Japanese schistosome fatty acid-binding protein gene and its
PT expression in Bombyx mori system.
XX
PS Claim 3; Page 1; 12pp; Chinese.
XX
CC The present invention relates to the preparation of a vaccine against
CC Japanese schistosomiasis. The vaccine comprises a gene encoding a fatty
CC acid binding protein (FABP). The FABP is expressed in a Bombyx mori
CC system as a fusion protein of 18kD. The fusion protein has an increased
CC immunogenicity and stronger anti-infective action than the wild-type
CC protein. The present sequence represents a PCR primer used to amplify DNA

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CC   encoding the FABP of the invention
XX
SQ   Sequence 29 BP; 2 A; 4 C; 3 G; 20 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         29 AAAAAAAAAAAAAAAAAA 12


RESULT 1612
AAD33515
ID   AAD33515 standard; DNA; 29 BP.
XX
AC   AAD33515;
XX
DT   01-JUL-2002  (first entry)
XX
DE   T7T18Apad_PS6-29-0001 probe for calibration of molecular array data.
XX
KW   Molecular array; probe; ss.
XX
OS   Unidentified.
XX
PN   EP1186673-A2.
XX
PD   13-MAR-2002.
XX
PF   10-SEP-2001; 2001EP-00307665.
XX
PR   11-SEP-2000; 2000US-00659173.
XX
PA   (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI   Wobler PK,  Delenstarr GC;
XX
DR   WPI; 2002-282886/33.
XX
PT   Calibration of molecular array data by employing calibration probes that
PT   generate signals proportional to total concentrations of labeled target
PT   molecules, and molecular arrays incorporating sets of calibration probes.
XX
PS   Disclosure; Page 14; 32pp; English.
XX
CC   The invention relates to a method for calibrating data scanned from a
CC   molecular array. The method involves employing calibration probes that
CC   generate signals proportional to the total concentrations of labelled
CC   target molecules to which the molecular array probes are directed over an
CC   entire range of sample solutions and molecular arrays incorporating sets
CC   of calibration probes. Method is useful for calibrating different types
CC   of signals scanned from a molecular array, or calibrating signals scanned
CC   from different molecular arrays. The present sequence is poly (A)
CC   normalisation probe used in calibration of molecular array data
XX
SQ   Sequence 29 BP; 23 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 1613
AAI69697/c
ID   AAI69697 standard; DNA; 29 BP.
XX
AC   AAI69697;
XX
DT   10-JAN-2002  (first entry)
XX
DE   Hepatitis E virus HEV-T1 sequence related PCR primer #62.
XX
KW   Hepatitis E virus; HEV-T1; hepatitis infection; PCR primer; ss.
XX
OS   Unidentified.
XX
PN   CN1300771-A.
XX
PD   27-JUN-2001.
XX
PF   23-DEC-1999;   99CN-00125741.
XX
PR   23-DEC-1999;   99CN-00125741.
XX
PA   (CHME-) CHINESE MEDICINE & BIOLOGIC PROD APPRAIS.
XX
PI   Wang Y,  Zhang H,  Li H;
XX
DR   WPI; 2001-550442/62.
XX
PT   Hepatitis E virus gene sequence and its application.
XX
PS   Example 1; Page 15(Disclosure); 34pp; Chinese.
XX
CC   The present invention relates to a novel nucleotide sequence and protein
CC   of a new hepatitis E virus HEV-T1 and the application of the nucleotide
CC   sequence and protein in diagnosing, preventing and treating hepatitis.
CC   The present sequence is a PCR primer described in the exemplification of
CC   the invention
XX
SQ   Sequence 29 BP; 3 A; 3 C; 3 G; 20 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         29 AAAAAAAAAAAAAAAAAA 12


RESULT 1614
AAD33517
ID   AAD33517 standard; DNA; 30 BP.
XX
AC   AAD33517;
XX
DT   01-JUL-2002  (first entry)
XX
DE   T7T18Apad_PS5-30-0001 probe for calibration of molecular array data.
XX
KW   Molecular array; probe; ss.
XX
OS   Unidentified.
XX
PN   EP1186673-A2.
XX
PD   13-MAR-2002.
XX
PF   10-SEP-2001; 2001EP-00307665.
XX
PR   11-SEP-2000; 2000US-00659173.
XX
PA   (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI   Wobler PK,  Delenstarr GC;
XX
DR   WPI; 2002-282886/33.
XX
PT   Calibration of molecular array data by employing calibration probes that
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```
PT   generate signals proportional to total concentrations of labeled target
PT   molecules, and molecular arrays incorporating sets of calibration probes.
XX
PS   Disclosure; Page 14; 32pp; English.
XX
CC   The invention relates to a method for calibrating data scanned from a
CC   molecular array. The method involves employing calibration probes that
CC   generate signals proportional to the total concentrations of labelled
CC   target molecules to which the molecular array probes are directed over an
CC   entire range of sample solutions and molecular arrays incorporating sets
CC   of calibration probes. Method is useful for calibrating different types
CC   of signals scanned from a molecular array, or calibrating signals scanned
CC   from different molecular arrays. The present sequence is poly (A)
CC   normalisation probe used in calibration of molecular array data
XX
SQ   Sequence 30 BP; 24 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 1615
AAV56638/c
ID   AAV56638 standard; DNA; 30 BP.
XX
AC   AAV56638;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAF cDNA primer #9.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease; primer; ss.
XX
OS   Synthetic.
OS   Felis catus.
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP001824.
XX
PR   04-JUN-1996;   96JP-00165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Imamura T,  Maeda H,  Fujiyasu T,  Imagawa Y,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
XX
PT   Novel feline cytokine protein - useful for treating feline auto:immune
PT   diseases, e.g. those caused by feline herpes virus or feline calcivirus.
XX
PS   Example 14; Page 66; 94pp; Japanese.
XX
CC   AAV56637-V56640 are primers used in the amplification of novel feline
CC   cytokine proteins, FLAFp40 and FLAFp35. This protein can be used in the
CC   production of a FLAFp35/FLAFp40 heterodimer which can potentiate the
CC   cytotoxic activity of feline cytotoxic T lymphocyte cells. Such proteins
CC   are used for treatment of feline autoimmune diseases e.g. as caused by
CC   feline herpes virus or feline calcivirus
XX
SQ   Sequence 30 BP; 3 A; 3 C; 3 G; 21 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 1616
AAF74908
ID   AAF74908 standard; DNA; 30 BP.
XX
AC   AAF74908;
XX
DT   23-MAY-2001  (first entry)
XX
DE   CD40L poly-A tract sequence SEQ ID NO:5.
XX
KW   Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW   diagnosis; antiarthritic; antirheumatic; immunosuppressive;
KW   antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200119844-A1.
XX
PD   22-MAR-2001.
XX
PF   13-SEP-2000; 2000WO-US024966.
XX
PR   13-SEP-1999;   99US-0153625P.
XX
PA   (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
PI   Crow MK,  Li Y;
XX
DR   WPI; 2001-244776/25.
XX
PT   New altered CD40L promoter for use in the study, diagnosis and treatment
PT   of a variety of inflammatory disorders and autoimmune diseases, such as
PT   rheumatoid arthritis.
XX
PS   Example 1; Fig 3; 90pp; English.
XX
CC   The present invention describes an isolated, purified nucleic acid, which
CC   is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC   residues 331-455 of the sequence comprising 455 nucleotides given in
CC   AAF74905 where A in the wild type sequence at position 331 (corresponding
CC   to position -125) is replaced with C. (I) has antiarthritic,
CC   antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC   be used in gene therapy. (I) is useful in the study, diagnosis and
CC   treatment of inflammatory and autoimmune diseases, as well as diseases in
CC   which elevated expression of CD40L is a factor, e.g., rheumatoid
CC   arthritis. The present sequence represents a CD40L poly-A tract sequence
CC   which is used in an example from the present invention
XX
SQ   Sequence 30 BP; 24 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 1617
AAD33519
ID   AAD33519 standard; DNA; 31 BP.
XX
AC   AAD33519;
XX
DT   01-JUL-2002  (first entry)
XX
```

```
DE   T7T18Apad_PS4-31-0001 probe for calibration of molecular array data.
XX
KW   Molecular array; probe; ss.
XX
OS   Unidentified.
XX
PN   EP1186673-A2.
XX
PD   13-MAR-2002.
XX
PF   10-SEP-2001; 2001EP-00307665.
XX
PR   11-SEP-2000; 2000US-00659173.
XX
PA   (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI   Wobler PK,  Delenstarr GC;
XX
DR   WPI; 2002-282886/33.
XX
PT   Calibration of molecular array data by employing calibration probes that
PT   generate signals proportional to total concentrations of labeled target
PT   molecules, and molecular arrays incorporating sets of calibration probes.
XX
PS   Disclosure; Page 14; 32pp; English.
XX
CC   The invention relates to a method for calibrating data scanned from a
CC   molecular array. The method involves employing calibration probes that
CC   generate signals proportional to the total concentrations of labelled
CC   target molecules to which the molecular array probes are directed over an
CC   entire range of sample solutions and molecular arrays incorporating sets
CC   of calibration probes. Method is useful for calibrating different types
CC   of signals scanned from a molecular array, or calibrating signals scanned
CC   from different molecular arrays. The present sequence is poly (A)
CC   normalisation probe used in calibration of molecular array data
XX
SQ   Sequence 31 BP; 25 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 1618
AAQ99582/c
ID   AAQ99582 standard; cDNA; 31 BP.
XX
AC   AAQ99582;
XX
DT   25-MAR-2003  (revised)
DT   30-APR-1996  (first entry)
XX
DE   Human TPO anti-sense primer hTPO-3mix #3.
XX
KW   Thrombopoietin; TPO; humoral factor; platelet; antibody; therapy; AIDS;
KW   thrombocytopenia; hypoplastic anaemia; thrombotic thombocytopenia;
KW   disseminated intravascular coagulation syndrome; PCR; primer; amplify;
KW   polymerase chain reaction; rat; human; ss.
XX
OS   Synthetic.
XX
PN   WO9521919-A2.
XX
PD   17-AUG-1995.
XX
PF   14-FEB-1995;   95WO-JP000208.
XX
PR   14-FEB-1994;   94JP-00039090.
PR   14-MAR-1994;   94US-00212164.
PR   25-MAR-1994;   94JP-00079842.
PR   01-APR-1994;   94US-00221020.
PR   01-JUN-1994;   94JP-00155126.
PR   15-JUN-1994;   94JP-00167328.
PR   20-JUL-1994;   94US-00278083.
PR   17-AUG-1994;   94JP-00193169.
PR   17-AUG-1994;   94JP-00227159.
PR   18-AUG-1994;   94JP-00193916.
PR   11-OCT-1994;   94US-00320300.
PR   01-NOV-1994;   94JP-00304167.
PR   01-DEC-1994;   94JP-00298669.
PR   22-DEC-1994;   94US-00361811.
PR   28-DEC-1994;   94JP-00341200.
PR   31-JAN-1995;   95US-00318478.
XX
PA   (KIRI ) KIRIN BREWERY KK.
XX
PI   Miyazaki H,  Kato T,  Ohgami K,  Iwamatsu A,  Akahori H,  Kuroki R;
PI   Shimizu T,  Muto T;
XX
DR   WPI; 1995-293120/38.
XX
PT   Thrombopoietin polypeptide which specifically stimulates or increases
PT   platelet production - useful in treatment of thrombocytopenia, also
PT   related DNA and vectors.
XX
PS   Example 19; Page 127; 383pp; English.
XX
CC   AAQ99576-Q99584 represent amplification primers based on regions of the
CC   human thrombopoietin (TPO) cDNA (see AAQ99552). These sequences were used
CC   to obtain a full length TPO sequence, as AAQ99552 did not have a complete
CC   3' terminus. TPO is a humoral factor capable of promoting platelet
CC   production. The protein encoded by the full length sequence can be
CC   purified by using a gel affinity column where Mpl has been coupled to a
CC   resin. AAQ99551 and AAQ99553 also encode TPO proteins. The DNA sequences
CC   are inserted into vectors which are used to transform prokaryotic and
CC   eukaryotic host cells. Using the proteins encoded by these sequences, and
CC   derivatives of them, antibodies specifically immunoreactive with a TPO
CC   protein can be created. The antibodies, DNA sequences and vectors are
CC   used to isolate the protein sequences. The TPO proteins can then be used
CC   in the treatment of platelet disorders. These include thrombocytopenia,
CC   hypoplastic anaemia, AIDS, disseminated intravascular coagulation
CC   syndrome and thrombotic thrombocytopenia. (Updated on 25-MAR-2003 to
CC   correct PR field.)
XX
SQ   Sequence 31 BP; 1 A; 5 C; 4 G; 21 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||
Db         28 GAAAAAAAAAAAAAAAAA 11


RESULT 1619
AAQ87894/c
ID   AAQ87894 standard; DNA; 32 BP.
XX
AC   AAQ87894;
XX
DT   25-MAR-2003  (revised)
DT   29-NOV-1995  (first entry)
XX
DE   Normalised library first strand cDNA synthesis primer.
XX
KW   Normalised cDNA library; directionally cloned cDNA library; screening;
KW   hybridisation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
```

```
FT   misc_feature    15. .18
FT                   /*tag=  a
FT                   /note= "characteristic sequence identifier"
XX
PN   WO9508647-A1.
XX
PD   30-MAR-1995.
XX
PF   23-SEP-1994;   94WO-US010821.
XX
PR   24-SEP-1993;   93US-00126594.
XX
PA   (UYCO ) UNIV COLUMBIA NEW YORK.
XX
PI   Soares MB,  Efstratiadis A;
XX
DR   WPI; 1995-139615/18.
XX
PT   New normalised directional cDNA libraries - used for isolating novel
PT   cDNA's, including tissue-specific and development-specific DNA.
XX
PS   Disclosure; Page 45; 186pp; English.
XX
CC   Human tissues were obtained for construction of a variety of cDNA
CC   libraries, including infant brain, adult brain and adult hippocampus.
CC   Each of the cDNA libraries had a characteristic sequence identifier,
CC   provided by the oligonucleotide utilised to prime first strand cDNA
CC   synthesis (see AAQ87894-Q87907 for these primer sequences; all these
CC   primers have the PacI restriction site for directional cloning of cDNAs).
CC   Each of the libraries was propagated in the form of single-stranded (ss)
CC   circles and normalised separately by a novel method. The method
CC   comprises: generating fragments complementary to the 3' non-coding
CC   sequence of the ss circles in the library to produce partial duplexes;
CC   purifying the partial duplexes; melting and reassociating them to
CC   appropriate Cot; and purifying the unassociated ss circles to generate a
CC   normalised cDNA library. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 32 BP; 4 A; 0 C; 0 G; 28 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
                ||||||||||||||||||
Db         32 AAAAAAAAAAAAAAAAAA 15


RESULT 1620
AAD33521
ID   AAD33521 standard; DNA; 32 BP.
XX
AC   AAD33521;
XX
DT   01-JUL-2002  (first entry)
XX
DE   T7T18Apad_PS3-32-0001 probe for calibration of molecular array data.
XX
KW   Molecular array; probe; ss.
XX
OS   Unidentified.
XX
PN   EP1186673-A2.
XX
PD   13-MAR-2002.
XX
PF   10-SEP-2001; 2001EP-00307665.
XX
PR   11-SEP-2000; 2000US-00659173.
XX
PA   (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI   Wobler PK,  Delenstarr GC;
XX
DR   WPI; 2002-282886/33.
XX
PT   Calibration of molecular array data by employing calibration probes that
PT   generate signals proportional to total concentrations of labeled target
PT   molecules, and molecular arrays incorporating sets of calibration probes.
XX
PS   Disclosure; Page 14; 32pp; English.
XX
CC   The invention relates to a method for calibrating data scanned from a
CC   molecular array. The method involves employing calibration probes that
CC   generate signals proportional to the total concentrations of labelled
CC   target molecules to which the molecular array probes are directed over an
CC   entire range of sample solutions and molecular arrays incorporating sets
CC   of calibration probes. Method is useful for calibrating different types
CC   of signals scanned from a molecular array, or calibrating signals scanned
CC   from different molecular arrays. The present sequence is poly (A)
CC   normalisation probe used in calibration of molecular array data
XX
SQ   Sequence 32 BP; 26 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
                ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 1621
AAT94579/c
ID   AAT94579 standard; DNA; 32 BP.
XX
AC   AAT94579;
XX
DT   12-MAY-1998  (first entry)
XX
DE   Antifungal polypeptide 3' antisense PCR primer.
XX
KW   Antifungal polypeptide; AlyAFP; inhibition; transgenic plants; primer;
KW   phytopathogenic fungus; resistance; rapid amplification of cDNA ends;
KW   PCR; RACE; antisense; ss.
XX
OS   Synthetic.
OS   Alyssum sp.
XX
PN   WO9737024-A2.
XX
PD   09-OCT-1997.
XX
PF   27-MAR-1997;   97WO-US005709.
XX
PR   29-MAR-1996;   96US-00627706.
XX
PA   (MONS ) MONSANTO CO.
XX
PI   Liang J,  Shah D,  Wu Y,  Rosenberger CA;
XX
DR   WPI; 1997-503109/46.
XX
PT   Alyssum antifungal polypeptide and corresponding DNA - used in the
PT   production of transgenic plants resistant to phytopathogenic fungi.
XX
PS   Example 4; Page 66; 92pp; English.
XX
CC   Primers AAT94578-9 were used to PCR amplify the 3' end of the sequence
CC   encoding the antifungal polypeptide AlyAFP (AAW35558), by a 3' RACE
CC   (Rapid Amplification of cDNA Ends) method. This 32-mer primer anneals to
CC   the polyA tail of the sequence. The primers amplify the sequence shown in
CC   AAT94580. The polypeptide can be used to control phytopathogenic fungi,
CC   whilst the coding DNA can be used to produce transgenic plants that
CC   express the polypeptide, making them resistant to the phytopathogenic
```

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CC   fungi
XX
SQ   Sequence 32 BP; 3 A; 3 C; 5 G; 21 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         32 AAAAAAAAAAAAAAAAAA 15


RESULT 1622
ADC87763/c
ID   ADC87763 standard; DNA; 32 BP.
XX
AC   ADC87763;
XX
DT   01-JAN-2004  (first entry)
XX
DE   F. culmorum  FCWP1 isolation PCR primer #4.
XX
KW   Antifungal protein; ribosomal protein; FCWP1; AlyAFP;
KW   plant fungal infection; Alternaria; Ascochyta; Botrytis; Cercospora;
KW   Colletotrichum; Diplodia; Fusarium; Gaeumanomyces; Helminthosporium;
KW   Macrophomina; Mycosphaerella; Nectria; Peronospora; Phoma;
KW   Phymatotrichum; Phytophthora; Plasmopara; Podosphaera; Puccinia; Puthium;
KW   Pyrenophora; Pyricularia; Pythium; Rhizoctonia; Scerotium; Sclerotinia;
KW   Septoria; Thielaviopsis; Venturia; Verticillium; ss; PCR; primer.
XX
OS   Synthetic.
OS   Fusarium culmorum.
XX
PN   US6573361-B1.
XX
PD   03-JUN-2003.
XX
PF   07-DEC-2000; 2000US-00732210.
XX
PR   07-DEC-1999;   99US-0169340P.
PR   07-DEC-1999;   99US-0169513P.
XX
PA   (MONS ) MONSANTO TECHNOLOGY LLC.
XX
PI   Bunkers GJ,  Liang J,  Mittanck CA,  Seale JW,  Wu YS;
XX
DR   WPI; 2003-754558/71.
XX
PT   Novel antifungal protein FCWP1, isolated from Fusarium culmorum, useful
PT   for controlling fungal infections in plants.
XX
PS   Example 11; SEQ ID NO 16; 27pp; English.
XX
CC   The invention relates to an isolated antifungal ribosomal protein from
CC   fusarium culmorum, FCWP1. Also included is a fusion protein between the
CC   signal peptide of the antifungal protein AlyAFP from Alyssum and FCWP1,
CC   encoded by the nucleic acid appearing as ADC87758. The FCWP1 proteins are
CC   useful for controlling fungal infections in plants, such as those caused
CC   by Alternaria (e.g. Alternaria brassicola , Alternaria solani ),
CC   Ascochyta (e.g. Ascochyta pisi ); Botrytis (e.g. Botrytis cinerea ),
CC   Cercospora (e.g. Cercospora kikuchii , Cercospora zaea-maydis ),
CC   Colletotrichum (e.g. Colletotrichum lindemuthianum ), Diplodia (e.g.
CC   Diplodia maydis ), Fusarium (e.g. Fusarium nivale , Fusarium oxysporum ,
CC   Fusarium graminearum , Fusarium culmorum , Fusarium solani , Fusarium
CC   moniliforme , Fusarium roseum ), Gaeumanomyces (e.g. Gaeumanomyces
CC   graminis f.sp. tritici), Helminthosporium (e.g. Helminthosporium turcicum
CC   , Helminthosporium carbonum , Helminthosporium maydis ), Macrophomina
CC   (e.g. Macrophomina phaseolina , Maganaporthe grisea ), Mycosphaerella
CC   (e.g. Mycosphaerella figiensis ), Nectria ( Nectria heamatococca ),
CC   Peronospora (e.g. Peronospora manshurica , Peronospora tabacina ), Phoma
CC   (e.g. Phoma betae ), Phymatotrichum (e.g. Phymatotrichum omnivorum ),
CC   Phytophthora (e.g. Phytophthora cinnamomi , Phytophthora cactorum ,
CC   Phytophthora phaseoli , Phytophthora parasitica , Phytophthora
CC   citrophthora , Phytophthora megasperma f.sp. sojae, Phytophthora
CC   infestans ), Plasmopara (e.g. Plasmopara viticola ), Podosphaera (e.g.
CC   Podosphaera leucotricha ), Puccinia (e.g. Puccinia sorghi , Puccinia
CC   striiformis , Puccinia graminis f.sp. tritici, Puccinia asparagi ,
CC   Puccinia recondita , Puccinia arachidis ), Puthium (e.g. Puthium
CC   aphanidermatum ), Pyrenophora (e.g. Pyrenophora tritici-repentens ),
CC   Pyricularia (e.g. Pyricularia oryzae ), Pythium (e.g. Pythium ultimum ),
CC   Rhizoctonia (e.g. Rhizoctonia solani , Rhizoctonia cerealis ), Scerotium
CC   (e.g. Scerotium rolfsii ), Sclerotinia (e.g. Sclerotinia sclerotiorum ),
CC   Septoria (e.g. Septoria lycopersici , Septoria glycines , Stagonospora
CC   nodorum / Phaeosphaeria nodorum , Septoria tritici ), Thielaviopsis (e.g.
CC   Thielaviopsis basicola ), Uncinula (e.g. Uncinula necator ), Venturia
CC   (e.g. Venturia inaequalis ) or Verticillium (e.g. Verticillium dahliae ,
CC   Verticillium albo-atrum ). Mutations in the proteolytic consensus
CC   sequences contained within FCWP1 provides improved stability of its
CC   antifungal activity. Also disclosed are ribosomal proteins with similar
CC   PI (>7|) and molecular weight (<20kDa) to FCWP1, which may act as
CC   antifungal proteins. The present sequence is a PCR primer used to isolate
CC   cDNA for FCWP1. Note: The sequence data for this patent did not form part
CC   of the printed specification, but was obtained in electronic format
CC   directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=6573361B1.
XX
SQ   Sequence 32 BP; 3 A; 3 C; 5 G; 21 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         32 AAAAAAAAAAAAAAAAAA 15


RESULT 1623
AAH28290/c
ID   AAH28290 standard; RNA; 32 BP.
XX
AC   AAH28290;
XX
DT   05-SEP-2001  (first entry)
XX
DE   3' untranslated region sequence from GADD45 gene.
XX
KW   mRNA protein complex; tumour development; cell aging; death;
KW   ribonomic profile; RNA-binding protein; ss.
XX
OS   Unidentified.
XX
PN   WO200148480-A1.
XX
PD   05-JUL-2001.
XX
PF   28-DEC-2000; 2000WO-US035583.
XX
PR   28-DEC-1999;   99US-0173338P.
XX
PA   (KEEN/) KEENE J D.
XX
PI   Keene JD,  Tenenbaum SA,  Carson C;
XX
DR   WPI; 2001-425706/45.
XX
PT   Partitioning endogenous mRNA-protein complexes in vivo, by contacting
PT   sample comprising the complex with ligand that binds to a component of
PT   the complex and separating complex by binding ligand with a binding
PT   molecule.
XX
PS   Example 6; Page 30; 49pp; English.
XX
CC   The specification describes a method for partitioning endogenous cellular
CC   mRNA-protein (mRNP) complexes. The method comprises contacting a
CC   biological sample comprising mRNP complex with ligand that specifically
```

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CC   binds a component of mRNP complex, separating mRNP complex by binding the
CC   ligand with a molecule specific for ligand, which is attached to the
CC   solid support and then collecting the mRNP complex by removing the
CC   complex from the support. The method is useful for in vivo partitioning
CC   of cellular mRNA protein complexes in a biological sample. The method is
CC   useful for determining the ribonomic profile of a cell which has numerous
CC   uses including monitoring of tumour development, state of growth or state
CC   of development, perturbations of a biological system such as disease,
CC   drug or toxin treatment and the state of cell aging or death,
CC   distinguishing ribonomic profiles among organisms, to discriminate
CC   between transcriptional and post-transcriptional contributions to gene
CC   expression and to track the movement of RNAs through RNP complexes,
CC   including the interactions of combinations of proteins with RNAs in RNP
CC   complexes. AAH28281-AAH28316 represent sequences derived from the 3'
CC   untranslated region (UTR) of mRNA of various genes. The sequences contain
CC   target sequences for RNA-binding proteins
XX
SQ   Sequence 32 BP; 2 A; 2 C; 2 G; 0 T; 26 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 32;
  Best Local Similarity   80.8%;  Pred. No. 2.5e+03;
  Matches   21;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
                |||    |||||||||| ||||||||
Db         28 AGACCAAAAAAAAAAAAGAAAAAAAA 3


RESULT 1624
AAC90605/c
ID   AAC90605 standard; RNA; 34 BP.
XX
AC   AAC90605;
XX
DT   20-MAR-2001  (first entry)
XX
DE   Tomato spotted wilt virus S RNA partial sequence #9.
XX
KW   Tospovirus resistance; transgenic plant; tomato spotted wilt virus;
KW   Impatiens necrotic spot virus; TSWV; ss.
XX
OS   Tomato spotted wilt virus.
XX
FH   Key             Location/Qualifiers
FT   misc_binding    1
FT                   /*tag=  a
FT                   /bound_moiety= "binds nucleotide 32 of AAC89654"
FT   misc_binding    2. .10
FT                   /*tag=  b
FT                   /bound_moiety= "binds nucleotides 30-22 of AAC89654"
FT   misc_binding    17. .32
FT                   /*tag=  c
FT                   /bound_moiety= "binds nucleotides 30-5 of AAC89564"
FT   misc_binding    33. .34
FT                   /*tag=  d
FT                   /bound_moiety= "binds nucleotides 1-2 of AAC89654"
XX
PN   US6150585-A.
XX
PD   21-NOV-2000.
XX
PF   26-NOV-1996;   96US-00757011.
XX
PR   03-NOV-1989;   89US-00431259.
PR   05-DEC-1989;   89US-00446024.
PR   02-MAY-1991;   91US-00694734.
PR   14-APR-1993;   93US-00047346.
PR   26-OCT-1993;   93US-00143397.
PR   27-JUL-1994;   94US-00280903.
XX
PA   (NOVS ) NOVARTIS FINANCE CORP.
XX
PI   Peters D,  Gielen JJL,  De Haan PT,  Van Grinsven MQJM,  Kool AJ;
PI   Goldbach RW;
XX
DR   WPI; 2001-060031/07.
XX
PT   Recombinant DNA construct comprising a DNA sequence encoding an RNA
PT   sequence that codes for a tospovirus protein, useful for producing plants
PT   with reduced susceptibility to tospovirus infection.
XX
PS   Example 9; Fig 16B; 49pp; English.
XX
CC   The present invention provides DNA constructs encoding RNA sequences from
CC   a tospovirus which can be used to produce transgenic plants with immunity
CC   to tospoviruses. Examples of tospoviruses include the tomato spotted wilt
CC   virus and the Impatiens necrotic spot virus
XX
SQ   Sequence 34 BP; 4 A; 0 C; 2 G; 0 T; 28 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 34;
  Best Local Similarity   80.8%;  Pred. No. 2.8e+03;
  Matches   21;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAAAAAAAAAA 2803
                || |||  |||| |||||| ||||||
Db         27 TAAAATAAAAAATAAAAAACAAAAAA 2


RESULT 1625
AAV12483/c
ID   AAV12483 standard; DNA; 39 BP.
XX
AC   AAV12483;
XX
DT   15-MAY-1998  (first entry)
XX
DE   Oligonucleotide SEQ ID NO:6 from US5174320 Example 2.
XX
KW   Synthesis; selection; amplification; circular oligonucleotide;
KW   rolling circle synthesis; diagnosis; therapeutic agent; ss.
XX
OS   Synthetic.
XX
PN   US5714320-A.
XX
PD   03-FEB-1998.
XX
PF   23-FEB-1995;   95US-00393439.
XX
PR   15-APR-1993;   93US-00047860.
XX
PA   (UYRP ) UNIV ROCHESTER.
XX
PI   Kool ET;
XX
DR   WPI; 1998-144278/13.
XX
PT   Rolling circle synthesis of oligo:nucleotide(s) - using primed circular
PT   template to produce oligonucleotide multimer for cleavage.
XX
PS   Example 2; Col 45; 38pp; English.
XX
CC   The present sequence represents an oligonucleotide used in an example of
CC   the present invention. The present invention describes a method for
CC   synthesising a selected oligonucleotide (I) having well defined ends. The
CC   method comprises: (a) annealing a primer to a single-stranded (ss)
CC   circular template to yield a primed circular template, where the template
CC   comprises: (i) at least one nucleotide sequence complementary to (I); and
CC   (ii) at least one nucleotide effective to produce a cleavage site in the
CC   oligonucleotide multimer; (b) combining the primed circular template with
CC   at least two types of nucleotide triphosphates and a polymerase enzyme
CC   without the addition of auxiliary proteins to yield a ss oligonucleotide
CC   multimer complementary to the circular oligonucleotide template,
CC   comprising multiple copies of (I); and (c) cleaving the oligonucleotide
CC   multimer at the cleavage site to produce (I) having well defined ends.
```

```
CC   The method is used for the large-scale synthesis of DNA and RNA oligomers
CC   for use, e.g. as probes and diagnostic agents and/or therapeutic agents
XX
SQ   Sequence 39 BP; 0 A; 0 C; 3 G; 36 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 39;
  Best Local Similarity   80.8%;  Pred. No. 3.1e+03;
  Matches   21;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
                | ||   |||||||||||| ||||||
Db         33 AAAAAACAAAAAAAAAAAACAAAAAA 8


RESULT 1626
AAX30019/c
ID   AAX30019 standard; DNA; 39 BP.
XX
AC   AAX30019;
XX
DT   16-JUN-1999  (first entry)
XX
DE   Multimer SEQ ID NO:6.
XX
KW   Multimer; probe; diagnosis; synthesis; detection; polymerase; ss.
XX
OS   Synthetic.
XX
PN   WO9909216-A2.
XX
PD   25-FEB-1999.
XX
PF   13-AUG-1998;   98WO-US016776.
XX
PR   13-AUG-1997;   97US-00910632.
XX
PA   (UYRP ) UNIV ROCHESTER.
XX
PI   Kool ET;
XX
DR   WPI; 1999-181062/15.
XX
PT   New detectably labelled oligonucleotide multimer, comprising multiple
PT   contiguous copies of a repeated oligonucleotide - useful for detecting
PT   target molecules in diagnosis and medicinal applications.
XX
PS   Example 2; Page 41; 103pp; English.
XX
CC   The present invention describes a detectably labelled oligonucleotide
CC   multimer, comprising multiple contiguous copies of a repeated
CC   oligonucleotides. The detectably labelled oligonucleotide multimer is
CC   useful for detecting a target molecule. Oligonucleotide multimers may be
CC   produced in sufficient quantity to be useful for diagnostic and medical
CC   applications. The multimers are useful for affinity labelling of
CC   proteins, and for signal amplification in highly sensitive affinity
CC   capture and sequence identification applications. The method provides a
CC   faster, cheaper and simpler way for large-scale production of DNA and RNA
CC   oligomers and multimers. The incorporation of labels enables the
CC   oligonucleotide multimers to be useful in diagnostics and medicine. The
CC   present sequence represents an oligonucleotide used in an example from
CC   the present invention
XX
SQ   Sequence 39 BP; 0 A; 0 C; 3 G; 36 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 18;  DB 1;  Length 39;
  Best Local Similarity   80.8%;  Pred. No. 3.1e+03;
  Matches   21;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
                | ||   |||||||||||| ||||||
Db         33 AAAAAACAAAAAAAAAAAACAAAAAA 8


RESULT 1627
AAT69640
ID   AAT69640 standard; DNA; 19 BP.
XX
AC   AAT69640;
XX
DT   20-FEB-1998  (first entry)
XX
DE   Telomerase Oligo-dT-Primer P3.
XX
KW   Telomerase; substrate; primer; detection; 5'-region; retrovirus;
KW   long terminal repeat 2; LTR-2; diagnosis; tumour; screening;
KW   effector compound; PCR; amplification; Oligo-dT-Primer; ss.
XX
OS   Synthetic.
XX
PN   DE19644302-A1.
XX
PD   05-JUN-1997.
XX
PF   24-OCT-1996;   96DE-01044302.
XX
PR   28-NOV-1995;   95DE-01044317.
XX
PA   (BOEF ) BOEHRINGER MANNHEIM GMBH.
XX
PI   Emrich T,  Leying H,  Hinzpeter M,  Karl G;
XX
DR   WPI; 1997-299542/28.
XX
PT   Measuring telomerase activity, useful for tumour diagnosis and compound
PT   screening - by extending substrate primer, followed by amplification and
PT   immobilising product for detection.
XX
PS   Example; Page 11; 21pp; German.
XX
CC   The present sequence is a telomerase Oliog-dT-Primer, which can be used
CC   in a novel method for detecting telomerase activity. The method comprises
CC   adding to a test sample a 1st primer, that serves as telomerase
CC   substrate, and nucleoside triphosphate (dNTP) and incubating to allow
CC   primer extension by the telomerase, amplifying the extension product,
CC   immobilising the amplification product (AP) on a solid phase and
CC   qualitative and/or quantitative detection of AP, where the substrate
CC   primer is preferably from the 5'-region of the long terminal repeat 2
CC   (LTR-2) sequence of a retrovirus. The method can be used to diagnose
CC   tumours and screen compounds for effector activity. Immobilisation of AP
CC   provides a signal that is reproducibly representative of telomerase
CC   activity, eliminates the need for gel electrophoretic separation and
CC   provides high sensitivity. Radioactive labels are not required and the
CC   method can be automated for routine use. Specific detection is achieved
CC   by proper choice of hybridisation conditions, without separation of the
CC   telomerase extension product. A specific signal is generated by 1-10 cell
CC   equivalents, but for tumour analysis 10-1000 ng of tissue is usually used
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 2 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 9.1e+02;
  Matches   17;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAA 2188
                ||||||||||||||||::
Db          1 TTTTTTTTTTTTTTTTTMH 19


RESULT 1628
AAT69640/c
ID   AAT69640 standard; DNA; 19 BP.
XX
AC   AAT69640;
XX
DT   20-FEB-1998  (first entry)
XX
```

```
DE   Telomerase Oligo-dT-Primer P3.
XX
KW   Telomerase; substrate; primer; detection; 5'-region; retrovirus;
KW   long terminal repeat 2; LTR-2; diagnosis; tumour; screening;
KW   effector compound; PCR; amplification; Oligo-dT-Primer; ss.
XX
OS   Synthetic.
XX
PN   DE19644302-A1.
XX
PD   05-JUN-1997.
XX
PF   24-OCT-1996;   96DE-01044302.
XX
PR   28-NOV-1995;   95DE-01044317.
XX
PA   (BOEF ) BOEHRINGER MANNHEIM GMBH.
XX
PI   Emrich T,  Leying H,  Hinzpeter M,  Karl G;
XX
DR   WPI; 1997-299542/28.
XX
PT   Measuring telomerase activity, useful for tumour diagnosis and compound
PT   screening - by extending substrate primer, followed by amplification and
PT   immobilising product for detection.
XX
PS   Example; Page 11; 21pp; German.
XX
CC   The present sequence is a telomerase Oliog-dT-Primer, which can be used
CC   in a novel method for detecting telomerase activity. The method comprises
CC   adding to a test sample a 1st primer, that serves as telomerase
CC   substrate, and nucleoside triphosphate (dNTP) and incubating to allow
CC   primer extension by the telomerase, amplifying the extension product,
CC   immobilising the amplification product (AP) on a solid phase and
CC   qualitative and/or quantitative detection of AP, where the substrate
CC   primer is preferably from the 5'-region of the long terminal repeat 2
CC   (LTR-2) sequence of a retrovirus. The method can be used to diagnose
CC   tumours and screen compounds for effector activity. Immobilisation of AP
CC   provides a signal that is reproducibly representative of telomerase
CC   activity, eliminates the need for gel electrophoretic separation and
CC   provides high sensitivity. Radioactive labels are not required and the
CC   method can be automated for routine use. Specific detection is achieved
CC   by proper choice of hybridisation conditions, without separation of the
CC   telomerase extension product. A specific signal is generated by 1-10 cell
CC   equivalents, but for tumour analysis 10-1000 ng of tissue is usually used
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 2 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 9.1e+02;
  Matches   17;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAA 2802
              ::||||||||||||||||||
Db         19 DKAAAAAAAAAAAAAAAAA 1


RESULT 1629
AAQ75733/c
ID   AAQ75733 standard; DNA; 21 BP.
XX
AC   AAQ75733;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAA 2801
              | ||  ||||||||||||||||
Db         21 AGTTAAAAAAAAAAAAAAAAA 1


RESULT 1630
AAQ75732/c
ID   AAQ75732 standard; DNA; 21 BP.
XX
AC   AAQ75732;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
```

```
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 3 A; 1 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAAA 2804
              ||  ||||||||||||||||||
Db         21 TGTTAAAAAAAAAAAAAAAAA 1


RESULT 1631
AAQ75648/c
ID   AAQ75648 standard; DNA; 21 BP.
XX
AC   AAQ75648;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAAA 2804
              \ \ ||||||||||||||||||
Db         21 TAACAAAAAAAAAAAAAAAAA 1


RESULT 1632
AAQ75676/c
ID   AAQ75676 standard; DNA; 21 BP.
XX
AC   AAQ75676;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 3 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAAA 2803
              ||  ||||||||||||||||||
Db         21 TTATAAAAAAAAAAAAAAAAA 1


RESULT 1633
AAQ75681/c
ID   AAQ75681 standard; DNA; 21 BP.
XX
AC   AAQ75681;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
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PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAA 2801
              || | ||||||||||||||||||
Db         21 AAATAAAAAAAAAAAAAAAAA 1


RESULT 1634
AAQ75780
ID   AAQ75780 standard; DNA; 21 BP.
XX
AC   AAQ75780;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTA 2187
                ||||||||||||||||||  |
Db          1 TTTTTTTTTTTTTTTTTCTCA 21


RESULT 1635
AAQ75660
ID   AAQ75660 standard; DNA; 21 BP.
XX
AC   AAQ75660;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTAA 2188
                ||||||||||||||||||  ||
Db          1 TTTTTTTTTTTTTTTTTGCAA 21


RESULT 1636
AAQ75652
ID   AAQ75652 standard; DNA; 21 BP.
XX
AC   AAQ75652;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
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```
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||  | |
Db          1 TTTTTTTTTTTTTTTTTGTCA 21


RESULT 1637
AAQ75753
ID   AAQ75753 standard; DNA; 21 BP.
XX
AC   AAQ75753;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTAACT 2190
              ||||||||||||||||||  | |
Db          1 TTTTTTTTTTTTTTTTTCAGT 21


RESULT 1638
AAQ75788
ID   AAQ75788 standard; DNA; 21 BP.
XX
AC   AAQ75788;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTAA 2188
              ||||||||||||||||||  ||
Db          1 TTTTTTTTTTTTTTTTTCCAA 21


RESULT 1639
AAQ75680/c
ID   AAQ75680 standard; DNA; 21 BP.
XX
AC   AAQ75680;
XX
DT   04-AUG-1995  (first entry)
```

XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2784 TGAAAAAAAAAAAAAAAAAAA 2804
| | ||||||||||||||||||
Db 21 TAATAAAAAAAAAAAAAAAAA 1

RESULT 1640
AAQ75697/c
ID AAQ75697 standard; DNA; 21 BP.
XX
AC AAQ75697;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2781 AATTGAAAAAAAAAAAAAAAA 2801
|| | |||||||||||||||||
Db 21 AAGTAAAAAAAAAAAAAAAAA 1

RESULT 1641
AAQ75637/c
ID AAQ75637 standard; DNA; 21 BP.
XX
AC AAQ75637;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 6; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2782 ATTGAAAAAAAAAAAAAAAA 2802
| | ||||||||||||||||||

```
Db         21 AGTCAAAAAAAAAAAAAAAAA 1

RESULT 1642
AAQ75644/c
ID   AAQ75644 standard; DNA; 21 BP.
XX
AC   AAQ75644;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAAA 2803
              ||  ||||||||||||||||||
Db         21 TTACAAAAAAAAAAAAAAAAA 1


RESULT 1643
AAQ75761
ID   AAQ75761 standard; DNA; 21 BP.
XX
AC   AAQ75761;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||  ||
Db          1 TTTTTTTTTTTTTTTTTCATT 21


RESULT 1644
AAQ75721/c
ID   AAQ75721 standard; DNA; 21 BP.
XX
AC   AAQ75721;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
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CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAA 2801
              | || ||||||||||||||||
Db         21 ACTTAAAAAAAAAAAAAAAAA 1


RESULT 1645
AAQ75762
ID   AAQ75762 standard; DNA; 21 BP.
XX
AC   AAQ75762;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTAAC 2189
              |||||||||||||||||  |
Db          1 TTTTTTTTTTTTTTTTCATC 21


RESULT 1646
AAQ75760
ID   AAQ75760 standard; DNA; 21 BP.
XX
AC   AAQ75760;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||  ||
Db          1 TTTTTTTTTTTTTTTTCATA 21


RESULT 1647
AAQ75754
ID   AAQ75754 standard; DNA; 21 BP.
XX
AC   AAQ75754;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
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XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTAAC 2189
              |||||||||||||||||  | |
Db          1 TTTTTTTTTTTTTTTTCAGC 21


RESULT 1648
AAQ75781
ID   AAQ75781 standard; DNA; 21 BP.
XX
AC   AAQ75781;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 2 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||  | |
Db          1 TTTTTTTTTTTTTTTTCTCT 21


RESULT 1649
AAQ75700/c
ID   AAQ75700 standard; DNA; 21 BP.
XX
AC   AAQ75700;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAAA 2803
              | | ||||||||||||||||||
Db         21 TGGTAAAAAAAAAAAAAAAAA 1


RESULT 1650
AAQ75742
ID   AAQ75742 standard; DNA; 21 BP.
XX
AC   AAQ75742;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
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PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTAAC 2189
              ||||||||||||||||||  ||
Db          1 TTTTTTTTTTTTTTTTTCGAC 21


RESULT 1651
AAQ75716/c
ID   AAQ75716 standard; DNA; 21 BP.
XX
AC   AAQ75716;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAA 2804
              ||  ||||||||||||||||||
Db         21 TGCTAAAAAAAAAAAAAAAAA 1


RESULT 1652
AAQ75740
ID   AAQ75740 standard; DNA; 21 BP.
XX
AC   AAQ75740;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTAA 2188
              ||||||||||||||||||  ||
Db          1 TTTTTTTTTTTTTTTTTCGAA 21


RESULT 1653
AAQ75636/c
ID   AAQ75636 standard; DNA; 21 BP.
XX
AC   AAQ75636;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
```

```
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAA 2804
              ||  ||||||||||||||||||
Db         21 TGTCAAAAAAAAAAAAAAAAA 1


RESULT 1654
AAQ75790
ID   AAQ75790 standard; DNA; 21 BP.
XX
AC   AAQ75790;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 3 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTAAC 2189
              ||||||||||||||||||  ||
Db          1 TTTTTTTTTTTTTTTTTCCAC 21


RESULT 1655
AAQ75645/c
ID   AAQ75645 standard; DNA; 21 BP.
XX
AC   AAQ75645;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAAA 2802
              ||  ||||||||||||||||||
Db         21 ATACAAAAAAAAAAAAAAAA 1
```

```
RESULT 1656
AAQ75662
ID   AAQ75662 standard; DNA; 21 BP.
XX
AC   AAQ75662;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTAAC 2189
              ||||||||||||||||||  ||
Db          1 TTTTTTTTTTTTTTTTTGCAC 21


RESULT 1657
AAQ75653
ID   AAQ75653 standard; DNA; 21 BP.
XX
AC   AAQ75653;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||  | |
Db          1 TTTTTTTTTTTTTTTTTGTCT 21


RESULT 1658
AAQ75677/c
ID   AAQ75677 standard; DNA; 21 BP.
XX
AC   AAQ75677;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
```

```
SQ   Sequence 21 BP; 2 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAAAA 2802
              ||  ||||||||||||||||||
Db         21 ATATAAAAAAAAAAAAAAAAA 1


RESULT 1659
AAQ75696/c
ID   AAQ75696 standard; DNA; 21 BP.
XX
AC   AAQ75696;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAA 2803
              | | ||||||||||||||||||
Db         21 TAGTAAAAAAAAAAAAAAAAA 1


RESULT 1660
AAQ75793
ID   AAQ75793 standard; DNA; 21 BP.
XX
AC   AAQ75793;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 2 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||  ||
Db          1 TTTTTTTTTTTTTTTTTCCTT 21


RESULT 1661
AAQ75688/c
ID   AAQ75688 standard; DNA; 21 BP.
XX
AC   AAQ75688;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
```

XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2783 TTGAAAAAAAAAAAAAAAAA 2803
| | ||||||||||||||||||
Db 21 TCGTAAAAAAAAAAAAAAAAA 1

RESULT 1662
AAQ75713/c
ID AAQ75713 standard; DNA; 21 BP.
XX
AC AAQ75713;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2781 AATTGAAAAAAAAAAAAAAA 2801
|| | ||||||||||||||||||
Db 21 AACTAAAAAAAAAAAAAAAAA 1

RESULT 1663
AAQ75769
ID AAQ75769 standard; DNA; 21 BP.
XX
AC AAQ75769;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 9; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2186
|||||||||||||||||| | |
Db 1 TTTTTTTTTTTTTTTTTCTGT 21

RESULT 1664
AAQ75797
ID AAQ75797 standard; DNA; 21 BP.
XX
AC AAQ75797;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX

```
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 3 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTAACT 2190
              ||||||||||||||||  ||
Db          1 TTTTTTTTTTTTTTTTCCCT 21


RESULT 1665
AAQ75672/c
ID   AAQ75672 standard; DNA; 21 BP.
XX
AC   AAQ75672;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAA 2804
              | | ||||||||||||||||||
Db         21 TCATAAAAAAAAAAAAAAAAA 1


RESULT 1666
AAQ75708/c
ID   AAQ75708 standard; DNA; 21 BP.
XX
AC   AAQ75708;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 3 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAA 2803
              ||  ||||||||||||||||
Db         21 TTCTAAAAAAAAAAAAAAAA 1


RESULT 1667
AAQ75768
ID   AAQ75768 standard; DNA; 21 BP.
XX
AC   AAQ75768;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
```

```
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||  ||
Db          1 TTTTTTTTTTTTTTTTTCTGA 21


RESULT 1668
AAQ75745
ID   AAQ75745 standard; DNA; 21 BP.
XX
AC   AAQ75745;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||  ||
Db          1 TTTTTTTTTTTTTTTTTCGTT 21


RESULT 1669
AAQ75749
ID   AAQ75749 standard; DNA; 21 BP.
XX
AC   AAQ75749;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAACT 2190
              ||||||||||||||||||  ||
Db          1 TTTTTTTTTTTTTTTTTCGCT 21


RESULT 1670
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```
AAQ75709/c
ID   AAQ75709 standard; DNA; 21 BP.
XX
AC   AAQ75709;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAAA 2802
              ||  ||||||||||||||||
Db         21 ATCTAAAAAAAAAAAAAAAA 1


RESULT 1671
AAQ75744
ID   AAQ75744 standard; DNA; 21 BP.
XX
AC   AAQ75744;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||  ||
Db          1 TTTTTTTTTTTTTTTTTCGTA 21


RESULT 1672
AAQ75792
ID   AAQ75792 standard; DNA; 21 BP.
XX
AC   AAQ75792;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;
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  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||  ||
Db          1 TTTTTTTTTTTTTTTTTCCTA 21


RESULT 1673
AAQ75633
ID   AAQ75633 standard; DNA; 21 BP.
XX
AC   AAQ75633;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||  ||
Db          1 TTTTTTTTTTTTTTTTTGATT 21


RESULT 1674
AAQ75633/c
ID   AAQ75633 standard; DNA; 21 BP.
XX
AC   AAQ75633;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAA 2801
              |||  ||||||||||||||||
Db         21 AATCAAAAAAAAAAAAAAAA 1


RESULT 1675
AAQ75620/c
ID   AAQ75620 standard; DNA; 21 BP.
XX
AC   AAQ75620;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
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CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAAA 2804
              ||  ||||||||||||||||||
Db         21 TGCCAAAAAAAAAAAAAAAAA 1


RESULT 1676
AAQ75626
ID   AAQ75626 standard; DNA; 21 BP.
XX
AC   AAQ75626;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTAAC 2189
              |||||||||||||||||  | |
Db          1 TTTTTTTTTTTTTTTTTGAGC 21


RESULT 1677
AAQ75664
ID   AAQ75664 standard; DNA; 21 BP.
XX
AC   AAQ75664;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||  ||
Db          1 TTTTTTTTTTTTTTTTTGCTA 21


RESULT 1678
AAQ75664/c
ID   AAQ75664 standard; DNA; 21 BP.
XX
AC   AAQ75664;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
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PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAAA 2803
              | | ||||||||||||||||||
Db         21 TAGCAAAAAAAAAAAAAAAAA 1


RESULT 1679
AAQ75669
ID   AAQ75669 standard; DNA; 21 BP.
XX
AC   AAQ75669;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTAACT 2190
              ||||||||||||||||  ||
Db          1 TTTTTTTTTTTTTTTTGCCT 21


RESULT 1680
AAQ75668/c
ID   AAQ75668 standard; DNA; 21 BP.
XX
AC   AAQ75668;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAAA 2803
              | | ||||||||||||||||||
Db         21 TGGCAAAAAAAAAAAAAAAAA 1


RESULT 1681
AAQ75625
ID   AAQ75625 standard; DNA; 21 BP.
XX
AC   AAQ75625;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
```

```
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAACT 2190
              ||||||||||||||||| | |
Db          1 TTTTTTTTTTTTTTTTTGAGT 21


RESULT 1682
AAQ75625/c
ID   AAQ75625 standard; DNA; 21 BP.
XX
AC   AAQ75625;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAAAA 2802
              | | |||||||||||||||||
Db         21 ACTCAAAAAAAAAAAAAAAAA 1


RESULT 1683
AAQ75634
ID   AAQ75634 standard; DNA; 21 BP.
XX
AC   AAQ75634;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTAAC 2189
              ||||||||||||||||| | |
Db          1 TTTTTTTTTTTTTTTTTGATC 21


RESULT 1684
AAQ75614
ID   AAQ75614 standard; DNA; 21 BP.
```

```
XX
AC   AAQ75614;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTAAC 2189
              |||||||||||||||||  ||
Db          1 TTTTTTTTTTTTTTTTTGGAC 21


RESULT 1685
AAQ75665
ID   AAQ75665 standard; DNA; 21 BP.
XX
AC   AAQ75665;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||  ||
Db          1 TTTTTTTTTTTTTTTTTGCTT 21


RESULT 1686
AAQ75612
ID   AAQ75612 standard; DNA; 21 BP.
XX
AC   AAQ75612;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
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  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTTAA 2188
              ||||||||||||||||||  ||
Db          1 TTTTTTTTTTTTTTTTTGGAA 21


RESULT 1687
AAQ75612/c
ID   AAQ75612 standard; DNA; 21 BP.
XX
AC   AAQ75612;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAAA 2803
              ||  ||||||||||||||||||
Db         21 TTCCAAAAAAAAAAAAAAAAA 1


RESULT 1688
AAQ75641
ID   AAQ75641 standard; DNA; 21 BP.
XX
AC   AAQ75641;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 0 C; 2 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||  |
Db          1 TTTTTTTTTTTTTTTTTGTGT 21


RESULT 1689
AAQ75632
ID   AAQ75632 standard; DNA; 21 BP.
XX
AC   AAQ75632;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
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CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||  ||
Db          1 TTTTTTTTTTTTTTTTGATA 21


RESULT 1690
AAQ75621
ID   AAQ75621 standard; DNA; 21 BP.
XX
AC   AAQ75621;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAACT 2190
              ||||||||||||||||||  ||
Db          1 TTTTTTTTTTTTTTTTTGGCT 21


RESULT 1691
AAQ75656/c
ID   AAQ75656 standard; DNA; 21 BP.
XX
AC   AAQ75656;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAAA 2803
              | | ||||||||||||||||||
Db         21 TCGCAAAAAAAAAAAAAAAAA 1


RESULT 1692
AAQ75617
ID   AAQ75617 standard; DNA; 21 BP.
XX
AC   AAQ75617;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
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DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 0 C; 2 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||  ||
Db          1 TTTTTTTTTTTTTTTTTGGTT 21


RESULT 1693
AAQ75640
ID   AAQ75640 standard; DNA; 21 BP.
XX
AC   AAQ75640;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||  |
Db          1 TTTTTTTTTTTTTTTTTGTGA 21


RESULT 1694
AAQ75640/c
ID   AAQ75640 standard; DNA; 21 BP.
XX
AC   AAQ75640;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAAA 2804
              | | ||||||||||||||||||
Db         21 TCACAAAAAAAAAAAAAAAAA 1


RESULT 1695
AAQ75613/c
ID   AAQ75613 standard; DNA; 21 BP.
XX
AC   AAQ75613;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
```

PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2782 ATTGAAAAAAAAAAAAAAAAA 2802
|| ||||||||||||||||||
Db 21 ATCCAAAAAAAAAAAAAAAAA 1

RESULT 1696
AAQ75616
ID AAQ75616 standard; DNA; 21 BP.
XX
AC AAQ75616;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 6; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2167 TTTTTTTTTTTTTTTTTTTA 2187
|||||||||||||||||| ||
Db 1 TTTTTTTTTTTTTTTTTGGTA 21

RESULT 1697
AAZ26563/c
ID AAZ26563 standard; DNA; 21 BP.
XX
AC AAZ26563;
XX
DT 30-NOV-1999 (first entry)
XX
DE Human polymorphic region 752.
XX
KW Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW cell viability; loss of heterozygosity; precancerous condition; ASI;
KW allele specific inhibitor; somatic cell; diagnosis; prevention;
KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW graft versus host disease; malignant cell removal; bone marrow; ss.
XX
OS Homo sapiens.
XX
PN WO9841648-A2.
XX
PD 24-SEP-1998.
XX
PF 19-MAR-1998; 98WO-US005419.
XX
PR 20-MAR-1997; 97US-0041057P.
XX
PA (VARI-) VARIAGENICS INC.
XX
PI Housman D, Ledley FD, Stanton VP;
XX
DR WPI; 1998-521232/44.
XX
PT Identifying target genes for allele-specific drugs - used for diagnosis,
PT prevention and treatment of, e.g. cancers, atherosclerotic plaque,
PT dysplastic lesions, endometriosis or graft versus host disease.
XX
PS Disclosure; Fig 7; 605pp; English.
XX
CC This invention describes a novel method for identifying an inhibitor
CC potentially useful for treatment of cancer, where the inhibitor is active
CC on a gene vital for cell growth or viability, and where the gene is
CC subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC used for preventing the development of cancer in a patient having a
CC precancerous condition, by administering to the patient a first allele
CC specific inhibitor (ASI) targeted to an allele of a first essential gene
CC present in cells of the precancerous condition, where the normal somatic
CC cells of the patient are heterozygous for the first gene, the inhibitor
CC is active on at least one but less than all allelic forms of the gene
CC present in a population and targets only one allelic form present in the
CC normal somatic cells, and the first gene. The products and methods can be
CC used in the diagnosis, prevention and treatment of LOH disorders, e.g.
CC cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
CC lesions, benign tumours, endometriosis, polycystic kidney disease, and
CC graft versus host disease. The method can also be used to remove
CC malignant cells from bone marrow transplants. AAZ25812-Z26825 represent
CC human polymorphic sites described in the method of the invention

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XX
SQ   Sequence 21 BP; 19 A; 1 C; 1 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              |||||||||||||| ||| ||
Db         21 TTTTTTTTTTTTTTCTTTGTT 1


RESULT 1698
AAF98936
ID   AAF98936 standard; DNA; 22 BP.
XX
AC   AAF98936;
XX
DT   12-JUN-2001  (first entry)
XX
DE   Immunostimulatory nucleic acid #52.
XX
KW   Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW   immunostimulatory; tumour; viral infection; bacterial infection;
KW   fungal infection; parasitic infection; cancer; asthma;
KW   infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS   Synthetic.
XX
PN   WO200122972-A2.
XX
PD   05-APR-2001.
XX
PF   25-SEP-2000; 2000WO-US026383.
XX
PR   25-SEP-1999;   99US-0156113P.
PR   27-SEP-1999;   99US-0156135P.
PR   23-AUG-2000; 2000US-0227436P.
XX
PA   (IOWA ) UNIV IOWA RES FOUND.
PA   (COLE-) COLEY PHARM GMBH.
XX
PI   Krieg AM,  Schetter C,  Vollmer J;
XX
DR   WPI; 2001-273485/28.
XX
PT   Vaccinating against tumors, infectious diseases, allergies and asthma
PT   using immunostimulatory Py-rich and TG nucleic acids.
XX
PS   Disclosure; Page 39; 338pp; English.
XX
CC   The present invention relates to a method for stimulating an immune
CC   response. The method comprises administering an immunostimulatory nucleic
CC   acid to a non-rodent subject in sufficient quantity to stimulate an
CC   immune response. The present sequence is one such immunostimulatory
CC   nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC   (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC   against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC   and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC   haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC   staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC   also useful for preventing cancer, asthma, infectious disease, allergy or
CC   immune deficiency. The present sequence can also be used to redirect a
CC   Th2 to a Th1 immune response and to activate immune cells. Note: the
CC   present sequence may have a phosphorothioate backbone
XX
SQ   Sequence 22 BP; 0 A; 0 C; 2 G; 20 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 22;
  Best Local Similarity   90.5%;  Pred. No. 1.3e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              |||||||| ||||||| ||||
Db          1 TTTTTTTTGTTTTTTTGTTTT 21


RESULT 1699
ABS77577
ID   ABS77577 standard; DNA; 22 BP.
XX
AC   ABS77577;
XX
DT   13-DEC-2002  (first entry)
XX
DE   Angiogenesis inhibitory oligonucleotide #61.
XX
KW   Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW   tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW   diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW   corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW   rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW   plaque neovascularisation; telangiectasia; haemophiliac joint;
KW   angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW   scleroderma; hypertrophic scar.
XX
OS   Synthetic.
XX
PN   WO200253141-A2.
XX
PD   11-JUL-2002.
XX
PF   14-DEC-2001; 2001WO-US048458.
XX
PR   14-DEC-2000; 2000US-0255534P.
XX
PA   (COLE-) COLEY PHARM GROUP INC.
XX
PI   Bratzler RL;
XX
DR   WPI; 2002-566690/60.
XX
PT   Inhibiting angiogenesis in a subject, involves administering at least one
PT   antiangiogenic nucleic acid molecule to the subject.
XX
PS   Claim 2; Page 20; 276pp; English.
XX
CC   The invention relates to inhibiting angiogenesis in a subject, comprising
CC   administering at least one antiangiogenic nucleic acid molecule. Also
CC   included is a kit comprising a first container housing the antiangiogenic
CC   nucleic acids, and instructions for administering them to a subject
CC   having a condition characterised by unwanted angiogenesis. The method is
CC   useful for inhibiting angiogenesis associated with solid tumour growth,
CC   tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC   diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC   corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC   rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC   neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,
CC   wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC   hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC   acid of the invention
XX
SQ   Sequence 22 BP; 0 A; 0 C; 2 G; 20 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 22;
  Best Local Similarity   90.5%;  Pred. No. 1.3e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              |||||||| ||||||| ||||
Db          1 TTTTTTTTGTTTTTTTGTTTT 21


RESULT 1700
ACD99369
ID   ACD99369 standard; DNA; 22 BP.
```

XX
AC ACD99369;
XX
DT 25-SEP-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #55.
XX
KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS Synthetic.
XX
PN US2003050268-A1.
XX
PD 13-MAR-2003.
XX
PF 29-MAR-2002; 2002US-00112653.
XX
PR 29-MAR-2001; 2001US-0279642P.
XX
PA (KRIE/) KRIEG A M.
PA (BERG/) BERG D J.
XX
PI Krieg AM, Berg DJ;
XX
DR WPI; 2003-521815/49.
XX
PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT disease by administering an immunostimulatory nucleic acid.
XX
PS Disclosure; Page 10; 229pp; English.
XX
CC The invention describes a method of treating non-allergic inflammatory
CC disease comprising administering to a subject having or at risk of
CC developing a non-allergic inflammatory disease an immunostimulatory
CC nucleic acid for prevention or treatment of the disease. The method is
CC useful for treating non-allergic inflammatory diseases, such as
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC This sequence represents an immunostimulatory nucleic acid
XX
SQ Sequence 22 BP; 0 A; 0 C; 2 G; 20 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.8; DB 1; Length 22;
Best Local Similarity 90.5%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2186
||||||| ||||||| ||||
Db 1 TTTTTTTTGTTTTTTTGTTTT 21

RESULT 1701
ADB36438
ID ADB36438 standard; DNA; 22 BP.
XX
AC ADB36438;
XX
DT 04-DEC-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #52.
XX
KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW hypo-responsive subject; immunostimulatory.
XX
OS Synthetic.
XX
PN US2003087848-A1.
XX
PD 08-MAY-2003.
XX
PF 02-FEB-2001; 2001US-00776479.
XX
PR 03-FEB-2000; 2000US-0179991P.
XX
PA (BRAT/) BRATZLER R L.
PA (PETE/) PETERSEN D M.
PA (FOUR/) FOURON Y.
XX
PI Bratzler RL, Petersen DM, Fouron Y;
XX
DR WPI; 2003-657977/62.
XX
PT Treating and/or preventing allergy or asthma using an immunostimulatory
PT nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS Claim 10; Page 6; 221pp; English.
XX
CC The invention relates to a method of treating or preventing allergy or
CC asthma which comprises administering to a subject a poly-G nucleic acid
CC in an aerosol formulation. The methods and compositions of the present
CC invention are useful for diagnosing and/or treating asthma and allergy
CC especially in a hypo-responsive subject. The present sequence represents
CC an immunostimulatory nucleic acid of the invention.
XX
SQ Sequence 22 BP; 0 A; 0 C; 2 G; 20 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.8; DB 1; Length 22;
Best Local Similarity 90.5%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2186
||||||| ||||||| ||||
Db 1 TTTTTTTTGTTTTTTTGTTTT 21

RESULT 1702
AAH91823
ID AAH91823 standard; DNA; 23 BP.
XX
AC AAH91823;
XX
DT 09-OCT-2001 (first entry)
XX
DE Human inflammatory bowel disease associated polymorphic site #898.
XX
KW Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
KW chromosome 5q31-33; forensic test; gene therapy; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT misc_feature 11
FT /*tag= a
FT /note= "SNP, optionally T or A at this position"
XX
PN WO200142511-A2.
XX
PD 14-JUN-2001.
XX
PF 11-DEC-2000; 2000WO-US033632.
XX
PR 10-DEC-1999; 99US-0170257P.
PR 10-APR-2000; 2000US-0196046P.
XX
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
PA (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.
XX
PI Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K;
XX
DR WPI; 2001-367874/38.
XX

```
PT   Testing for the presence of polymorphisms associated with inflammatory
PT   bowel disease, using a hybridization assay.
XX
PS   Claim 1; Page 76; 463pp; English.
XX
CC   The present invention describes a method for detecting the presence of
CC   polymorphisms associated with inflammatory bowel diseases such as
CC   ulcerative colitis and Crohn's disease. The methods can be used to detect
CC   the presence of genetic polymorphisms associated with inflammatory bowel
CC   disease and correlating their occurrence with disease states. They may be
CC   used in this way for phenotypic correlations, forensics, paternity
CC   testing, medicine and genetic analysis. The present sequence is a
CC   polymorphic site described in the exemplification of the invention
XX
SQ   Sequence 23 BP; 0 A; 4 C; 0 G; 18 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 23;
  Best Local Similarity   86.4%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2157 TTTTTCTCCTTTTTTTTTTTT 2178
              || |||| | ||||||||||||
Db          2 TTCTTCTTCNTTTTTTTTTTT 23


RESULT 1703
AAF98935
ID   AAF98935 standard; DNA; 24 BP.
XX
AC   AAF98935;
XX
DT   12-JUN-2001  (first entry)
XX
DE   Immunostimulatory nucleic acid #51.
XX
KW   Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW   immunostimulatory; tumour; viral infection; bacterial infection;
KW   fungal infection; parasitic infection; cancer; asthma;
KW   infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS   Synthetic.
XX
PN   WO200122972-A2.
XX
PD   05-APR-2001.
XX
PF   25-SEP-2000; 2000WO-US026383.
XX
PR   25-SEP-1999;   99US-0156113P.
PR   27-SEP-1999;   99US-0156135P.
PR   23-AUG-2000; 2000US-0227436P.
XX
PA   (IOWA ) UNIV IOWA RES FOUND.
PA   (COLE-) COLEY PHARM GMBH.
XX
PI   Krieg AM,  Schetter C,  Vollmer J;
XX
DR   WPI; 2001-273485/28.
XX
PT   Vaccinating against tumors, infectious diseases, allergies and asthma
PT   using immunostimulatory Py-rich and TG nucleic acids.
XX
PS   Disclosure; Page 39; 338pp; English.
XX
CC   The present invention relates to a method for stimulating an immune
CC   response. The method comprises administering an immunostimulatory nucleic
CC   acid to a non-rodent subject in sufficient quantity to stimulate an
CC   immune response. The present sequence is one such immunostimulatory
CC   nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC   (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC   against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC   and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC   haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC   staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC   also useful for preventing cancer, asthma, infectious disease, allergy or
CC   immune deficiency. The present sequence can also be used to redirect a
CC   Th2 to a Th1 immune response and to activate immune cells. Note: the
CC   present sequence may have a phosphorothioate backbone
XX
SQ   Sequence 24 BP; 0 A; 0 C; 3 G; 21 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 24;
  Best Local Similarity   90.5%;  Pred. No. 1.6e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||| ||||||| |||||
Db          4 TTTTTTGTTTTTTTGTTTTT 24


RESULT 1704
AAI64873
ID   AAI64873 standard; DNA; 24 BP.
XX
AC   AAI64873;
XX
DT   04-DEC-2001  (first entry)
XX
DE   Human serine/threonine protein kinase 48 cDNA PCR primer #2.
XX
KW   Human; serine/threonine protein kinase 48; cancer; HIV infection;
KW   gene therapy; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1300831-A.
XX
PD   27-JUN-2001.
XX
PF   22-DEC-1999;   99CN-00125686.
XX
PR   22-DEC-1999;   99CN-00125686.
XX
PA   (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2001-530471/59.
XX
PT   New human serine/threonine protein kinase 48 and its encoding
PT   polynucleotide, useful for treating cancer and human immunodeficiency
PT   virus infection.
XX
PS   Example 3; Page 17(Disclosure); 33pp; Chinese.
XX
CC   The present invention provides the protein and coding sequences of human
CC   serine/threonine protein kinase 48. The sequences can be used in the
CC   treatment of cancer and HIV infection. The present sequence is a PCR
CC   primer for the coding sequence of the invention
XX
SQ   Sequence 24 BP; 3 A; 1 C; 3 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 24;
  Best Local Similarity   90.5%;  Pred. No. 1.6e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAACT 2190
              |||||||||||||||| ||| |
Db          1 TTTTTTTTTTTTTTTGTAAAT 21


RESULT 1705
AAI64873/c
ID   AAI64873 standard; DNA; 24 BP.
XX
AC   AAI64873;
```

XX
DT 04-DEC-2001 (first entry)
XX
DE Human serine/threonine protein kinase 48 cDNA PCR primer #2.
XX
KW Human; serine/threonine protein kinase 48; cancer; HIV infection;
KW gene therapy; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN CN1300831-A.
XX
PD 27-JUN-2001.
XX
PF 22-DEC-1999; 99CN-00125686.
XX
PR 22-DEC-1999; 99CN-00125686.
XX
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2001-530471/59.
XX
PT New human serine/threonine protein kinase 48 and its encoding
PT polynucleotide, useful for treating cancer and human immunodeficiency
PT virus infection.
XX
PS Example 3; Page 17(Disclosure); 33pp; Chinese.
XX
CC The present invention provides the protein and coding sequences of human
CC serine/threonine protein kinase 48. The sequences can be used in the
CC treatment of cancer and HIV infection. The present sequence is a PCR
CC primer for the coding sequence of the invention
XX
SQ Sequence 24 BP; 3 A; 1 C; 3 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.8; DB 1; Length 24;
Best Local Similarity 90.5%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2782 ATTGAAAAAAAAAAAAAAAA 2802
||| | ||||||||||||||||
Db 21 ATTTACAAAAAAAAAAAAAA 1

RESULT 1706
AAI65187
ID AAI65187 standard; DNA; 24 BP.
XX
AC AAI65187;
XX
DT 12-DEC-2001 (first entry)
XX
DE Human gap connexin 10 PCR primer #1.
XX
KW Human; gap connexin 10; cytostatic; virucidal; immunomodulatory;
KW antiinflammatory; haemostatic; gene therapy; malignant tumour;
KW PCR primer; haemopathy; HIV infection; immunological disease;
KW inflammation; ss.
XX
OS Homo sapiens.
XX
PN WO200172818-A1.
XX
PD 04-OCT-2001.
XX
PF 26-MAR-2001; 2001WO-CN000511.
XX
PR 29-MAR-2000; 2000CN-00115275.
XX
PA (BIOW-) BIOWINDOW GENE DEV INC.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2001-602853/68.
XX
PT Human gap connexin 10 polynucleotide and polypeptide, useful in diagnosis
PT and treatment of malignant tumor, hemopathy, HIV infection, immunological
PT diseases and various inflammatory diseases.
XX
PS Example 2; Page 12; 36pp; Chinese.
XX
CC The present invention relates to human gap connexin 10 (see AAI65186 and
CC AAG78856). The protein and its coding sequence are useful in the
CC diagnosis and treatment of malignant tumours, haemopathy, HIV infection,
CC immunological diseases and various inflammations. The present sequence is
CC a PCR primer which was used in an example from the present invention
XX
SQ Sequence 24 BP; 2 A; 0 C; 3 G; 19 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.8; DB 1; Length 24;
Best Local Similarity 90.5%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2186
||| ||||||||||||||||
Db 3 TTTAATTTTTTTTTTTTTTT 23

RESULT 1707
ABS77576
ID ABS77576 standard; DNA; 24 BP.
XX
AC ABS77576;
XX
DT 13-DEC-2002 (first entry)
XX
DE Angiogenesis inhibitory oligonucleotide #60.
XX
KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW plaque neovascularisation; telangiectasia; haemophiliac joint;
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW scleroderma; hypertrophic scar.
XX
OS Synthetic.
XX
PN WO200253141-A2.
XX
PD 11-JUL-2002.
XX
PF 14-DEC-2001; 2001WO-US048458.
XX
PR 14-DEC-2000; 2000US-0255534P.
XX
PA (COLE-) COLEY PHARM GROUP INC.
XX
PI Bratzler RL;
XX
DR WPI; 2002-566690/60.
XX
PT Inhibiting angiogenesis in a subject, involves administering at least one
PT antiangiogenic nucleic acid molecule to the subject.
XX
PS Claim 2; Page 20; 276pp; English.
XX
CC The invention relates to inhibiting angiogenesis in a subject, comprising
CC administering at least one antiangiogenic nucleic acid molecule. Also
CC included is a kit comprising a first container housing the antiangiogenic
CC nucleic acids, and instructions for administering them to a subject
CC having a condition characterised by unwanted angiogenesis. The method is
CC useful for inhibiting angiogenesis associated with solid tumour growth,

```
CC   tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC   diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC   corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC   rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC   neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,
CC   wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC   hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC   acid of the invention
XX
SQ   Sequence 24 BP; 0 A; 0 C; 3 G; 21 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 24;
  Best Local Similarity   90.5%;  Pred. No. 1.6e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||| ||||||| |||||
Db          4 TTTTTTTGTTTTTTTGTTTTT 24


RESULT 1708
ABA01048
ID   ABA01048 standard; DNA; 24 BP.
XX
AC   ABA01048;
XX
DT   24-JAN-2002  (first entry)
XX
DE   Human sodium pump subunit 12 PCR primer 1.
XX
KW   Human; sodium pump; subunit 12; cytostatic; virucide; immunomodulator;
KW   antiinflammatory; haemostatic; gene therapy; cancer; haemopathy;
KW   human immunodeficiency virus; HIV; infection; immunological disease;
KW   inflammatory disorder; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200177162-A1.
XX
PD   18-OCT-2001.
XX
PF   26-MAR-2001; 2001WO-CN000422.
XX
PR   27-MAR-2000; 2000CN-00115156.
XX
PA   (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-017442/02.
XX
PT   Human sodium pump subunit 12 of sodium pump and encoded polynucleotide,
PT   used in diagnosis and treatment of malignant tumors, hemopathy, human
PT   immunodeficiency virus infection, immunological diseases and
PT   inflammation.
XX
PS   Example 2; Page 16; 35pp; Chinese.
XX
CC   The invention relates to an isolated polypeptide of human sodium pump
CC   subunit 12 comprising a 110 residue amino acid sequence, fully defined in
CC   the specification, or its fragment, analogue or derivative. The
CC   polypeptide is used in the diagnosis and treatment of malignant tumours,
CC   haemopathy, human immunodeficiency virus (HIV) infection, immunological
CC   diseases and various inflammatory disorders. The present sequence is a
CC   primer used to isolate a polynucleotide encoding the polypeptide of the
CC   invention
XX
SQ   Sequence 24 BP; 0 A; 0 C; 4 G; 20 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 24;
  Best Local Similarity   90.5%;  Pred. No. 1.6e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||| |||||||| ||||||||
Db          2 TTTGTTTTTTTTGTTTTTTT 22


RESULT 1709
ABN86902
ID   ABN86902 standard; DNA; 24 BP.
XX
AC   ABN86902;
XX
DT   23-JUL-2002  (first entry)
XX
DE   Human macroprotein 21.78 PCR primer 2 SEQ ID NO:4.
XX
KW   Human; macroprotein 21.78; embryo development teratogenesis; tumour;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1331245-A.
XX
PD   16-JAN-2002.
XX
PF   30-JUN-2000; 2000CN-00116981.
XX
PR   30-JUN-2000; 2000CN-00116981.
XX
PA   (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-292882/34.
XX
PT   New polypeptide-human macroprotein 21.78 and polynucleotide encoding it,
PT   for treating diseases such as embryo development teratogenesis and tumor.
XX
PS   Example 2; Page 19 (Disclosure); 35pp; Chinese.
XX
CC   The present invention describes human macroprotein 21.78 (I). Also
CC   described is a process for preparing (I) using DNA recombination
CC   techniques. (I) and the polynucleotide sequence encoding it (II) can be
CC   used in the treatment of diseases such as embryo development
CC   teratogenesis and tumours. The present sequence represents a PCR primer
CC   for (I), which is used in an example from the present invention
XX
SQ   Sequence 24 BP; 0 A; 1 C; 2 G; 21 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 24;
  Best Local Similarity   90.5%;  Pred. No. 1.6e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              |||||| ||||| ||||||||
Db          1 TTTTTTGTTTTTGTTTTTTT 21


RESULT 1710
ACD99368
ID   ACD99368 standard; DNA; 24 BP.
XX
AC   ACD99368;
XX
DT   25-SEP-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #54.
XX
KW   Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW   antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW   psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW   inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS   Synthetic.
```

XX
PN US2003050268-A1.
XX
PD 13-MAR-2003.
XX
PF 29-MAR-2002; 2002US-00112653.
XX
PR 29-MAR-2001; 2001US-0279642P.
XX
PA (KRIE/) KRIEG A M.
PA (BERG/) BERG D J.
XX
PI Krieg AM, Berg DJ;
XX
DR WPI; 2003-521815/49.
XX
PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT disease by administering an immunostimulatory nucleic acid.
XX
PS Disclosure; Page 10; 229pp; English.
XX
CC The invention describes a method of treating non-allergic inflammatory
CC disease comprising administering to a subject having or at risk of
CC developing a non-allergic inflammatory disease an immunostimulatory
CC nucleic acid for prevention or treatment of the disease. The method is
CC useful for treating non-allergic inflammatory diseases, such as
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC This sequence represents an immunostimulatory nucleic acid
XX
SQ Sequence 24 BP; 0 A; 0 C; 3 G; 21 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.8; DB 1; Length 24;
Best Local Similarity 90.5%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2186
||||||| ||||||| |||||
Db 4 TTTTTTTGTTTTTTTGTTTT 24

RESULT 1711
ADB36437
ID ADB36437 standard; DNA; 24 BP.
XX
AC ADB36437;
XX
DT 04-DEC-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #51.
XX
KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW hypo-responsive subject; immunostimulatory.
XX
OS Synthetic.
XX
PN US2003087848-A1.
XX
PD 08-MAY-2003.
XX
PF 02-FEB-2001; 2001US-00776479.
XX
PR 03-FEB-2000; 2000US-0179991P.
XX
PA (BRAT/) BRATZLER R L.
PA (PETE/) PETERSEN D M.
PA (FOUR/) FOURON Y.
XX
PI Bratzler RL, Petersen DM, Fouron Y;
XX
DR WPI; 2003-657977/62.
XX
PT Treating and/or preventing allergy or asthma using an immunostimulatory
PT nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS Disclosure; Page 6; 221pp; English.
XX
CC The invention relates to a method of treating or preventing allergy or
CC asthma which comprises administering to a subject a poly-G nucleic acid
CC in an aerosol formulation. The methods and compositions of the present
CC invention are useful for diagnosing and/or treating asthma and allergy
CC especially in a hypo-responsive subject. The present sequence represents
CC an immunostimulatory nucleic acid of the invention.
XX
SQ Sequence 24 BP; 0 A; 0 C; 3 G; 21 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.8; DB 1; Length 24;
Best Local Similarity 90.5%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2186
||||||| ||||||| |||||
Db 4 TTTTTTTGTTTTTTTGTTTT 24

RESULT 1712
AAV30657/c
ID AAV30657 standard; DNA; 25 BP.
XX
AC AAV30657;
XX
DT 13-AUG-1998 (first entry)
XX
DE Telomerase reverse transcriptase PCR primer TCP1.62.
XX
KW Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis; prognosis;
KW cell proliferation; cancer; ageing; ribonucleoprotein; PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN GB2317891-A.
XX
PD 08-APR-1998.
XX
PF 01-OCT-1997; 97GB-00020890.
XX
PR 01-OCT-1996; 96US-00724643.
PR 18-APR-1997; 97US-00844419.
PR 25-APR-1997; 97US-00846017.
PR 06-MAY-1997; 97US-00851843.
PR 09-MAY-1997; 97US-00854050.
PR 14-AUG-1997; 97US-00911312.
PR 14-AUG-1997; 97US-00912951.
PR 14-AUG-1997; 97US-00915503.
XX
PA (GERO-) GERON CORP.
PA (UYTE-) UNIV TECHNOLOGY CORP.
XX
PI Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;
PI Andrews WH;
XX
DR WPI; 1998-171633/16.
XX
PT Pure and recombinant human Telomerase Reverse Transcriptase and its
PT variants - are useful in the diagnosis, prognosis and treatment of cell
PT proliferation conditions especially cancer and ageing.
XX
PS Disclosure; Page 41; 387pp; English.
XX
CC The present sequence represents a PCR primer from the present invention
CC which describes human telomerase reverse transcriptase (hTRT). The
CC present invention also describes the following methods: (A) determining
CC whether a test compound is a modulator of hTRT, by detecting the change
CC in hTRT recombinant protein or polynucleotide, on administration of the

```
CC   compound; (B) preparation of recombinant telomerase by contacting a
CC   protein preparation of hTRT with a telomerase RNA component; (C)
CC   detection of the hTRT RNA or protein in a sample by binding a relevant
CC   probe to the sample and detecting the complex formed or in the case of
CC   RNA detection, amplifying the product and correlating the presence of
CC   complex or amplification product with presence of hTRT in the sample; and
CC   (D) increasing the proliferation of a vertebrate cell by increasing hTRT
CC   expression; and (E) the use of an agent that causes an increase in cell
CC   vertebrate cell proliferation to create a medicament that inhibits
CC   ageing. A protein preparation of hTRT and the polynucleotide encoding
CC   hTRT can be used in the manufacture of medicaments for inhibiting the
CC   effect of ageing or cancer. Inhibitors of telomerase activity can be used
CC   to treat conditions that are associated with high telomerase activity. A
CC   protein preparation of hTRT can also be used in the new methods
XX
SQ   Sequence 25 BP; 6 A; 11 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.7e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        789 CCTGTCAGAAGGAGCTGGTGG 809
              |||| | ||||||||||||||||
Db         21 CCTGCCTGAAGGAGCTGGTGG 1


RESULT 1713
AAC96118
ID   AAC96118 standard; DNA; 25 BP.
XX
AC   AAC96118;
XX
DT   26-FEB-2001  (first entry)
XX
DE   16s rRNA gene PCR primer #85.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 45; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 3 A; 2 C; 3 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.7e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAACT 2190
              |||||||||||||||  ||||
Db          1 TTTTTTTTTTTTTTTGGAACT 21


RESULT 1714
AAC95708/c
ID   AAC95708 standard; DNA; 25 BP.
XX
AC   AAC95708;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DQA1 gene PCR primer #5.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 38; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 2 A; 6 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.7e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAA 2799
              ||| ||| ||||||||||||||
Db         21 AGACTTGGAAAAAAAAAAAAA 1


RESULT 1715
AAH38199
ID   AAH38199 standard; DNA; 25 BP.
XX
AC   AAH38199;
XX
DT   14-AUG-2001  (first entry)
XX
```

```
DE   SNP specific SNPE primer SEQ ID 995.
XX
KW   Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW   SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
KW   Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW   polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW   acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW   inflammation; forensic investigation; paternity analysis; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200129262-A2.
XX
PD   26-APR-2001.
XX
PF   13-OCT-2000; 2000WO-US028436.
XX
PR   15-OCT-1999;   99US-0160096P.
XX
PA   (ORCH-) ORCHID BIOSCIENCES INC.
XX
PI   Picoult-Newburg L,  Pohl M;
XX
DR   WPI; 2001-290930/30.
XX
PT   New genotyping oligonucleotide, useful for detecting the presence,
PT   absence or identity of single polynucleotide polymorphism in a nucleic
PT   acid sample.
XX
PS   Claim 1; Page 55; 83pp; English.
XX
CC   Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC   primer extension (SNPE) primers, and the sequences of regions flanking
CC   sites of single nucleotide polymorphisms SNPs. The present invention
CC   includes kits for determining the presence or absence of a SNP, using the
CC   oligonucleotides of the invention. The PCR primers are used to amplify a
CC   SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC   The oligonucleotides are useful for genotyping a nucleic acid sample by
CC   performing a single-nucleotide primer extension reaction. The
CC   oligonucleotides are useful for determining the presence, absence or
CC   identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC   assess by association analysis the genotype of an individual or group of
CC   individuals, having a pathological phenotypic trait suspected of being
CC   caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC   agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC   dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC   osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC   traits also include symptoms of or susceptibility to multifactorial
CC   disease of which a component is or may be genetic such as autoimmune
CC   diseases, including, rheumatoid arthritis, multiple sclerosis,
CC   inflammation, cancer, nervous system diseases and infection by pathogenic
CC   microorganism. The method is also useful in forensic investigations and
CC   paternity analysis. The present sequence represents a single nucleotide
CC   primer extension (SNPE) primer specific for a human SNP containing DNA
CC   sequence
XX
SQ   Sequence 25 BP; 1 A; 2 C; 1 G; 21 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.7e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTT 2186
              |||||| ||||| ||||||||
Db          5 TTTTTTCTTTTTCTTTTTTTT 25


RESULT 1716
ABS98709
ID   ABS98709 standard; DNA; 25 BP.
XX
AC   ABS98709;
XX
DT   18-DEC-2002  (first entry)
XX
DE   Human p53 PCR primer #5.
XX
KW   PCR; ss; primer; electronic microarray; primer extension;
KW   RNA polymerase recognition site; oncogenesis; cell growth;
KW   differentiation.
XX
OS   Homo sapiens.
XX
PN   US2002119484-A1.
XX
PD   29-AUG-2002.
XX
PF   12-FEB-2002; 2002US-00075579.
XX
PR   07-JUL-1994;   94US-00271882.
PR   24-JAN-2000; 2000US-00490965.
PR   09-NOV-2000; 2000US-00710200.
XX
PA   (NANO-) NANOGEN INC.
XX
PI   Weidenhammer EM,  Xu X,  Heller MJ,  Kahl BF;
XX
DR   WPI; 2002-750052/81.
XX
PT   Determining mRNA expression in sample, by producing shortened amplicons
PT   from mRNA isolated from sample, electronically hybridizing amplicons to
PT   probes bound to a support, and detecting the amount of hybridized
PT   amplicons.
XX
PS   Example 6; Page 13; 37pp; English.
XX
CC   The invention relates to detecting (M1) relative amounts of at least 2
CC   mRNA sequences in a biological sample (BS), comprises isolating mRNA from
CC   BS, amplifying at least 2 mRNA transcripts from each BS to produce
CC   amplicons (A) less than about 300 bases in length, electronically
CC   hybridising (A) to at least 2 probes bound to a support at predetermined
CC   locations, and detecting amounts of each (A) hybridised to the bound
CC   probes. Also included are (1) preserving (M2) and reusing a nucleic acid
CC   library produced from a patient biological sample, by: (a) isolating mRNA
CC   from a patient biological sample; (b) reverse- transcribing the mRNA to
CC   produce a cDNA library; (c) amplifying the cDNA library by a DNA
CC   polymerase reaction utilising at least one chimaeric primer comprising a
CC   RNA polymerase recognition site upstream of a sequence specific for a
CC   mRNA transcript of interest and a fill-in primer for the complementary
CC   nucleic acid strand chosen from sequence specific primers and random
CC   primers (at least 1 of the primers used is chosen from 5' affinity-moiety
CC   labeled chimaeric primers and 5' affinity-moiety labeled sequence
CC   specific fill-in primers); (d) binding the amplification products to a
CC   solid support coated with an affinity-binding moiety; (e) utilising the
CC   bound amplification products as a template for an in vitro transcription
CC   reaction; (f) separating the in vitro transcription products from the
CC   amplification products bound to the solid support; and (g) utilising the
CC   bound amplification products from step (h) as a template for at least one
CC   additional in vitro transcription reaction (the amount of in vitro
CC   transcription product produced is not significantly less than that
CC   produced in step (e)); (2) detecting (M3) the extent of hybridisation of
CC   a nucleic acid in a sample to a probe nucleic acid sequence; and (3)
CC   providing (M4) an internal control for an individual test site in a
CC   nucleic acid hybridisation reaction assay to determine the presence of at
CC   least one nucleic aid sequence of interest in at least one nucleic acid
CC   containing sample (the nucleic acid hybridisation assay is performed on
CC   an electronically controlled microarray comprising at least two test
CC   sites). M1 Is useful for detecting the relative amounts of at least two
CC   mRNA sequences in a biological sample. M1 is useful for determining the
CC   level of mRNA expression in the cells of a biological sample, for
CC   gathering data to correlate difference in expression patterns with
CC   specific physiological and/or pathological states, for studying
CC   expression of genes in organisms under various physiological conditions,
CC   for studying the role of gene expression in diseases and oncogenesis,
CC   physio-chemical cellular responses to stimuli, and cell growth and
CC   differentiation, for titrating the amount of amplified mRNA present in a
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CC   sample, and to compare, side by side, the expression levels of mRNA in a
CC   cell type that has undergone two physical or chemical stimuli. The method
CC   uses primer extension and an active electronic microarray. The present
CC   sequence is a gene specific primer used in the method of the invention
XX
SQ   Sequence 25 BP; 5 A; 6 C; 12 G; 2 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.7e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        487 GAGCCAGGAGGGAGCGGGGCT 507
              ||||||||  ||||||  |||||
Db          1 GAGCCAGGGGGGAGCAGGGCT 21


RESULT 1717
AAD44166
ID   AAD44166 standard; DNA; 25 BP.
XX
AC   AAD44166;
XX
DT   13-DEC-2002  (first entry)
XX
DE   Probe 261 targetted to human tumour suppressor p53 gene.
XX
KW   Target nucleotide; analyte; signal; drug discovery; human; probe; ss.
XX
OS   Homo sapiens.
XX
PN   US2002051973-A1.
XX
PD   02-MAY-2002.
XX
PF   17-SEP-1999;   99US-00398399.
XX
PR   17-SEP-1999;   99US-00398399.
XX
PA   (DELE/) DELENSTARR G C.
PA   (LEFK/) LEFKOWITZ S M.
PA   (LUEB/) LUEBKE K J.
PA   (OVER/) OVERMAN L B.
PA   (SAMP/) SAMPRAS N M.
PA   (SAMP/) SAMPSON J R.
PA   (WOLB/) WOLBER P K.
XX
PI   Delenstarr GC,  Lefkowitz SM,  Luebke KJ,  Overman LB,  Sampras NM;
PI   Sampson JR,  Wolber PK;
XX
DR   WPI; 2002-443693/47.
XX
PT   Detecting a target nucleotide sequence in an analyte, for use in e.g.
PT   drug discovery, comprises using a set of features having
PT   oligophosphodiester probes, and subtracting a background signal from an
PT   observed signal.
XX
PS   Claim 5; Page 19; 35pp; English.
XX
CC   The invention relates to a method for detecting the presence and/or
CC   amount of a target nucleotide sequence in an analyte. The method
CC   comprising: contacting an aliquot of an analyte suspected of containing
CC   the target sequence with a set of features comprising oligophosphodiester
CC   probes; and subtracting a background signal from an observed signal to
CC   determine the presence and/or amount of the target sequence in the
CC   analyte. The method is used to detect the presence and/or amount of a
CC   target sequence in an analyte. The method is used for estimating
CC   background noise in a nucleic acid hybridisation assay and for validating
CC   a test-background feature. The method is useful in chemical, biological
CC   medical and diagnostic techniques, and for drug discovery. The present
CC   sequence is a probe targetted to human tumour suppressor p53 gene
XX
SQ   Sequence 25 BP; 5 A; 6 C; 13 G; 1 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.7e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        487 GAGCCAGGAGGGAGCGGGGCT 507
              ||||||||  ||||||  |||||
Db          2 GAGCCAGGGGGGAGCAGGGCT 22


RESULT 1718
ABS76275
ID   ABS76275 standard; DNA; 25 BP.
XX
AC   ABS76275;
XX
DT   27-DEC-2002  (first entry)
XX
DE   Human PAPP-E exon 7 associated 25-mer SEQ ID 1801.
XX
KW   PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW   contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW   dysgenetic pregnancy; primer; ss.
XX
OS   Homo sapiens.
XX
PN   US2002102252-A1.
XX
PD   01-AUG-2002.
XX
PF   06-APR-2001; 2001US-00827998.
XX
PR   26-MAY-2000; 2000US-0207456P.
XX
PA   (GUYY/) GU Y.
PA   (SHAN/) SHANNON M E.
XX
PI   Gu Y,  Shannon ME;
XX
DR   WPI; 2002-697817/75.
XX
PT   New isolated nucleic acid encoding an isoform of human pregnancy
PT   associated plasma protein E, for preventing or aborting pregnancy.
XX
PS   Example 2; Page 312; 353pp; English.
XX
CC   This invention describes a novel isolated nucleic acid that encodes one
CC   of three new isoforms of human pregnancy associated plasma protein E,
CC   hPAPP-E. The products of the invention have abortive and contraceptive
CC   activity and can be used for gene therapy or in a vaccine. The nucleic
CC   acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC   used in pharmaceutical compositions or vaccines for preventing or
CC   aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC   dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC   the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC   antibodies can be used to assess the expression levels of PAPP-E isoform
CC   proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC   antenatally. This sequence represents an oligomer used in scanning the
CC   human PAPP-E genes described in the disclosure of the invention
XX
SQ   Sequence 25 BP; 3 A; 4 C; 7 G; 11 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.7e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2310 AAGCAATTTGTTGCTGCTTGT 2330
              ||||  | ||||||||||||||
Db          2 AAGCCAGTTGTTGCTGCTTGT 22


RESULT 1719
ABS76276
ID   ABS76276 standard; DNA; 25 BP.
```

```
XX
AC   ABS76276;
XX
DT   27-DEC-2002  (first entry)
XX
DE   Human PAPP-E exon 7 associated 25-mer SEQ ID 1802.
XX
KW   PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW   contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW   dysgenetic pregnancy; primer; ss.
XX
OS   Homo sapiens.
XX
PN   US2002102252-A1.
XX
PD   01-AUG-2002.
XX
PF   06-APR-2001; 2001US-00827998.
XX
PR   26-MAY-2000; 2000US-0207456P.
XX
PA   (GUYY/) GU Y.
PA   (SHAN/) SHANNON M E.
XX
PI   Gu Y,  Shannon ME;
XX
DR   WPI; 2002-697817/75.
XX
PT   New isolated nucleic acid encoding an isoform of human pregnancy
PT   associated plasma protein E, for preventing or aborting pregnancy.
XX
PS   Example 2; Page 312; 353pp; English.
XX
CC   This invention describes a novel isolated nucleic acid that encodes one
CC   of three new isoforms of human pregnancy associated plasma protein E,
CC   hPAPP-E. The products of the invention have abortive and contraceptive
CC   activity and can be used for gene therapy or in a vaccine. The nucleic
CC   acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC   used in pharmaceutical compositions or vaccines for preventing or
CC   aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC   dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC   the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC   antibodies can be used to assess the expression levels of PAPP-E isoform
CC   proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC   antenatally. This sequence represents an oligomer used in scanning the
CC   human PAPP-E genes described in the disclosure of the invention
XX
SQ   Sequence 25 BP; 3 A; 5 C; 7 G; 10 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.7e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2310 AAGCAATTTGTTGCTGCTTGT 2330
              |||| | ||||||||||||||||
Db          1 AAGCCAGTTGTTGCTGCTTGT 21


RESULT 1720
ABS76274
ID   ABS76274 standard; DNA; 25 BP.
XX
AC   ABS76274;
XX
DT   27-DEC-2002  (first entry)
XX
DE   Human PAPP-E exon 7 associated 25-mer SEQ ID 1800.
XX
KW   PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW   contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW   dysgenetic pregnancy; primer; ss.
XX
OS   Homo sapiens.
XX
PN   US2002102252-A1.
XX
PD   01-AUG-2002.
XX
PF   06-APR-2001; 2001US-00827998.
XX
PR   26-MAY-2000; 2000US-0207456P.
XX
PA   (GUYY/) GU Y.
PA   (SHAN/) SHANNON M E.
XX
PI   Gu Y,  Shannon ME;
XX
DR   WPI; 2002-697817/75.
XX
PT   New isolated nucleic acid encoding an isoform of human pregnancy
PT   associated plasma protein E, for preventing or aborting pregnancy.
XX
PS   Example 2; Page 312; 353pp; English.
XX
CC   This invention describes a novel isolated nucleic acid that encodes one
CC   of three new isoforms of human pregnancy associated plasma protein E,
CC   hPAPP-E. The products of the invention have abortive and contraceptive
CC   activity and can be used for gene therapy or in a vaccine. The nucleic
CC   acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC   used in pharmaceutical compositions or vaccines for preventing or
CC   aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC   dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC   the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC   antibodies can be used to assess the expression levels of PAPP-E isoform
CC   proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC   antenatally. This sequence represents an oligomer used in scanning the
CC   human PAPP-E genes described in the disclosure of the invention
XX
SQ   Sequence 25 BP; 4 A; 4 C; 7 G; 10 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.7e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2310 AAGCAATTTGTTGCTGCTTGT 2330
              |||| | ||||||||||||||||
Db          3 AAGCCAGTTGTTGCTGCTTGT 23


RESULT 1721
ABS76273
ID   ABS76273 standard; DNA; 25 BP.
XX
AC   ABS76273;
XX
DT   27-DEC-2002  (first entry)
XX
DE   Human PAPP-E exon 7 associated 25-mer SEQ ID 1799.
XX
KW   PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW   contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW   dysgenetic pregnancy; primer; ss.
XX
OS   Homo sapiens.
XX
PN   US2002102252-A1.
XX
PD   01-AUG-2002.
XX
PF   06-APR-2001; 2001US-00827998.
XX
PR   26-MAY-2000; 2000US-0207456P.
XX
PA   (GUYY/) GU Y.
PA   (SHAN/) SHANNON M E.
XX
```

PI Gu Y, Shannon ME;
XX
DR WPI; 2002-697817/75.
XX
PT New isolated nucleic acid encoding an isoform of human pregnancy
PT associated plasma protein E, for preventing or aborting pregnancy.
XX
PS Example 2; Page 311; 353pp; English.
XX
CC This invention describes a novel isolated nucleic acid that encodes one
CC of three new isoforms of human pregnancy associated plasma protein E,
CC hPAPP-E. The products of the invention have abortive and contraceptive
CC activity and can be used for gene therapy or in a vaccine. The nucleic
CC acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC used in pharmaceutical compositions or vaccines for preventing or
CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC antibodies can be used to assess the expression levels of PAPP-E isoform
CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC antenatally. This sequence represents an oligomer used in scanning the
CC human PAPP-E genes described in the disclosure of the invention
XX
SQ Sequence 25 BP; 4 A; 5 C; 7 G; 9 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 1.7e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2310 AAGCAATTTGTTGCTGCTTGT 2330
|||| | ||||||||||||||
Db 4 AAGCCAGTTGTTGCTGCTTGT 24

RESULT 1722
ABS76272
ID ABS76272 standard; DNA; 25 BP.
XX
AC ABS76272;
XX
DT 27-DEC-2002 (first entry)
XX
DE Human PAPP-E exon 7 associated 25-mer SEQ ID 1798.
XX
KW PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW dysgenetic pregnancy; primer; ss.
XX
OS Homo sapiens.
XX
PN US2002102252-A1.
XX
PD 01-AUG-2002.
XX
PF 06-APR-2001; 2001US-00827998.
XX
PR 26-MAY-2000; 2000US-0207456P.
XX
PA (GUYY/) GU Y.
PA (SHAN/) SHANNON M E.
XX
PI Gu Y, Shannon ME;
XX
DR WPI; 2002-697817/75.
XX
PT New isolated nucleic acid encoding an isoform of human pregnancy
PT associated plasma protein E, for preventing or aborting pregnancy.
XX
PS Example 2; Page 311; 353pp; English.
XX
CC This invention describes a novel isolated nucleic acid that encodes one
CC of three new isoforms of human pregnancy associated plasma protein E,
CC hPAPP-E. The products of the invention have abortive and contraceptive
CC activity and can be used for gene therapy or in a vaccine. The nucleic
CC acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC used in pharmaceutical compositions or vaccines for preventing or
CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC antibodies can be used to assess the expression levels of PAPP-E isoform
CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC antenatally. This sequence represents an oligomer used in scanning the
CC human PAPP-E genes described in the disclosure of the invention
XX
SQ Sequence 25 BP; 4 A; 5 C; 6 G; 10 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 1.7e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2310 AAGCAATTTGTTGCTGCTTGT 2330
|||| | ||||||||||||||
Db 5 AAGCCAGTTGTTGCTGCTTGT 25

RESULT 1723
ABK99538
ID ABK99538 standard; DNA; 25 BP.
XX
AC ABK99538;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human p53 gene hybridisation probe #8.
XX
KW Nucleic acid microarray; probe; ss.
XX
OS Homo sapiens.
XX
PN US2002068293-A1.
XX
PD 06-JUN-2002.
XX
PF 02-JUL-2001; 2001US-00899381.
XX
PR 17-SEP-1999; 99US-00398399.
XX
PA (DELE/) DELENSTARR G C.
PA (WOLB/) WOLBER P K.
PA (SANA/) SANA T R.
XX
PI Delenstarr GC, Wolber PK, Sana TR;
XX
DR WPI; 2002-582474/62.
XX
PT Nucleic acid arrays for qualitatively or quantitatively determining the
PT presence of analyte target nucleic acid in a sample comprises both
PT hybridization features and background features.
XX
PS Claim 8; Page 15; 38pp; English.
XX
CC The invention relates to a nucleic acid array (I) comprising at least one
CC hybridisation feature and at least one background feature. (I) is useful
CC for detecting the presence of an analyte nucleic acid in a sample. The
CC detection comprises contacting the nucleic acid array with the sample
CC under stringent hybridisation conditions, subtracting the background
CC signal from the hybridisation signal to obtain a background corrected
CC hybridisation signal and relating the background corrected hybridisation
CC signal to the presence of the analyte target nucleic acid in the sample
CC The method further comprises a labeling step comprising labeling any
CC analyte target nucleic acids present in the sample with a member of a
CC signal producing system prior to contacting the array with the sample.
CC ABK99529-ABK99544 and ABK99549-ABK99578 represent nucleic acid probes of
CC the invention
XX
SQ Sequence 25 BP; 5 A; 6 C; 13 G; 1 T; 0 U; 0 Other;

```
  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.7e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        487 GAGCCAGGAGGGAGCGGGGCT 507
              ||||||| |||||| |||||
Db          2 GAGCCAGGGGGGAGCAGGGCT 22


RESULT 1724
AAD39915
ID   AAD39915 standard; DNA; 25 BP.
XX
AC   AAD39915;
XX
DT   22-OCT-2002  (first entry)
XX
DE   Human PCR primer #5 used for amplifying p53 target gene.
XX
KW   Human; amplicon; electronic hybridisation; gene expression; oncogenesis;
KW   physio-chemical cellular response; stimuli; cell growth; differentiation;
KW   PCR; primer; p53; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Biotinylated"
XX
PN   US6379897-B1.
XX
PD   30-APR-2002.
XX
PF   09-NOV-2000; 2000US-00710200.
XX
PR   09-NOV-2000; 2000US-00710200.
XX
PA   (NANO-) NANOGEN INC.
XX
PI   Weidenhammer EM,  Wang L,  Xu X,  Heller MJ,  Kahl BF;
XX
DR   WPI; 2002-424785/45.
XX
PT   Detecting relative amounts of at least two different mRNAs in biological
PT   samples by electronically hybridizing amplicons to probes, useful to
PT   monitor gene expression in disease and in cell response studies.
XX
PS   Example 6; Col 45; 36pp; English.
XX
CC   The invention relates to a method for detecting the relative amounts of
CC   at least two different mRNA sequences in biological samples. The method
CC   comprising isolating sample mRNA, amplifying at least two mRNAs to
CC   produce amplicons of not more than 300 bases, electronically hybridising
CC   the amplicons to probes bound to a support at predetermined locations and
CC   detecting amounts of hybridised amplicons. The method may be used to
CC   monitor gene expression in the study of disease and oncogenesis, physio-
CC   chemical cellular responses to stimuli and cell growth and
CC   differentiation. The present sequence is a human PCR primer used for
CC   amplifying p53 target gene
XX
SQ   Sequence 25 BP; 5 A; 6 C; 12 G; 2 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.7e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        487 GAGCCAGGAGGGAGCGGGGCT 507
              ||||||| |||||| |||||
Db          1 GAGCCAGGGGGGAGCAGGGCT 21


RESULT 1725
ACD00131
ID   ACD00131 standard; DNA; 25 BP.
XX
AC   ACD00131;
XX
DT   28-JUL-2003  (first entry)
XX
DE   G-protein coupled receptor GPCR-A-1 analysis oligonucleotide #604.
XX
KW   Human; G-protein coupled receptor; GPCR-A-1; cancer; tumour;
KW   G-Protein-Agonist; G-Protein-Antagonist; gene therapy; cytostatic; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003031621-A2.
XX
PD   17-APR-2003.
XX
PF   11-OCT-2002; 2002WO-US032599.
XX
PR   12-OCT-2001; 2001US-0329000P.
XX
PA   (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
XX
PI   Zhang J;
XX
DR   WPI; 2003-381720/36.
XX
PT   New GPCR-A-1 nucleic acid and polypeptide, useful for diagnosing,
PT   investigating and/or treating disorders associated with aberrant
PT   expression or activity of GPCR-A-1, such as tumors and cancers.
XX
PS   Example 2; SEQ ID NO 628; 156pp; English.
XX
CC   The invention describes an isolated nucleic acid encoding a G protein
CC   coupled receptor (GPCR), mutations of which cause cancer, comprising a
CC   2225 or 1921 base pair sequence, or their degenerate variants, encoding a
CC   409 residue amino acid sequence, all given in the specification, with or
CC   without conservative amino acid substitutions, or complements of the
CC   sequence of them. The encoding nucleic acid is not more than 100 kbase in
CC   length. The methods and compositions of the present invention are useful
CC   for diagnosing, investigating and/or treating disorders associated with
CC   aberrant expression or activity of GPCR-A-1, such as tumours and cancers.
CC   This sequence represents an oligonucleotide used to analyse the gene
CC   encoding human G-protein coupled receptor GPCR-A-1
XX
SQ   Sequence 25 BP; 4 A; 4 C; 10 G; 7 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.7e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2105 GGGGGCCTTCTGGTTTTAGGA 2125
              |||| |||||||||| ||||||
Db          4 GGGGACCTTCTGGTCTTAGGA 24


RESULT 1726
ACD00133
ID   ACD00133 standard; DNA; 25 BP.
XX
AC   ACD00133;
XX
DT   28-JUL-2003  (first entry)
XX
DE   G-protein coupled receptor GPCR-A-1 analysis oligonucleotide #606.
XX
KW   Human; G-protein coupled receptor; GPCR-A-1; cancer; tumour;
KW   G-Protein-Agonist; G-Protein-Antagonist; gene therapy; cytostatic; ss.
XX
OS   Homo sapiens.
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XX
PN   WO2003031621-A2.
XX
PD   17-APR-2003.
XX
PF   11-OCT-2002; 2002WO-US032599.
XX
PR   12-OCT-2001; 2001US-0329000P.
XX
PA   (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
XX
PI   Zhang J;
XX
DR   WPI; 2003-381720/36.
XX
PT   New GPCR-A-1 nucleic acid and polypeptide, useful for diagnosing,
PT   investigating and/or treating disorders associated with aberrant
PT   expression or activity of GPCR-A-1, such as tumors and cancers.
XX
PS   Example 2; SEQ ID NO 630; 156pp; English.
XX
CC   The invention describes an isolated nucleic acid encoding a G protein
CC   coupled receptor (GPCR), mutations of which cause cancer, comprising a
CC   2225 or 1921 base pair sequence, or their degenerate variants, encoding a
CC   409 residue amino acid sequence, all given in the specification, with or
CC   without conservative amino acid substitutions, or complements of the
CC   sequence of them. The encoding nucleic acid is not more than 100 kbase in
CC   length. The methods and compositions of the present invention are useful
CC   for diagnosing, investigating and/or treating disorders associated with
CC   aberrant expression or activity of GPCR-A-1, such as tumours and cancers.
CC   This sequence represents an oligonucleotide used to analyse the gene
CC   encoding human G-protein coupled receptor GPCR-A-1
XX
SQ   Sequence 25 BP; 5 A; 4 C; 10 G; 6 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.7e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2105 GGGGGCCTTCTGGTTTTAGGA 2125
              |||| ||||||||| ||||||
Db          2 GGGGACCTTCTGGTCTTAGGA 22


RESULT 1727
ACD00132
ID   ACD00132 standard; DNA; 25 BP.
XX
AC   ACD00132;
XX
DT   28-JUL-2003  (first entry)
XX
DE   G-protein coupled receptor GPCR-A-1 analysis oligonucleotide #605.
XX
KW   Human; G-protein coupled receptor; GPCR-A-1; cancer; tumour;
KW   G-Protein-Agonist; G-Protein-Antagonist; gene therapy; cytostatic; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003031621-A2.
XX
PD   17-APR-2003.
XX
PF   11-OCT-2002; 2002WO-US032599.
XX
PR   12-OCT-2001; 2001US-0329000P.
XX
PA   (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
XX
PI   Zhang J;
XX
DR   WPI; 2003-381720/36.
XX
PT   New GPCR-A-1 nucleic acid and polypeptide, useful for diagnosing,
PT   investigating and/or treating disorders associated with aberrant
PT   expression or activity of GPCR-A-1, such as tumors and cancers.
XX
PS   Example 2; SEQ ID NO 629; 156pp; English.
XX
CC   The invention describes an isolated nucleic acid encoding a G protein
CC   coupled receptor (GPCR), mutations of which cause cancer, comprising a
CC   2225 or 1921 base pair sequence, or their degenerate variants, encoding a
CC   409 residue amino acid sequence, all given in the specification, with or
CC   without conservative amino acid substitutions, or complements of the
CC   sequence of them. The encoding nucleic acid is not more than 100 kbase in
CC   length. The methods and compositions of the present invention are useful
CC   for diagnosing, investigating and/or treating disorders associated with
CC   aberrant expression or activity of GPCR-A-1, such as tumours and cancers.
CC   This sequence represents an oligonucleotide used to analyse the gene
CC   encoding human G-protein coupled receptor GPCR-A-1
XX
SQ   Sequence 25 BP; 4 A; 4 C; 10 G; 7 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.7e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2105 GGGGGCCTTCTGGTTTTAGGA 2125
              |||| ||||||||| ||||||
Db          3 GGGGACCTTCTGGTCTTAGGA 23


RESULT 1728
ACD00130
ID   ACD00130 standard; DNA; 25 BP.
XX
AC   ACD00130;
XX
DT   28-JUL-2003  (first entry)
XX
DE   G-protein coupled receptor GPCR-A-1 analysis oligonucleotide #603.
XX
KW   Human; G-protein coupled receptor; GPCR-A-1; cancer; tumour;
KW   G-Protein-Agonist; G-Protein-Antagonist; gene therapy; cytostatic; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003031621-A2.
XX
PD   17-APR-2003.
XX
PF   11-OCT-2002; 2002WO-US032599.
XX
PR   12-OCT-2001; 2001US-0329000P.
XX
PA   (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
XX
PI   Zhang J;
XX
DR   WPI; 2003-381720/36.
XX
PT   New GPCR-A-1 nucleic acid and polypeptide, useful for diagnosing,
PT   investigating and/or treating disorders associated with aberrant
PT   expression or activity of GPCR-A-1, such as tumors and cancers.
XX
PS   Example 2; SEQ ID NO 627; 156pp; English.
XX
CC   The invention describes an isolated nucleic acid encoding a G protein
CC   coupled receptor (GPCR), mutations of which cause cancer, comprising a
CC   2225 or 1921 base pair sequence, or their degenerate variants, encoding a
CC   409 residue amino acid sequence, all given in the specification, with or
CC   without conservative amino acid substitutions, or complements of the
CC   sequence of them. The encoding nucleic acid is not more than 100 kbase in
CC   length. The methods and compositions of the present invention are useful
CC   for diagnosing, investigating and/or treating disorders associated with
CC   aberrant expression or activity of GPCR-A-1, such as tumours and cancers.
```

```
CC   This sequence represents an oligonucleotide used to analyse the gene
CC   encoding human G-protein coupled receptor GPCR-A-1
XX
SQ   Sequence 25 BP; 4 A; 4 C; 10 G; 7 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.7e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2105 GGGGGCCTTCTGGTTTTAGGA 2125
              |||| ||||||||| ||||||
Db          5 GGGGACCTTCTGGTCTTAGGA 25


RESULT 1729
ACD00134
ID   ACD00134 standard; DNA; 25 BP.
XX
AC   ACD00134;
XX
DT   28-JUL-2003  (first entry)
XX
DE   G-protein coupled receptor GPCR-A-1 analysis oligonucleotide #607.
XX
KW   Human; G-protein coupled receptor; GPCR-A-1; cancer; tumour;
KW   G-Protein-Agonist; G-Protein-Antagonist; gene therapy; cytostatic; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003031621-A2.
XX
PD   17-APR-2003.
XX
PF   11-OCT-2002; 2002WO-US032599.
XX
PR   12-OCT-2001; 2001US-0329000P.
XX
PA   (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
XX
PI   Zhang J;
XX
DR   WPI; 2003-381720/36.
XX
PT   New GPCR-A-1 nucleic acid and polypeptide, useful for diagnosing,
PT   investigating and/or treating disorders associated with aberrant
PT   expression or activity of GPCR-A-1, such as tumors and cancers.
XX
PS   Example 2; SEQ ID NO 631; 156pp; English.
XX
CC   The invention describes an isolated nucleic acid encoding a G protein
CC   coupled receptor (GPCR), mutations of which cause cancer, comprising a
CC   2225 or 1921 base pair sequence, or their degenerate variants, encoding a
CC   409 residue amino acid sequence, all given in the specification, with or
CC   without conservative amino acid substitutions, or complements of the
CC   sequence of them. The encoding nucleic acid is not more than 100 kbase in
CC   length. The methods and compositions of the present invention are useful
CC   for diagnosing, investigating and/or treating disorders associated with
CC   aberrant expression or activity of GPCR-A-1, such as tumours and cancers.
CC   This sequence represents an oligonucleotide used to analyse the gene
CC   encoding human G-protein coupled receptor GPCR-A-1
XX
SQ   Sequence 25 BP; 4 A; 4 C; 11 G; 6 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.7e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2105 GGGGGCCTTCTGGTTTTAGGA 2125
              |||| ||||||||| ||||||
Db          1 GGGGACCTTCTGGTCTTAGGA 21


RESULT 1730
ADB04569
ID   ADB04569 standard; DNA; 25 BP.
XX
AC   ADB04569;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ7 scanning oligonucleotide SEQ ID 5555.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 5555; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 25 BP; 3 A; 1 C; 3 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.7e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTA 2187
              || |||||||||||||||| |
Db          5 TTCTTTTTTTTTTTTTTTGA 25


RESULT 1731
ADB04569/c
ID   ADB04569 standard; DNA; 25 BP.
XX
AC   ADB04569;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ7 scanning oligonucleotide SEQ ID 5555.
```

```
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 5555; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 25 BP; 3 A; 1 C; 3 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.7e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAAA 2804
              | |||||||||||||||| ||
Db         25 TCAAAAAAAAAAAAAAAAGAA 5


RESULT 1732
ADB04572
ID   ADB04572 standard; DNA; 25 BP.
XX
AC   ADB04572;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ7 scanning oligonucleotide SEQ ID 5558.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 5558; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 25 BP; 3 A; 2 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.7e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTA 2187
              || |||||||||||||||| |
Db          2 TTCTTTTTTTTTTTTTTTGA 22


RESULT 1733
ADB04572/c
ID   ADB04572 standard; DNA; 25 BP.
XX
AC   ADB04572;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ7 scanning oligonucleotide SEQ ID 5558.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
```

PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
DR WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS Example 8; SEQ ID NO 5558; 103pp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 25 BP; 3 A; 2 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 1.7e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       2784 TGAAAAAAAAAAAAAAAAAAA 2804
              | |||||||||||||||| ||
Db         22 TCAAAAAAAAAAAAAAAAGAA 2
```

RESULT 1734
ADB04573
ID ADB04573 standard; DNA; 25 BP.
XX
AC ADB04573;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ7 scanning oligonucleotide SEQ ID 5559.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
DR WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS Example 8; SEQ ID NO 5559; 103pp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 25 BP; 3 A; 2 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 1.7e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       2167 TTTTTTTTTTTTTTTTTTTA 2187
              || |||||||||||||||| |
Db          1 TTCTTTTTTTTTTTTTTTGA 21
```

RESULT 1735
ADB04573/c
ID ADB04573 standard; DNA; 25 BP.
XX
AC ADB04573;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ7 scanning oligonucleotide SEQ ID 5559.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
DR WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS Example 8; SEQ ID NO 5559; 103pp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,

```
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 25 BP; 3 A; 2 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.7e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAA 2804
              | ||||||||||||||||| ||
Db         21 TCAAAAAAAAAAAAAAAAGAA 1


RESULT 1736
ADB04571
ID   ADB04571 standard; DNA; 25 BP.
XX
AC   ADB04571;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ7 scanning oligonucleotide SEQ ID 5557.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 5557; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 25 BP; 3 A; 1 C; 3 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.7e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTA 2187
              || |||||||||||||||| |
Db          3 TTCTTTTTTTTTTTTTTTGA 23


RESULT 1737
ADB04571/c
ID   ADB04571 standard; DNA; 25 BP.
XX
AC   ADB04571;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ7 scanning oligonucleotide SEQ ID 5557.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 5557; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 25 BP; 3 A; 1 C; 3 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
```

```
  Best Local Similarity   90.5%;  Pred. No. 1.7e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAA 2804
              | ||||||||||||||||| ||
Db         23 TCAAAAAAAAAAAAAAAAGAA 3
```

RESULT 1738
ADB04570
ID ADB04570 standard; DNA; 25 BP.
XX
AC ADB04570;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ7 scanning oligonucleotide SEQ ID 5556.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
DR WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS Example 8; SEQ ID NO 5556; 103pp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 25 BP; 2 A; 1 C; 4 G; 18 T; 0 U; 0 Other;

```
  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.7e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTA 2187
              || |||||||||||||||| |
Db          4 TTCTTTTTTTTTTTTTTTGA 24
```

RESULT 1739
ADB04570/c
ID ADB04570 standard; DNA; 25 BP.
XX
AC ADB04570;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ7 scanning oligonucleotide SEQ ID 5556.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
DR WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS Example 8; SEQ ID NO 5556; 103pp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 25 BP; 2 A; 1 C; 4 G; 18 T; 0 U; 0 Other;

```
  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.7e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAA 2804
              | ||||||||||||||||| ||
Db         24 TCAAAAAAAAAAAAAAAAGAA 4
```

RESULT 1740
ABX79024
ID ABX79024 standard; DNA; 25 BP.
XX
AC ABX79024;
XX
DT 15-APR-2003 (first entry)
XX

```
DE   Electronic microarray associated p53 oligonucleotide #5.
XX
KW   Electronic microarray; utilising gene expression experimental model;
KW   oncogenesis; physio-chemical cellular response; cell growth;
KW   cell differentiation; ss.
XX
OS   Homo sapiens.
XX
PN   US2002150917-A1.
XX
PD   17-OCT-2002.
XX
PF   10-OCT-2001; 2001US-00975408.
XX
PR   09-NOV-2000; 2000US-00710200.
XX
PA   (NANO-) NANOGEN INC.
XX
PI   Weidenhammer EM,  Wang L,  Xu X,  Heller MJ,  Kahl BF;
XX
DR   WPI; 2003-198284/19.
XX
PT   Detecting relative amounts of at least two mRNA utilizing microelectronic
PT   arrays in a sample, useful for studying disease and oncogenesis, physio-
PT   chemical cellular responses to stimuli, and cell growth and
PT   differentiation.
XX
PS   Example 6; Page 14; 39pp; English.
XX
CC   The invention describes a method of detecting the relative amounts of at
CC   least two mRNA sequences in at least one biological sample, comprising:
CC   (a) isolating mRNA from the sample; (b) amplifying at least two mRNA
CC   transcripts to produce amplicons; (c) electronically hybridising the
CC   amplicons produced to at least two probes bound to a support at
CC   predetermined locations; and (d) detecting the amounts of each amplicon
CC   hybridised to the bound probes at the predetermined locations. The
CC   methods and compositions are useful for utilising gene expression
CC   experimental models for use in studying disease and oncogenesis, physio-
CC   chemical cellular responses to stimuli, and cell growth and
CC   differentiation. This sequence represents an oligonucleotide targeted to
CC   a human gene and used to demonstrate the methods described in the
CC   invention
XX
SQ   Sequence 25 BP; 5 A; 6 C; 12 G; 2 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.7e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        487 GAGCCAGGAGGGAGCGGGGCT 507
              ||||||||  ||||||  |||||
Db          1 GAGCCAGGGGGGAGCAGGGCT 21


RESULT 1741
AAA13806/c
ID   AAA13806 standard; DNA; 26 BP.
XX
AC   AAA13806;
XX
DT   27-JUL-2000  (first entry)
XX
DE   Yeast DOG2 stress responsive gene PCR primer SEQ ID NO:5.
XX
KW   Yeast; stress responsive gene; promoter; brewing; beer; wine; sake;
KW   bread; oxidative stress; osmotic pressure; stress; glucose starvation;
KW   PCR primer; ss.
XX
OS   Saccharomyces cerevisiae.
XX
PN   JP2000078977-A.
XX
PD   21-MAR-2000.
XX
PF   04-SEP-1998;  98JP-00251390.
XX
PR   04-SEP-1998;  98JP-00251390.
XX
PA   (TAIF ) MARUHA CORP.
XX
DR   WPI; 2000-285929/25.
XX
PT   A stress-responsive gene promotor.
XX
PS   Example 3; Page 10; 12pp; Japanese.
XX
CC   The present invention describes a stress responsive gene promoter
CC   isolated from Saccharomyces cerevisiae (yeast). Also described in the
CC   present invention are: (1) a promoter containing a DNA hybridising with
CC   the above DNA under a stringent condition and having stress-responsive
CC   promoter activity; (2) a gene expression cassette containing the above
CC   promoter; (3) an expression vector containing the above gene expression
CC   cassette; (4) a recombinant vector in which a gene encoding an optional
CC   polypeptide is recombined to the above expression vector; (5) a
CC   transformant containing the above recombinant vector; and (6) a method
CC   for the preparation of the above polypeptide in which the above
CC   transformant is cultured and the polypeptide is collected from the
CC   resultant culture. Saccharomyces cerevisiae is used for the brewing of
CC   beer, wine and sake and production of bread. The gene is responsive to
CC   the stresses such as oxidative stress, osmotic pressure stress and
CC   glucose starvation stress. The present sequence represents a PCR primer
CC   for the yeast DOG2 stress responsive gene, which is used in an example
CC   from the present invention
XX
SQ   Sequence 26 BP; 3 A; 2 C; 2 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 26;
  Best Local Similarity   90.5%;  Pred. No. 1.9e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAAA 2804
              | |||||||  ||||||||||
Db         24 TCAAAAAAATAAAAAAAAAAA 4


RESULT 1742
AAQ05023
ID   AAQ05023 standard; DNA; 27 BP.
XX
AC   AAQ05023;
XX
DT   25-MAR-2003  (revised)
DT   31-OCT-1990  (first entry)
XX
DE   Sequence binding to and inhibiting the Beta-globin gene.
XX
KW   C-myc; cancer; HIV-I; AIDS; collagenase; Alzheimers disease; EGF;
KW   epidermal growth factor; GSTpi; HMGCoA; thallasemia;
KW   Herpes simplex virus; nerve growth factor receptor; globin; ss.
XX
OS   Synthetic.
XX
PN   EP375408-A.
XX
PD   27-JUN-1990.
XX
PF   20-DEC-1989;  89EP-00313391.
XX
PR   20-DEC-1988;  88US-00287359.
XX
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (HOGA/) HOGAN M E.
XX
PI   Hogan ME,  Kessler DJ;
XX
DR   WPI; 1990-195509/26.
```

```
XX
PT   Synthetic oligo-nucleotide(s) which bind target duplex DNA - forming co-
PT   linear triplex to control transcription process in gene-specific fashion.
XX
PS   Claim 47; Page 31; 40pp; English.
XX
CC   Sequence forms triplex with the double stranded target sequence with G
CC   binding to G-C and T to A-T. The strand runs 3' to 5' in an antiparallel
CC   orientation and when targeted to a specific sequence will deactivate it.
CC   This allows for growth inhibition in cancerous cells; manipulation of
CC   cellular structural protein content; inhibition of IL-2 chain receptor;
CC   disbursing plaque formation in Alzheimer's disease; inhibiting EGF gene;
CC   modulating cholestrol synthesis through the HMGCoA gene; suppressing NGF
CC   gene expression; arresting HSV-I replication and suppressing Beta- globin
CC   expression in thallassaemia and sicle cell anaemia patients. (Updated on
CC   25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA
CC   field.)
XX
SQ   Sequence 27 BP; 0 A; 0 C; 6 G; 21 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 27;
  Best Local Similarity   90.5%;  Pred. No. 2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
                || |||||||| |||||||||
Db          6 TTGTTTTTTTTGTTTTTTTT 26


RESULT 1743
AAQ36361
ID   AAQ36361 standard; DNA; 27 BP.
XX
AC   AAQ36361;
XX
DT   25-MAR-2003  (revised)
DT   07-JUN-1993  (first entry)
XX
DE   GL6par, targetted to human beta globin sequence.
XX
KW   Heamoglobin; beta thalassemia; sickle cell anaemia; delta protein;
KW   triplex; target; duplex; promoter; coding domain; 3'-5'; ss.
XX
OS   Synthetic.
XX
PN   US5176996-A.
XX
PD   05-JAN-1993.
XX
PF   22-DEC-1989;   89US-00453532.
XX
PR   20-DEC-1988;   88US-00287359.
XX
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PI   Hogan ME,  Kessler DJ;
XX
DR   WPI; 1993-035718/04.
XX
PT   Synthetic oligo-nucleotide(s), prodn. useful e.g. for HIV-1 inhibition -
PT   which bind to target sequence in duplex DNA forming colinear triplex by
PT   binding to major groove.
XX
PS   Example 13; Col 35; 29pp; English.
XX
CC   The beta globin gene encodes on of the proteins comprising human adult
CC   haemoglobin. Mutation in this gene is responsible for beta thalassemia
CC   and sickle cell anaemia. Expression of the gene may be prevented by the
CC   formation of a triplex between the duplex target DNA sequence and an anti
CC   parallel or parallel synthetic oligonucleotide. The triplex
CC   oligonucleotides are designed to inhibit the beta globin gene in
CC   thallassemics and in patients with sickle cell anaemia, to be replaced by
CC   the naturally occurring delta protein. Two classes of triplex
CC   oligonucleotides may be used, targetted against the 5' enhancer or the
CC   promoter/coding domain, in this case from base 874 to 900 (numbering is
CC   relative to the principal mRNA start site). A suitable parallel
CC   oligonucleotide is GL6par (3'-5'). See also AAQ36219-362. (Updated on 25-
CC   MAR-2003 to correct PF field.)
XX
SQ   Sequence 27 BP; 0 A; 0 C; 6 G; 21 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 27;
  Best Local Similarity   90.5%;  Pred. No. 2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
                || |||||||| |||||||||
Db          6 TTGTTTTTTTTGTTTTTTTT 26


RESULT 1744
ABK52620/c
ID   ABK52620 standard; DNA; 27 BP.
XX
AC   ABK52620;
XX
DT   27-AUG-2002  (first entry)
XX
DE   Minority genome method VFA-MUT-11 DNA sequence.
XX
KW   Minority genome method; viral quasi-species; majority genome;
KW   genetic diagnosis; viral infection; human immune deficiency virus;
KW   hepatitis B; hepatitis C; antiviral therapy; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1
FT                   /*tag=  a
FT                   /label= unknown
FT                   /note= "C6 aminolinker sequence"
XX
PN   WO200183815-A1.
XX
PD   08-NOV-2001.
XX
PF   27-APR-2001; 2001WO-ES000165.
XX
PR   27-APR-2000; 2000ES-00001068.
XX
PA   (CNSJ ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
XX
PI   Arias Esteban A,  Baranowski E,  Briones Llorente C;
PI   Domingo Solans E,  Escarmis Homs C,  Gomez Castilla J;
PI   Martin Ruiz- Jarabo C,  Parro Garcia V;
XX
DR   WPI; 2002-147445/19.
XX
PT   Detecting minority genomes in viral quasi-species, useful for identifying
PT   mutants responsible for drug resistance and to individualize therapy.
XX
PS   Example 1; Page 53; 107pp; Spanish.
XX
CC   The present invention relates to a new method for detecting minority
CC   genomes, present at less than 50%, in a population of nucleic acids of a
CC   viral quasi-species and having at least one mutation with respect to the
CC   majority genome. The invention can be used for genetic diagnosis of viral
CC   infections, especially human immune deficiency virus and hepatitis B or
CC   C, particularly to detect memory minority genomes that are implicated in
CC   failure of antiviral therapy, so the method may make possible design of
CC   therapies customised for individual patients. The present nucleic acid
CC   sequence represents the VFA-MUT-11 DNA sequence that was used in the
CC   methods of the invention
XX
SQ   Sequence 27 BP; 2 A; 4 C; 2 G; 18 T; 0 U; 1 Other;
```

```
  Query Match             0.6%;  Score 17.8;  DB 1;  Length 27;
  Best Local Similarity   90.5%;  Pred. No. 2e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAA 2799
              || ||| ||||||||||||||
Db         22 AGGATTAAAAAAAAAAAAAAA 2

RESULT 1745
ABA05517
ID   ABA05517 standard; DNA; 24 BP.
XX
AC   ABA05517;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Human Tre carcinogenic gene protein 10.56 PCR primer 2.
XX
KW   Human; Tre carcinogenic gene protein 10.56; cytostatic; haemostatic;
KW   virucide; immunomodulatory; antiinflammatory; gene therapy; cancer;
KW   haemopathy; human immunodeficiency virus; HIV; infection;
KW   immunological disease; inflammatory disorder; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200190131-A1.
XX
PD   29-NOV-2001.
XX
PF   21-MAY-2001; 2001WO-CN000833.
XX
PR   24-MAY-2000; 2000CN-00115824.
XX
PA   (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-083078/11.
XX
PT   Human tre carcinogenic gene protein 10.56 and encoding polynucleotide,
PT   used in diagnosis and treatment of malignant tumors, hemopathy, human
PT   immunodeficiency virus infection, immunological diseases and
PT   inflammation.
XX
PS   Example 2; Page 17; 36pp; Chinese.
XX
CC   The invention relates to an isolated polypeptide of human tre
CC   carcinogenic gene protein 10.56 comprising a 96 residue amino acid
CC   sequence, fully defined in the specification, or its fragment, analogue
CC   or derivative. The polypeptide is useful in the diagnosis and treatment
CC   of malignant tumours, haemopathy, human immunodeficiency virus (HIV)
CC   infection, immunological diseases and various inflammatory disorders. The
CC   present sequence is a primer used to amplify a polynucleotide encoding
CC   the polypeptide of the invention
XX
SQ   Sequence 24 BP; 0 A; 3 C; 0 G; 21 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 24;
  Best Local Similarity   83.3%;  Pred. No. 1.7e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2157 TTTTTCTCCTTTTTTTTTTTTTT 2180
              ||||| || || ||| ||||||||
Db          1 TTTTTTTCTTTCTTTCTTTTTTT 24

RESULT 1746
ABQ73262
ID   ABQ73262 standard; DNA; 24 BP.
XX
AC   ABQ73262;
XX
DT   30-SEP-2002  (first entry)
XX
DE   Human ribosomal protein L312.54 PCR primer 2 SEQ ID NO:4.
XX
KW   Human; ribosomal protein L312.54; malignant tumour; inflammation;
KW   development disorder; immunological disease; haemopathy; HIV infection;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1339454-A.
XX
PD   13-MAR-2002.
XX
PF   23-AUG-2000; 2000CN-00119720.
XX
PR   23-AUG-2000; 2000CN-00119720.
XX
PA   (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-455356/49.
XX
PT   New polypeptide-ribosomal protein L312.54 and polynucleotide for encoding
PT   said polypeptide.
XX
PS   Example 2; Page 17 (Disclosure); 33pp; Chinese.
XX
CC   The present invention describes human ribosomal protein L312.54 (I). Also
CC   described is a process for producing (I) using DNA recombination
CC   technology. (I) and the polynucleotide encoding it can be used for
CC   treating various diseases, such as malignant tumour, inflammations,
CC   development disorder, immunological diseases, haemopathy and HIV
CC   infection. The present sequence represents a PCR primer for (I), which is
CC   used in an example from the present invention
XX
SQ   Sequence 24 BP; 3 A; 2 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 24;
  Best Local Similarity   83.3%;  Pred. No. 1.7e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTTTTT 2184
              | ||||||| | ||||||||||
Db          1 TATCCTTTTAATGTTTTTTTTTT 24

RESULT 1747
ABQ04183
ID   ABQ04183 standard; DNA; 24 BP.
XX
AC   ABQ04183;
XX
DT   11-JUN-2002  (first entry)
XX
DE   Oligonucleotide adapter/capture probe 4174.
XX
KW   Oligonucleotide array; adapter sequence; probe; ss.
XX
OS   Synthetic.
XX
PN   WO200216649-A2.
XX
PD   28-FEB-2002.
XX
PF   27-AUG-2001; 2001WO-US026519.
XX
PR   25-AUG-2000; 2000US-0227948P.
PR   29-AUG-2000; 2000US-0228854P.
XX
PA   (ILLU-) ILLUMINA INC.
XX
```

PI Gunderson K;
XX
DR WPI; 2002-292068/33.
XX
PT Array comprising adapter sequences useful for immobilizing or detecting a
PT target nucleic acid sequence, has different addresses comprising
PT different specific capture probes.
XX
PS Claim 1; Page 141; 261pp; English.
XX
CC The invention relates to an oligonucleotide array (I) comprising at least
CC 25 different addresses (adapter sequences) with each comprising a
CC different capture probe selected from a group consisting of the sequences
CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
CC and contacting the modified target nucleic acid with (I). The steps of
CC above method is useful for detecting a target nucleic acid, which further
CC comprises detecting the presence of the modified target nucleic acid
XX
SQ Sequence 24 BP; 5 A; 4 C; 7 G; 8 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 1.7e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1086 AAGGTGAAGCTGTTCATTTGGCTA 1109
|||||| || ||||||||||||
Db 1 AAGGTGGTGCCATTCATTTGGCTA 24

RESULT 1748
ABQ00107
ID ABQ00107 standard; DNA; 24 BP.
XX
AC ABQ00107;
XX
DT 11-JUN-2002 (first entry)
XX
DE Oligonucleotide adapter/capture probe 98.
XX
KW Oligonucleotide array; adapter sequence; probe; ss.
XX
OS Synthetic.
XX
PN WO200216649-A2.
XX
PD 28-FEB-2002.
XX
PF 27-AUG-2001; 2001WO-US026519.
XX
PR 25-AUG-2000; 2000US-0227948P.
PR 29-AUG-2000; 2000US-0228854P.
XX
PA (ILLU-) ILLUMINA INC.
XX
PI Gunderson K;
XX
DR WPI; 2002-292068/33.
XX
PT Array comprising adapter sequences useful for immobilizing or detecting a
PT target nucleic acid sequence, has different addresses comprising
PT different specific capture probes.
XX
PS Claim 1; Page 46; 261pp; English.
XX
CC The invention relates to an oligonucleotide array (I) comprising at least
CC 25 different addresses (adapter sequences) with each comprising a
CC different capture probe selected from a group consisting of the sequences
CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
CC and contacting the modified target nucleic acid with (I). The steps of
CC above method is useful for detecting a target nucleic acid, which further
CC comprises detecting the presence of the modified target nucleic acid
XX
SQ Sequence 24 BP; 5 A; 4 C; 7 G; 8 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 1.7e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1086 AAGGTGAAGCTGTTCATTTGGCTA 1109
|||||| || ||||||||||||
Db 1 AAGGTGGTGCCATTCATTTGGCTA 24

RESULT 1749
ABQ04224/c
ID ABQ04224 standard; DNA; 24 BP.
XX
AC ABQ04224;
XX
DT 11-JUN-2002 (first entry)
XX
DE Oligonucleotide adapter/capture probe 4215.
XX
KW Oligonucleotide array; adapter sequence; probe; ss.
XX
OS Synthetic.
XX
PN WO200216649-A2.
XX
PD 28-FEB-2002.
XX
PF 27-AUG-2001; 2001WO-US026519.
XX
PR 25-AUG-2000; 2000US-0227948P.
PR 29-AUG-2000; 2000US-0228854P.
XX
PA (ILLU-) ILLUMINA INC.
XX
PI Gunderson K;
XX
DR WPI; 2002-292068/33.
XX
PT Array comprising adapter sequences useful for immobilizing or detecting a
PT target nucleic acid sequence, has different addresses comprising
PT different specific capture probes.
XX
PS Claim 1; Page 141; 261pp; English.
XX
CC The invention relates to an oligonucleotide array (I) comprising at least
CC 25 different addresses (adapter sequences) with each comprising a
CC different capture probe selected from a group consisting of the sequences
CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
CC and contacting the modified target nucleic acid with (I). The steps of
CC above method is useful for detecting a target nucleic acid, which further
CC comprises detecting the presence of the modified target nucleic acid
XX
SQ Sequence 24 BP; 8 A; 7 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 1.7e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1086 AAGGTGAAGCTGTTCATTTGGCTA 1109
|||||| || ||||||||||||
Db 24 AAGGTGGTGCCATTCATTTGGCTA 1

RESULT 1750
ABA99264
ID ABA99264 standard; DNA; 24 BP.

```
XX
AC   ABA99264;
XX
DT   08-MAY-2002  (first entry)
XX
DE   Human tra oncogene 10-56 RT-PCR primer 2.
XX
KW   Oncogene; tra oncogene 10.56; human; treatment; gene therapy; cytostatic;
KW   haemostatic; virucide; immunomodulatory; antiinflammatory; diagnosis;
KW   malignant tumour; haemopathy; human immunodeficiency virus;
KW   HIV infection; immunological disease; inflammation; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200200824-A2.
XX
PD   03-JAN-2002.
XX
PF   11-JUN-2001; 2001WO-CN000936.
XX
PR   12-JUN-2000; 2000CN-00116436.
XX
PA   (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-075668/10.
XX
PT   human tre oncogene 10.56 and encoding polynucleotide, used in diagnosis
PT   and treatment of malignant tumors, hemopathy, human immunodeficiency
PT   virus infection, immunological diseases and inflammation.
XX
PS   Example 2; Page 12; 32pp; Chinese.
XX
CC   This invention describes a novel human tre oncogene 10.56 which has
CC   cytostatic, haemostatic, virucide, immunomodulatory and antiinflammatory
CC   activity and can be used for gene therapy. The polypeptide of the
CC   invention and its encoding polynucleotide are used in diagnosis and
CC   treatment of malignant tumours, haemopathy, human immunodeficiency virus
CC   (HIV) infection, immunological diseases and various inflammations. This
CC   sequence represents an RT-PCR primer used in the amplification of the
CC   human tre oncogene 10.56 gene which is described in the disclosure of the
CC   invention
XX
SQ   Sequence 24 BP; 0 A; 3 C; 0 G; 21 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 24;
  Best Local Similarity   83.3%;  Pred. No. 1.7e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2157 TTTTTCTCCTTTTTTTTTTTTTT 2180
             ||||| || || ||| |||||||||
Db          1 TTTTTTTCTTTCTTTCTTTTTTT 24


RESULT 1751
ABK11020
ID   ABK11020 standard; DNA; 24 BP.
XX
AC   ABK11020;
XX
DT   05-JUN-2002  (first entry)
XX
DE   Gamma-COP13 polypeptide, RT-PCR primer #2.
XX
KW   Gamma-COP13; cytostatic; haemostatic; virucide; immunomodulatory;
KW   antiinflammatory; malignant tumour; haemopathy; inflammation;
KW   human immunodeficiency virus; HIV; immunological disease;
KW   reverse transcriptase PCR; RT-PCR; primer; ss.
XX
OS   Unidentified.
XX
PN   WO200202616-A1.
XX
PD   10-JAN-2002.
XX
PF   11-JUN-2001; 2001WO-CN000961.
XX
PR   14-JUN-2000; 2000CN-00116482.
XX
PA   (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-090536/12.
XX
PT   Gamma-cop 13 polypeptide and encoded polynucleotide, used in diagnosis
PT   and treatment of malignant tumors, hemopathy, human immunodeficiency
PT   virus infection, immunological diseases and inflammation.
XX
PS   Example 2; Page 11; 33pp; Chinese.
XX
CC   The invention relates to an isolated polypeptide (I), of gamma-COP13 and
CC   the polynucleotide (II) encoding it. (I) and (II) are used in diagnosis
CC   and treatment of malignant tumour, haemopathy, human immunodeficiency
CC   virus (HIV) infection, immunological diseases and various inflammations.
CC   The present sequence represents a reverse transcriptase (RT)-PCR primer
CC   used to isolate the coding sequence of gamma-COP13 polypeptide
XX
SQ   Sequence 24 BP; 3 A; 2 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 24;
  Best Local Similarity   83.3%;  Pred. No. 1.7e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTAACT 2190
             ||||||| ||| ||||| ||| ||
Db          1 TTTTTTTATTTATTTTTCTTATCT 24


RESULT 1752
AAV27258
ID   AAV27258 standard; cDNA; 25 BP.
XX
AC   AAV27258;
XX
DT   28-SEP-1998  (first entry)
XX
DE   Sunflower antifungal protein MS59 5'RACE primer.
XX
KW   Antifungal; fungicide; MS59; sunflower; carbohydrate oxidase;
KW   glucose oxidase; transgenic plant; Phytophthora; Pythium;
KW   crop protection; disease resistance; RACE; PCR; primer; ss.
XX
OS   Synthetic.
OS   Helianthus annuus; cv. zebulon.
XX
PN   WO9813478-A2.
XX
PD   02-APR-1998.
XX
PF   04-SEP-1997;  97WO-EP004923.
XX
PR   04-SEP-1996;   96EP-00202466.
PR   19-MAR-1997;   97EP-00200831.
XX
PA   (MOGE-) MOGEN INT NV.
XX
PI   Stuiver MH,  Custers JHHV,  Sela-Buurlage MB,  Melchers LS;
PI   Van Deventer- Troost JPE,  Lageweg W,  Ponstein AS;
XX
DR   WPI; 1998-230692/20.
XX
PT   New plant proteins having anti-fungal activity - useful as, e.g.
PT   carbohydrate oxidase(s) for protection against Phytophthora and Pythium
PT   sp.
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```
XX
PS   Example 11; Page 37; 139pp; English.
XX
CC   Primers for 5'RACE (see AAV27256 and AAV27258), for nested 5'RACE (see
CC   AAV27259), for 3'RACE (see AAV27255) and for nested 3'RACE (see AAV27257)
CC   are based on previously obtained 5' and 3'RACE products of sodium
CC   salicylate-treated sunflower cv. zebulon leaf cDNA (see AAV27252-54).
CC   They were used to obtain further sequence information related to the
CC   novel antifungal protein MS59. 4 Partial cDNA clones were obtained, and
CC   these were used to produce a full-length sequence (see AAV27260) for
CC   sunflower leaf antifungal MS59 protein (see AAW55053). Claimed antifungal
CC   proteins, including MS59, have a mol.wt. of 55-65 kDa (SDS-PAGE), have
CC   carbohydrate oxidase (especially glucose oxidase) activity, show anti-
CC   Phytophthora and/or anti-Pythium activity, can be expressed in transgenic
CC   plants to reduce susceptibility to infection by fungi, or expressed in
CC   host cells for use in antifungal compositions. Plants engineered to
CC   express the antifungal proteins require reduced treatments with
CC   fungicides and have a longer shelf-life
XX
SQ   Sequence 25 BP; 6 A; 2 C; 11 G; 6 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 25;
  Best Local Similarity   83.3%;  Pred. No. 1.9e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1004 GAGAAGTTGGACAAGATCGGGTTG 1027
             | ||||||| | ||||| ||||||
Db          2 GGGAAGTTGCAGAAGATTGGGTTG 25


RESULT 1753
AAA68966
ID   AAA68966 standard; DNA; 25 BP.
XX
AC   AAA68966;
XX
DT   15-SEP-2003  (revised)
DT   06-AUG-2003  (revised)
DT   27-OCT-2000  (first entry)
XX
DE   Bacteriophage 96 ORF RBS sequence 96ORF358.
XX
KW   Bacteriophage; antimicrobial; genome; identification; antibacterial;
KW   bacterial growth inhibition; PCR primer; RBS; ribosome biding site;
KW   bacterial infection; ss.
XX
OS   Staphylococcus aureus; bacteriophage 96.
XX
PN   WO200032825-A2.
XX
PD   08-JUN-2000.
XX
PF   03-DEC-1999;   99WO-IB002040.
XX
PR   03-DEC-1998;   98US-0110992P.
PR   03-JUN-1999;   99US-00326144.
PR   28-SEP-1999;   99US-00407804.
PR   30-SEP-1999;   99US-0157218P.
PR   01-DEC-1999;   99US-0168777P.
PR   02-DEC-1999;   99US-00454252.
XX
PA   (PHAG-) PHAGETECH INC.
XX
PI   Pelletier J,  Gros P,  Dubow M;
XX
DR   WPI; 2000-412361/35.
XX
PT   Identifying a bacteriophage coding region for treating bacterial
PT   infections comprises identifying a nucleic acid encoding a product that
PT   inhibits bacteria when a bacteriophage infects a bacterium.
XX
PS   Disclosure; Page 204; 456pp; English.
XX
CC   The present invention describes a method for identifying a bacteriophage
CC   coding region encoding a product active on an essential bacterial target.
CC   The method comprises identifying a nucleic acid sequence encoding a gene
CC   product that provides a bacteria-inhibiting function when an
CC   uncharacterised bacteriophage infects a pathogenic bacterium. The
CC   compound active on a target of a bacteriophage inhibitor protein in a
CC   bacteria is used to treat or prevent a bacterial infection in an animal.
CC   AAA68243 to AAA69442 and AAB16523 to AAB16954 represent bacteriophage
CC   nucleotide and protein sequences which are used in the exemplification of
CC   the present invention. (Updated on 06-AUG-2003 to correct OS field.)
CC   (Updated on 15-SEP-2003 to standardise OS field)
XX
SQ   Sequence 25 BP; 8 A; 2 C; 3 G; 12 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 25;
  Best Local Similarity   83.3%;  Pred. No. 1.9e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2760 TAATAAAAGTATTCTTGTTAGAAT 2783
              | ||||||||||||||  ||| ||
Db          2 TCATAAAAGTATTCTTTGTAGTAT 25


RESULT 1754
AAC96038/c
ID   AAC96038 standard; DNA; 25 BP.
XX
AC   AAC96038;
XX
DT   26-FEB-2001  (first entry)
XX
DE   16s rRNA gene PCR primer #5.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 44; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 4 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 25;
  Best Local Similarity   83.3%;  Pred. No. 1.9e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;
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```
Qy       2781 AATTGAAAAAAAAAAAAAAAAAA 2804
              ||||   || ||||||||||||||
Db         24 AATTCCGAATAAAAAAAAAAAAAA 1
```

RESULT 1755
AAC96289/c
ID AAC96289 standard; DNA; 25 BP.
XX
AC AAC96289;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA DPB1 gene PCR primer #21.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 48; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 4 A; 2 C; 3 G; 16 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy       2775 TGTTAGAATTGAAAAAAAAAAAAA 2798
              || || | || ||||||||||||
Db         24 TGGTACACTTAAAAAAAAAAAAAA 1
```

RESULT 1756
AAC96549
ID AAC96549 standard; DNA; 25 BP.
XX
AC AAC96549;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA DRB345 gene PCR primer #20.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 53; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 1 A; 2 C; 4 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy       2167 TTTTTTTTTTTTTTTTTTTAACT 2190
              |||||||||||||||| ||  | ||
Db          1 TTTTTTTTTTTTTTTCTTGGAGCT 24
```

RESULT 1757
AAC96427/c
ID AAC96427 standard; DNA; 25 BP.
XX
AC AAC96427;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA DQA1 gene PCR primer #29.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX

```
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 51; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 0 A; 6 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 25;
  Best Local Similarity   83.3%;  Pred. No. 1.9e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAA 2802
                ||||  ||  ||||||||||||||||
Db         24 AGAAGGGAGGAAAAAAAAAAAAAA 1


RESULT 1758
AAC95726/c
ID   AAC95726 standard; DNA; 25 BP.
XX
AC   AAC95726;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DQA1 gene PCR primer #23.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 39; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 0 A; 6 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 25;
  Best Local Similarity   83.3%;  Pred. No. 1.9e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAA 2802
                ||||  ||  ||||||||||||||||
Db         24 AGAAGGGAGGAAAAAAAAAAAAAA 1


RESULT 1759
AAC96237/c
ID   AAC96237 standard; DNA; 25 BP.
XX
AC   AAC96237;
XX
DT   26-FEB-2001  (first entry)
XX
DE   16s rRNA gene PCR primer #204.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 47; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 5 A; 2 C; 4 G; 14 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 25;
  Best Local Similarity   83.3%;  Pred. No. 1.9e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2776 GTTAGAATTGAAAAAAAAAAAAAA 2799
                |||  | |||  ||||||||||||
Db         24 GTTCTACTTGCAAAAAAAAAAAAA 1


RESULT 1760
AAC96446/c
ID   AAC96446 standard; DNA; 25 BP.
XX
AC   AAC96446;
XX
```

DT 26-FEB-2001 (first entry)
XX
DE HLA DQA1 gene PCR primer #48.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 51; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 4 A; 5 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2778 TAGAATTGAAAAAAAAAAAAAAAA 2801
|||| ||| | ||||||||||||
Db 24 TAGAGTTGTAGCAAAAAAAAAAAA 1

RESULT 1761
AAH38027/c
ID AAH38027 standard; DNA; 25 BP.
XX
AC AAH38027;
XX
DT 14-AUG-2001 (first entry)
XX
DE SNP specific SNPE primer SEQ ID 823.
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW inflammation; forensic investigation; paternity analysis; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200129262-A2.
XX
PD 26-APR-2001.
XX
PF 13-OCT-2000; 2000WO-US028436.
XX
PR 15-OCT-1999; 99US-0160096P.
XX
PA (ORCH-) ORCHID BIOSCIENCES INC.
XX
PI Picoult-Newburg L, Pohl M;
XX
DR WPI; 2001-290930/30.
XX
PT New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample.
XX
PS Claim 1; Page 54; 83pp; English.
XX
CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a single nucleotide
CC primer extension (SNPE) primer specific for a human SNP containing DNA
CC sequence
XX
SQ Sequence 25 BP; 18 A; 1 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2165 CTTTTTTTTTTTTTTTTTTTTAA 2188
|| | |||||||||||||| ||||
Db 25 CTGATCTTTTTTTTTTTTTCTTAA 2

RESULT 1762
ACK08350/c
ID ACK08350 standard; DNA; 25 BP.
XX
AC ACK08350;
XX
DT 14-OCT-2003 (first entry)
XX
DE Human microarray DNA oligonucleotide SEQ ID NO 108331.
XX
KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.
XX
OS Homo sapiens.
XX
PN US2003104410-A1.
XX
PD 05-JUN-2003.
XX
PF 15-MAR-2002; 2002US-00098263.

```
XX
PR   16-MAR-2001; 2001US-0276759P.
XX
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Mittmann MP;
XX
DR   WPI; 2003-567953/53.
XX
PT   New array of nucleic acid probes, useful for in situ hybridization, in
PT   Southern, Northern or dot-blot hybridization to identify or detect the
PT   sequence or specific mutations of any gene.
XX
PS   Claim 1; SEQ ID NO 108331; 9pp; English.
XX
CC   The invention discloses a microarray comprising a plurality of nucleic
CC   acid probes including one of 2,018,500 fully defined sequences, or its
CC   perfect match, perfect mismatch, antisense match or antisense mismatch.
CC   Also disclosed is a method of gene expression analysis. The array is used
CC   in monitoring gene expression levels by hybridisation to a DNA library,
CC   in analysis of genetic variation or in hybridisation of tag-labelled
CC   compounds. The nucleic acid probes are specifically designed for analysis
CC   of at least one target sequence. The method of analysis comprises
CC   hybridising at least one or more nucleic acids to at least two or more
CC   nucleic acid probes and detecting the hybridisation. The nucleic acid
CC   probes are attached to a solid support. The analysis comprises monitoring
CC   gene expression levels, identifying biallelic markers or polymorphisms,
CC   or family members of a gene and a cross-species comparison. Each of the
CC   nucleic acids further comprises a tag sequence. The array of nucleic acid
CC   probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC   blot hybridisation to identify or detect the sequence or specific
CC   mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC   primer extensions or in screening cDNA or genomic libraries or subclones
CC   for additional subclones containing segments of DNA that have been
CC   isolated and previously sequenced. The sequence presented is one of the
CC   nucleic acid probes incorporated in the microarray. Note: The sequence
CC   data for this patent can also be obtained in electronic format directly
CC   from USPTO at seqdata.uspto.goc/sequence.html
XX
SQ   Sequence 25 BP; 4 A; 11 C; 7 G; 3 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 25;
  Best Local Similarity   83.3%;  Pred. No. 1.9e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         53 GGCGGGGGCGGCGGCAGACGCCTG 76
              ||| |||| |||  ||||||||||
Db         25 GGCAGGGGTGGCTTCAGACGCCTG 2


RESULT 1763
ACI33260
ID   ACI33260 standard; DNA; 25 BP.
XX
AC   ACI33260;
XX
DT   13-OCT-2003  (first entry)
XX
DE   Human microarray DNA oligonucleotide SEQ ID NO 33251.
XX
KW   EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW   genetic variation; biallelic marker; polymorphism; human;
KW   cross-species comparison.
XX
OS   Homo sapiens.
XX
PN   US2003104410-A1.
XX
PD   05-JUN-2003.
XX
PF   15-MAR-2002; 2002US-00098263.
XX
PR   16-MAR-2001; 2001US-0276759P.
XX
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Mittmann MP;
XX
DR   WPI; 2003-567953/53.
XX
PT   New array of nucleic acid probes, useful for in situ hybridization, in
PT   Southern, Northern or dot-blot hybridization to identify or detect the
PT   sequence or specific mutations of any gene.
XX
PS   Claim 1; SEQ ID NO 33251; 9pp; English.
XX
CC   The invention discloses a microarray comprising a plurality of nucleic
CC   acid probes including one of 2,018,500 fully defined sequences, or its
CC   perfect match, perfect mismatch, antisense match or antisense mismatch.
CC   Also disclosed is a method of gene expression analysis. The array is used
CC   in monitoring gene expression levels by hybridisation to a DNA library,
CC   in analysis of genetic variation or in hybridisation of tag-labelled
CC   compounds. The nucleic acid probes are specifically designed for analysis
CC   of at least one target sequence. The method of analysis comprises
CC   hybridising at least one or more nucleic acids to at least two or more
CC   nucleic acid probes and detecting the hybridisation. The nucleic acid
CC   probes are attached to a solid support. The analysis comprises monitoring
CC   gene expression levels, identifying biallelic markers or polymorphisms,
CC   or family members of a gene and a cross-species comparison. Each of the
CC   nucleic acids further comprises a tag sequence. The array of nucleic acid
CC   probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC   blot hybridisation to identify or detect the sequence or specific
CC   mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC   primer extensions or in screening cDNA or genomic libraries or subclones
CC   for additional subclones containing segments of DNA that have been
CC   isolated and previously sequenced. The sequence presented is one of the
CC   nucleic acid probes incorporated in the microarray. Note: The sequence
CC   data for this patent can also be obtained in electronic format directly
CC   from USPTO at seqdata.uspto.goc/sequence.html
XX
SQ   Sequence 25 BP; 7 A; 6 C; 4 G; 8 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 25;
  Best Local Similarity   83.3%;  Pred. No. 1.9e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        180 TAACCGATAATGTCAAGTACGAAG 203
              |||||  | |||||| ||||||||
Db          2 TAACCCTTCATGTCATGTACGAAG 25


RESULT 1764
ACK08351/c
ID   ACK08351 standard; DNA; 25 BP.
XX
AC   ACK08351;
XX
DT   14-OCT-2003  (first entry)
XX
DE   Human microarray DNA oligonucleotide SEQ ID NO 108332.
XX
KW   EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW   genetic variation; biallelic marker; polymorphism; human;
KW   cross-species comparison.
XX
OS   Homo sapiens.
XX
PN   US2003104410-A1.
XX
PD   05-JUN-2003.
XX
PF   15-MAR-2002; 2002US-00098263.
XX
PR   16-MAR-2001; 2001US-0276759P.
XX
PA   (AFFY-) AFFYMETRIX INC.
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XX
PI   Mittmann MP;
XX
DR   WPI; 2003-567953/53.
XX
PT   New array of nucleic acid probes, useful for in situ hybridization, in
PT   Southern, Northern or dot-blot hybridization to identify or detect the
PT   sequence or specific mutations of any gene.
XX
PS   Claim 1; SEQ ID NO 108332; 9pp; English.
XX
CC   The invention discloses a microarray comprising a plurality of nucleic
CC   acid probes including one of 2,018,500 fully defined sequences, or its
CC   perfect match, perfect mismatch, antisense match or antisense mismatch.
CC   Also disclosed is a method of gene expression analysis. The array is used
CC   in monitoring gene expression levels by hybridisation to a DNA library,
CC   in analysis of genetic variation or in hybridisation of tag-labelled
CC   compounds. The nucleic acid probes are specifically designed for analysis
CC   of at least one target sequence. The method of analysis comprises
CC   hybridising at least one or more nucleic acids to at least two or more
CC   nucleic acid probes and detecting the hybridisation. The nucleic acid
CC   probes are attached to a solid support. The analysis comprises monitoring
CC   gene expression levels, identifying biallelic markers or polymorphisms,
CC   or family members of a gene and a cross-species comparison. Each of the
CC   nucleic acids further comprises a tag sequence. The array of nucleic acid
CC   probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC   blot hybridisation to identify or detect the sequence or specific
CC   mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC   primer extensions or in screening cDNA or genomic libraries or subclones
CC   for additional subclones containing segments of DNA that have been
CC   isolated and previously sequenced. The sequence presented is one of the
CC   nucleic acid probes incorporated in the microarray. Note: The sequence
CC   data for this patent can also be obtained in electronic format directly
CC   from USPTO at seqdata.uspto.goc/sequence.html
XX
SQ   Sequence 25 BP; 3 A; 11 C; 7 G; 4 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 25;
  Best Local Similarity   83.3%;  Pred. No. 1.9e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         53 GGCGGGGGCGGCGGCAGACGCCTG 76
              ||| |||| ||| |||||||||| |
Db         25 GGCAGGGGTGGCATCAGACGCCTG 2


RESULT 1765
AAV12482
ID   AAV12482 standard; DNA; 26 BP.
XX
AC   AAV12482;
XX
DT   15-MAY-1998  (first entry)
XX
DE   Oligonucleotide SEQ ID NO:5 from US5174320 Example 2.
XX
KW   Synthesis; selection; amplification; circular oligonucleotide;
KW   rolling circle synthesis; diagnosis; therapeutic agent; ss.
XX
OS   Synthetic.
XX
PN   US5714320-A.
XX
PD   03-FEB-1998.
XX
PF   23-FEB-1995;   95US-00393439.
XX
PR   15-APR-1993;   93US-00047860.
XX
PA   (UYRP ) UNIV ROCHESTER.
XX
PI   Kool ET;
XX
DR   WPI; 1998-144278/13.
XX
PT   Rolling circle synthesis of oligo:nucleotide(s) - using primed circular
PT   template to produce oligonucleotide multimer for cleavage.
XX
PS   Example 2; Col 45; 38pp; English.
XX
CC   The present sequence represents an oligonucleotide used in an example of
CC   the present invention. The present invention describes a method for
CC   synthesising a selected oligonucleotide (I) having well defined ends. The
CC   method comprises: (a) annealing a primer to a single-stranded (ss)
CC   circular template to yield a primed circular template, where the template
CC   comprises: (i) at least one nucleotide sequence complementary to (I); and
CC   (ii) at least one nucleotide effective to produce a cleavage site in the
CC   oligonucleotide multimer; (b) combining the primed circular template with
CC   at least two types of nucleotide triphosphates and a polymerase enzyme
CC   without the addition of auxiliary proteins to yield a ss oligonucleotide
CC   multimer complementary to the circular oligonucleotide template,
CC   comprising multiple copies of (I); and (c) cleaving the oligonucleotide
CC   multimer at the cleavage site to produce (I) having well defined ends.
CC   The method is used for the large-scale synthesis of DNA and RNA oligomers
CC   for use, e.g. as probes and diagnostic agents and/or therapeutic agents
XX
SQ   Sequence 26 BP; 24 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 26;
  Best Local Similarity   83.3%;  Pred. No. 2e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
                 ||   ||||||| ||||||||||
Db          2 AAAAAAAAAAAACAAAAAAAAAAA 25


RESULT 1766
AAV59215
ID   AAV59215 standard; DNA; 26 BP.
XX
AC   AAV59215;
XX
DT   14-DEC-1998  (first entry)
XX
DE   Circular template for linear oligomer dT12.
XX
KW   ss; circular; cyclic; RNA oligonucleotide; probe; standard; diagnostic;
KW   therapeutic agent.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_binding    1
FT                   /*tag=  a
FT                   /note= "Position 1 optionally bound to position 26"
FT   misc_binding    26
FT                   /*tag=  b
FT                   /note= "Position 26 optionally bound to position 1"
XX
PN   WO9838300-A1.
XX
PD   03-SEP-1998.
XX
PF   26-FEB-1998;   98WO-US003784.
XX
PR   26-FEB-1997;   97US-00805631.
XX
PA   (UYRP ) UNIV ROCHESTER.
XX
PI   Kool ET;
XX
DR   WPI; 1998-481202/41.
XX
PT   Synthesis of oligo:nucleotide(s) - using a single-stranded circular
PT   oligo:nucleotide template ribonucleotide tri:phosphate(s) and a
```

PT polymerase to form multimer(s) which can be cleaved.
XX
PS Example 2; Page 36; 100pp; English.
XX
CC The circular template was used for the synthesis of the oligomer dT12 in
CC an example of the method of the invention for synthesising an RNA
CC oligonucleotide, comprising combining a single-stranded circular
CC oligonucleotide template comprising at least one copy of a nucleotide
CC sequence complementary to the sequence of the desired RNA oligonucleotide
CC with at least 2 types of ribonucleotide triphosphate and a polymerase
CC enzyme to yield a single-stranded RNA oligonucleotide multimer
CC complementary to the circular oligonucleotide template, where the RNA
CC oligonucleotide multimer comprises multiple copies of the desired RNA
CC oligonucleotide. The methods can be used for producing RNA
CC oligonucleotides having a specific sequence and well defined ends. The
CC RNA oligonucleotides produced can be used as probes, standards and
CC diagnostic or therapeutic agents. They can be used for modifying the
CC structure or function of a target molecule. They can also be used to
CC cleave disease-associated RNA, DNA or protein
XX
SQ Sequence 26 BP; 24 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.6; DB 1; Length 26;
Best Local Similarity 83.3%; Pred. No. 2e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
|| ||||||| ||||||||||
Db 2 AAAAAAAAAAAACAAAAAAAAAAA 25

RESULT 1767
AAX30018
ID AAX30018 standard; DNA; 26 BP.
XX
AC AAX30018;
XX
DT 16-JUN-1999 (first entry)
XX
DE Precircle DNA oligonucleotide SEQ ID NO:5.
XX
KW Multimer; probe; diagnosis; synthesis; detection; polymerase; ss.
XX
OS Synthetic.
XX
PN WO9909216-A2.
XX
PD 25-FEB-1999.
XX
PF 13-AUG-1998; 98WO-US016776.
XX
PR 13-AUG-1997; 97US-00910632.
XX
PA (UYRP) UNIV ROCHESTER.
XX
PI Kool ET;
XX
DR WPI; 1999-181062/15.
XX
PT New detectably labelled oligonucleotide multimer, comprising multiple
PT contiguous copies of a repeated oligonucleotide - useful for detecting
PT target molecules in diagnosis and medicinal applications.
XX
PS Example 2; Page 41; 103pp; English.
XX
CC The present invention describes a detectably labelled oligonucleotide
CC multimer, comprising multiple contiguous copies of a repeated
CC oligonucleotides. The detectably labelled oligonucleotide multimer is
CC useful for detecting a target molecule. Oligonucleotide multimers may be
CC produced in sufficient quantity to be useful for diagnostic and medical
CC applications. The multimers are useful for affinity labelling of
CC proteins, and for signal amplification in highly sensitive affinity
CC capture and sequence identification applications. The method provides a
CC faster, cheaper and simpler way for large-scale production of DNA and RNA
CC oligomers and multimers. The incorporation of labels enables the
CC oligonucleotide multimers to be useful in diagnostics and medicine. The
CC present sequence represents an oligonucleotide used in an example from
CC the present invention
XX
SQ Sequence 26 BP; 24 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.6; DB 1; Length 26;
Best Local Similarity 83.3%; Pred. No. 2e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
|| ||||||| ||||||||||
Db 2 AAAAAAAAAAAACAAAAAAAAAAA 25

RESULT 1768
ADC65872
ID ADC65872 standard; DNA; 26 BP.
XX
AC ADC65872;
XX
DT 18-DEC-2003 (first entry)
XX
DE DNA oligonucleotide #5.
XX
KW RNA oligonucleotide synthesis; ribonucleotide triphosphate; polymerase;
KW electroporation; calcium phosphate treatment; lipid-mediated delivery;
KW cation-mediated delivery; bacterial infection; viral infection;
KW drug resistant infection; double stranded DNA oligomer; ss.
XX
OS Synthetic.
XX
PN US2003087241-A1.
XX
PD 08-MAY-2003.
XX
PF 30-NOV-2001; 2001US-00997931.
XX
PR 15-APR-1993; 93US-00047860.
PR 23-FEB-1995; 95US-00393439.
PR 26-FEB-1997; 97US-00805631.
PR 11-MAY-2000; 2000US-00569344.
XX
PA (UYRP) UNIV ROCHESTER.
XX
PI Kool ET;
XX
DR WPI; 2003-755141/71.
XX
PT Synthesizing RNA oligonucleotide involves combining single-stranded
PT circular oligonucleotide, ribonucleotide triphosphate and polymerase
PT enzyme to yield desired RNA complementary to circular oligonucleotide
PT template.
XX
PS Example 2; SEQ ID NO 5; 78pp; English.
XX
CC The invention relates to a method for synthesising an RNA
CC oligonucleotide, comprising combining a single-stranded circular
CC oligonucleotide template with at least two types of ribonucleotide
CC triphosphate and a polymerase enzyme to yield a single-stranded RNA
CC oligonucleotide multimer complementary to the circular oligonucleotide
CC template, where the RNA oligonucleotide multimer comprises multiple
CC copies of the desired RNA oligonucleotide. The method is useful for
CC synthesising an RNA oligonucleotide with well-defined ends. The circular
CC oligonucleotide is introduced into the cell using direct injection,
CC electroporation, calcium phosphate treatment, lipid-mediated delivery, or
CC cation-mediated delivery. The method is useful for treating bacterial
CC and/or viral infections in mammals, particularly drug resistant
CC infections, and for producing double stranded DNA oligomers. The method
CC is performed in the absence of an oligonucleotide primer, or without the
CC addition of auxiliary proteins. This sequence represents an

```
CC   oligonucleotide used in the method of the invention.
XX
SQ   Sequence 26 BP; 24 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 26;
  Best Local Similarity   83.3%;  Pred. No. 2e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||| ||||||||||||
Db          2 AAAAAAAAAAAACAAAAAAAAAAA 25


RESULT 1769
AAS01617
ID   AAS01617 standard; DNA; 26 BP.
XX
AC   AAS01617;
XX
DT   18-JUL-2001  (first entry)
XX
DE   Human MINT31/CACNA1G region 6 bisulfite GM6 reverse PCR primer.
XX
KW   Human; T-type calcium channel; CACNA1G; cytosine methylation; CpG island;
KW   cellular proliferative disorder; colorectal cancer; age related disease;
KW   apolipoprotein B; APOB; caudal type homeobox transcription factor 2;
KW   CDX2; epidermal growth factor receptor; EGFR; fibrillin-1; FBN1;
KW   G protein-coupled receptor 37; GPR37; heat shock 70kD protein 6; HSP70B';
KW   HSPA6; RasGAP-related protein; IQGAP2; proteinase-activated receptor 2;
KW   PAR2; paired-like homeodomain transcription factor 2; PITX2; klotho; KL;
KW   patched A; patched B; PTCHA; PTCHB; syndecan 1; syndecan 4; SDC1; SDC4;
KW   chromosome 17; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200119845-A1.
XX
PD   22-MAR-2001.
XX
PF   14-SEP-2000; 2000WO-US025479.
XX
PR   15-SEP-1999;   99US-00398522.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI   Issa J;
XX
DR   WPI; 2001-244777/25.
XX
PT   New nucleic acid molecule for use as a marker for screening cancer,
PT   comprises the coding region for a T-type calcium channel and regulatory
PT   sequences associated with the channel.
XX
PS   Claim 21; Page 35; 125pp; English.
XX
CC   The present sequence for bisulfite GM6 reverse PCR primer is used to
CC   study the methylation state of region 6 in human MINT31/T-type calcium
CC   channel CACNA1G which map to chromosome 17. The methylation state of
CC   specific regions within CpG islands associated with the CACNA1G gene
CC   correlate with several cancerous phenotypes involving various tissue and
CC   cell types. Since aberrant methylation of normally unmethylated CpG
CC   islands is often observed in immortalised and transformed cells, CACNA1G
CC   is implicated in cellular proliferative disorders e.g. leukaemia,
CC   colorectal, lung, breast and other cancers. The nucleic acid coding for
CC   CACNA1G is useful as a marker for screening cancer and age related
CC   diseases. A diagnostic kit containing primers (AAS01574-AAS01623) for
CC   amplification of a CpG-containing nucleic acid, where the primer
CC   hybridises with a target polynucleotide sequence (AAS01627-AAS01676), can
CC   be used for detecting aberrant methylation. The CpG island sequences
CC   (AAS01677-AAS01692) are selected from genes encoding CACNA1G,
CC   apolipoprotein B (APOB), caudal type homeobox transcription factor 2
CC   (CDX2), epidermal growth factor receptor (EGFR), fibrillin-1 (FBN1), G
CC   protein-coupled receptor 37 (GPR37), heat shock 70kD protein 6 (HSP70B';
CC   HSPA6), RasGAP-related protein (IQGAP2), klotho (KL), proteinase-
CC   activated receptor 2 (PAR2), paired-like homeodomain transcription factor
CC   2 (PITX2), patched A and B (PTCHA; PTCHB) and syndecan 1 and 4 (SDC1;
CC   SDC4) or a MINT31 sequence
XX
SQ   Sequence 26 BP; 18 A; 3 C; 0 G; 4 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 26;
  Best Local Similarity   94.4%;  Pred. No. 2e+03;
  Matches   17;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              :||||||||||||||||||
Db          3 RAAAAAAAAAAAAAAAAA 20


RESULT 1770
AAS01577
ID   AAS01577 standard; DNA; 26 BP.
XX
AC   AAS01577;
XX
DT   18-JUL-2001  (first entry)
XX
DE   Human T-type calcium channel CACNA1G R6 3'-bisulfite PCR primer.
XX
KW   Human; T-type calcium channel; CACNA1G; cytosine methylation; CpG island;
KW   cellular proliferative disorder; colorectal cancer; age related disease;
KW   apolipoprotein B; APOB; caudal type homeobox transcription factor 2;
KW   CDX2; epidermal growth factor receptor; EGFR; fibrillin-1; FBN1;
KW   G protein-coupled receptor 37; GPR37; heat shock 70kD protein 6; HSP70B';
KW   HSPA6; RasGAP-related protein; IQGAP2; proteinase-activated receptor 2;
KW   PAR2; paired-like homeodomain transcription factor 2; PITX2; klotho; KL;
KW   patched A; patched B; PTCHA; PTCHB; syndecan 1; syndecan 4; SDC1; SDC4;
KW   chromosome 17; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200119845-A1.
XX
PD   22-MAR-2001.
XX
PF   14-SEP-2000; 2000WO-US025479.
XX
PR   15-SEP-1999;   99US-00398522.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI   Issa J;
XX
DR   WPI; 2001-244777/25.
XX
PT   New nucleic acid molecule for use as a marker for screening cancer,
PT   comprises the coding region for a T-type calcium channel and regulatory
PT   sequences associated with the channel.
XX
PS   Claim 21; Page 34; 125pp; English.
XX
CC   The present sequence for 3'-bisulfite PCR primer is used to study the
CC   methylation state of region R6 in a novel human T-type calcium channel
CC   CACNA1G which maps to chromosome 17. The methylation state of specific
CC   regions within CpG islands associated with the CACNA1G gene correlate
CC   with several cancerous phenotypes involving various tissue and cell
CC   types. Since aberrant methylation of normally unmethylated CpG islands is
CC   often observed in immortalised and transformed cells, CACNA1G is
CC   implicated in cellular proliferative disorders e.g. leukaemia,
CC   colorectal, lung, breast and other cancers. The nucleic acid coding for
CC   CACNA1G is useful as a marker for screening cancer and age related
CC   diseases. A diagnostic kit containing primers (AAS01574-AAS01623) for
CC   amplification of a CpG-containing nucleic acid, where the primer
CC   hybridises with a target polynucleotide sequence (AAS01627-AAS01676), can
CC   be used for detecting aberrant methylation. The CpG island sequences
CC   (AAS01677-AAS01692) are selected from genes encoding CACNA1G,
```

```
CC   apolipoprotein B (APOB), caudal type homeobox transcription factor 2
CC   (CDX2), epidermal growth factor receptor (EGFR), fibrillin-1 (FBN1), G
CC   protein-coupled receptor 37 (GPR37), heat shock 70kD protein 6 (HSP70B';
CC   HSPA6), RasGAP-related protein (IQGAP2), klotho (KL), proteinase-
CC   activated receptor 2 (PAR2), paired-like homeodomain transcription factor
CC   2 (PITX2), patched A and B (PTCHA; PTCHB) and syndecan 1 and 4 (SDC1;
CC   SDC4) or a MINT31 sequence
XX
SQ   Sequence 26 BP; 18 A; 3 C; 0 G; 4 T; 0 U; 1 Other;

  Query Match              0.6%;  Score 17.6;  DB 1;  Length 26;
  Best Local Similarity   94.4%;  Pred. No. 2e+03;
  Matches   17;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              :||||||||||||||||||
Db          3 RAAAAAAAAAAAAAAAAA 20


RESULT 1771
AAS01670/c
ID   AAS01670 standard; DNA; 26 BP.
XX
AC   AAS01670;
XX
DT   18-JUL-2001  (first entry)
XX
DE   Human MINT31/CACNA1G region 6 reverse target sequence for bisulfite PCR.
XX
KW   Human; T-type calcium channel; CACNA1G; cytosine methylation; CpG island;
KW   cellular proliferative disorder; colorectal cancer; age related disease;
KW   apolipoprotein B; APOB; caudal type homeobox transcription factor 2;
KW   CDX2; epidermal growth factor receptor; EGFR; fibrillin-1; FBN1;
KW   G protein-coupled receptor 37; GPR37; heat shock 70kD protein 6; HSP70B';
KW   HSPA6; RasGAP-related protein; IQGAP2; proteinase-activated receptor 2;
KW   PAR2; paired-like homeodomain transcription factor 2; PITX2; klotho; KL;
KW   patched A; patched B; PTCHA; PTCHB; syndecan 1; syndecan 4; SDC1; SDC4;
KW   chromosome 17; ds.
XX
OS   Homo sapiens.
XX
PN   WO200119845-A1.
XX
PD   22-MAR-2001.
XX
PF   14-SEP-2000; 2000WO-US025479.
XX
PR   15-SEP-1999;   99US-00398522.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI   Issa J;
XX
DR   WPI; 2001-244777/25.
XX
PT   New nucleic acid molecule for use as a marker for screening cancer,
PT   comprises the coding region for a T-type calcium channel and regulatory
PT   sequences associated with the channel.
XX
PS   Claim 20; Page 36; 125pp; English.
XX
CC   The present sequence for human MINT31/T-type calcium channel CACNA1G
CC   region 6 reverse target sequence is used to study the methylation state
CC   of region 6 in MINT31/CACNA1G which map to chromosome 17. The methylation
CC   state of specific regions within CpG islands associated with the CACNA1G
CC   gene correlate with several cancerous phenotypes involving various tissue
CC   and cell types. Since aberrant methylation of normally unmethylated CpG
CC   islands is often observed in immortalised and transformed cells, CACNA1G
CC   is implicated in cellular proliferative disorders e.g. leukaemia,
CC   colorectal, lung, breast and other cancers. The nucleic acid coding for
CC   CACNA1G is useful as a marker for screening cancer and age related
CC   diseases. A diagnostic kit containing primers (AAS01574-AAS01623) for
CC   amplification of a CpG-containing nucleic acid, where the primer
CC   hybridises with a target polynucleotide sequence (AAS01627-AAS01676), can
CC   be used for detecting aberrant methylation. The CpG island sequences
CC   (AAS01677-AAS01692) are selected from genes encoding CACNA1G,
CC   apolipoprotein B (APOB), caudal type homeobox transcription factor 2
CC   (CDX2), epidermal growth factor receptor (EGFR), fibrillin-1 (FBN1), G
CC   protein-coupled receptor 37 (GPR37), heat shock 70kD protein 6 (HSP70B';
CC   HSPA6), RasGAP-related protein (IQGAP2), klotho (KL), proteinase-
CC   activated receptor 2 (PAR2), paired-like homeodomain transcription factor
CC   2 (PITX2), patched A and B (PTCHA; PTCHB) and syndecan 1 and 4 (SDC1;
CC   SDC4) or a MINT31 sequence
XX
SQ   Sequence 26 BP; 4 A; 0 C; 3 G; 18 T; 0 U; 1 Other;

  Query Match              0.6%;  Score 17.6;  DB 1;  Length 26;
  Best Local Similarity   94.4%;  Pred. No. 2e+03;
  Matches   17;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              :||||||||||||||||||
Db         24 RAAAAAAAAAAAAAAAAA 7


RESULT 1772
AAS01630
ID   AAS01630 standard; DNA; 26 BP.
XX
AC   AAS01630;
XX
DT   18-JUL-2001  (first entry)
XX
DE   Human CACNA1G R6 3'-target sequence for bisulfite PCR.
XX
KW   Human; T-type calcium channel; CACNA1G; cytosine methylation; CpG island;
KW   cellular proliferative disorder; colorectal cancer; age related disease;
KW   apolipoprotein B; APOB; caudal type homeobox transcription factor 2;
KW   CDX2; epidermal growth factor receptor; EGFR; fibrillin-1; FBN1;
KW   G protein-coupled receptor 37; GPR37; heat shock 70kD protein 6; HSP70B';
KW   HSPA6; RasGAP-related protein; IQGAP2; proteinase-activated receptor 2;
KW   PAR2; paired-like homeodomain transcription factor 2; PITX2; klotho; KL;
KW   patched A; patched B; PTCHA; PTCHB; syndecan 1; syndecan 4; SDC1; SDC4;
KW   chromosome 17; ds.
XX
OS   Homo sapiens.
XX
PN   WO200119845-A1.
XX
PD   22-MAR-2001.
XX
PF   14-SEP-2000; 2000WO-US025479.
XX
PR   15-SEP-1999;   99US-00398522.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI   Issa J;
XX
DR   WPI; 2001-244777/25.
XX
PT   New nucleic acid molecule for use as a marker for screening cancer,
PT   comprises the coding region for a T-type calcium channel and regulatory
PT   sequences associated with the channel.
XX
PS   Claim 20; Page 37; 125pp; English.
XX
CC   The present sequence for human T-type calcium channel R6 3'-target
CC   sequence (complementary to the 3'-bisulfite PCR primer) is used to study
CC   the methylation state of R6 of CACNA1G which maps to chromosome 17. The
CC   methylation state of specific regions within CpG islands associated with
CC   the CACNA1G gene correlate with several cancerous phenotypes involving
CC   various tissue and cell types. Since aberrant methylation of normally
CC   unmethylated CpG islands is often observed in immortalised and
CC   transformed cells, CACNA1G is implicated in cellular proliferative
CC   disorders e.g. leukaemia, colorectal, lung, breast and other cancers. The
```

```
CC   nucleic acid coding for CACNA1G is useful as a marker for screening
CC   cancer and age related diseases. A diagnostic kit containing primers
CC   (AAS01574-AAS01623) for amplification of a CpG-containing nucleic acid,
CC   where the primer hybridises with a target polynucleotide sequence
CC   (AAS01627-AAS01676), can be used for detecting aberrant methylation. The
CC   CpG island sequences (AAS01677-AAS01692) are selected from genes encoding
CC   CACNA1G, apolipoprotein B (APOB), caudal type homeobox transcription
CC   factor 2 (CDX2), epidermal growth factor receptor (EGFR), fibrillin-1
CC   (FBN1), G protein-coupled receptor 37 (GPR37), heat shock 70kD protein 6
CC   (HSP70B'; HSPA6), RasGAP-related protein (IQGAP2), klotho (KL),
CC   proteinase-activated receptor 2 (PAR2), paired-like homeodomain
CC   transcription factor 2 (PITX2), patched A and B (PTCHA; PTCHB) and
CC   syndecan 1 and 4 (SDC1; SDC4) or a MINT31 sequence
XX
SQ   Sequence 26 BP; 4 A; 0 C; 3 G; 18 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 26;
  Best Local Similarity   94.4%;  Pred. No. 2e+03;
  Matches   17;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTA 2187
                ||||||||||||||||:
Db          7 TTTTTTTTTTTTTTTTTR 24


RESULT 1773
AAD49491/c
ID   AAD49491 standard; DNA; 27 BP.
XX
AC   AAD49491;
XX
DT   24-MAR-2003  (first entry)
XX
DE   Oligonucleotide #2 used to clone C3Basic3 reverse HIV Tat protein.
XX
KW   Drug delivery construct; axon growth; nerve injury; ischaemic damage;
KW   stroke injury; gene therapy; neuroleptic; neuroprotective; ss.
XX
OS   Unidentified.
XX
PN   WO200283179-A2.
XX
PD   24-OCT-2002.
XX
PF   08-APR-2002; 2002WO-CA000480.
XX
PR   12-APR-2001; 2001CA-02342970.
PR   13-NOV-2001; 2001CA-02362004.
PR   15-JAN-2002; 2002CA-02367636.
XX
PA   (BIOA-) BIOAXONE THERAPEUTIQUE INC.
XX
PI   Mckerracher L;
XX
DR   WPI; 2003-092963/08.
XX
PT   New drug delivery construct comprising a transport and active agent
PT   region, useful for the manufacture of a pharmaceutical composition for
PT   treating nerve injury.
XX
PS   Example 14; Page 86; 188pp; English.
XX
CC   The invention relates to a new drug delivery construct comprises at least
CC   one transport agent region and an active agent region. The transport
CC   agent region is able to facilitate the uptake of the active agent region
CC   into a cell. The active agent region is an active therapeutic agent
CC   region able to facilitate axon growth and an analogue. The drug delivery
CC   construct is useful for suppressing the inhibition of neuronal axon
CC   growth, facilitating axon growth, treating nerve injury, treating
CC   ischaemic damage related to stroke injury. The drug delivery construct
CC   and the drug conjugate are useful for the manufacture of a pharmaceutical
CC   composition for treating nerve injury. The invention is useful in gene
CC   therapy. The present sequence is an oligonucleotide used to clone
CC   C3Basic3 reverse HIV Tat protein
XX
SQ   Sequence 27 BP; 0 A; 7 C; 1 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 27;
  Best Local Similarity   83.3%;  Pred. No. 2.2e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1492 GGAGAAAATGGAGAAACACAGGAA 1515
              | |||||| | ||||||| |||||
Db         26 GAAGAAAAAGAAGAAACAAAGGAA 3


RESULT 1774
AAV59216/c
ID   AAV59216 standard; DNA; 29 BP.
XX
AC   AAV59216;
XX
DT   14-DEC-1998  (first entry)
XX
DE   Linear multimer produced by rolling circle synthesis.
XX
KW   ss; RNA oligonucleotide; probe; standard; diagnostic; therapeutic agent.
XX
OS   Synthetic.
XX
PN   WO9838300-A1.
XX
PD   03-SEP-1998.
XX
PF   26-FEB-1998;   98WO-US003784.
XX
PR   26-FEB-1997;   97US-00805631.
XX
PA   (UYRP ) UNIV ROCHESTER.
XX
PI   Kool ET;
XX
DR   WPI; 1998-481202/41.
XX
PT   Synthesis of oligo:nucleotide(s) - using a single-stranded circular
PT   oligo:nucleotide template ribonucleotide tri:phosphate(s) and a
PT   polymerase to form multimer(s) which can be cleaved.
XX
PS   Example 2; Page 36; 100pp; English.
XX
CC   The linear multimer was produced by rolling circle synthesis in an
CC   example of the method of the invention for synthesising an RNA
CC   oligonucleotide, comprising combining a single-stranded circular
CC   oligonucleotide template comprising at least one copy of a nucleotide
CC   sequence complementary to the sequence of the desired RNA oligonucleotide
CC   with at least 2 types of ribonucleotide triphosphate and a polymerase
CC   enzyme to yield a single-stranded RNA oligonucleotide multimer
CC   complementary to the circular oligonucleotide template, where the RNA
CC   oligonucleotide multimer comprises multiple copies of the desired RNA
CC   oligonucleotide. The methods can be used for producing RNA
CC   oligonucleotides having a specific sequence and well defined ends. The
CC   RNA oligonucleotides produced can be used as probes, standards and
CC   diagnostic or therapeutic agents. They can be used for modifying the
CC   structure or function of a target molecule. They can also be used to
CC   cleave disease-associated RNA, DNA or protein
XX
SQ   Sequence 29 BP; 0 A; 0 C; 2 G; 27 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 29;
  Best Local Similarity   83.3%;  Pred. No. 2.5e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAAA 2804
                ||   ||||||| ||||||||||
Db         29 AAAAAAAAAAAACAAAAAAAAAAA 6
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```
RESULT 1775
ADC65873/c
ID   ADC65873 standard; DNA; 29 BP.
XX
AC   ADC65873;
XX
DT   18-DEC-2003  (first entry)
XX
DE   DNA oligonucleotide #6.
XX
KW   RNA oligonucleotide synthesis; ribonucleotide triphosphate; polymerase;
KW   electroporation; calcium phosphate treatment; lipid-mediated delivery;
KW   cation-mediated delivery; bacterial infection; viral infection;
KW   drug resistant infection; double stranded DNA oligomer; ss.
XX
OS   Synthetic.
XX
PN   US2003087241-A1.
XX
PD   08-MAY-2003.
XX
PF   30-NOV-2001; 2001US-00997931.
XX
PR   15-APR-1993;   93US-00047860.
PR   23-FEB-1995;   95US-00393439.
PR   26-FEB-1997;   97US-00805631.
PR   11-MAY-2000; 2000US-00569344.
XX
PA   (UYRP ) UNIV ROCHESTER.
XX
PI   Kool ET;
XX
DR   WPI; 2003-755141/71.
XX
PT   Synthesizing RNA oligonucleotide involves combining single-stranded
PT   circular oligonucleotide, ribonucleotide triphosphate and polymerase
PT   enzyme to yield desired RNA complementary to circular oligonucleotide
PT   template.
XX
PS   Example 2; SEQ ID NO 6; 78pp; English.
XX
CC   The invention relates to a method for synthesising an RNA
CC   oligonucleotide, comprising combining a single-stranded circular
CC   oligonucleotide template with at least two types of ribonucleotide
CC   triphosphate and a polymerase enzyme to yield a single-stranded RNA
CC   oligonucleotide multimer complementary to the circular oligonucleotide
CC   template, where the RNA oligonucleotide multimer comprises multiple
CC   copies of the desired RNA oligonucleotide. The method is useful for
CC   synthesising an RNA oligonucleotide with well-defined ends. The circular
CC   oligonucleotide is introduced into the cell using direct injection,
CC   electroporation, calcium phosphate treatment, lipid-mediated delivery, or
CC   cation-mediated delivery. The method is useful for treating bacterial
CC   and/or viral infections in mammals, particularly drug resistant
CC   infections, and for producing double stranded DNA oligomers. The method
CC   is performed in the absence of an oligonucleotide primer, or without the
CC   addition of auxiliary proteins. This sequence represents an
CC   oligonucleotide used in the method of the invention.
XX
SQ   Sequence 29 BP; 0 A; 0 C; 2 G; 27 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 29;
  Best Local Similarity   83.3%;  Pred. No. 2.5e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
                ||   ||||||| ||||||||||
Db         29 AAAAAAAAAAAACAAAAAAAAAA 6


RESULT 1776
AAF74918
ID   AAF74918 standard; DNA; 29 BP.
XX
AC   AAF74918;
XX
DT   23-MAY-2001  (first entry)
XX
DE   CD40L poly-A tract sequence SEQ ID NO:15.
XX
KW   Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW   diagnosis; antiarthritic; antirheumatic; immunosuppressive;
KW   antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200119844-A1.
XX
PD   22-MAR-2001.
XX
PF   13-SEP-2000; 2000WO-US024966.
XX
PR   13-SEP-1999;   99US-0153625P.
XX
PA   (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
PI   Crow MK,  Li Y;
XX
DR   WPI; 2001-244776/25.
XX
PT   New altered CD40L promoter for use in the study, diagnosis and treatment
PT   of a variety of inflammatory disorders and autoimmune diseases, such as
PT   rheumatoid arthritis.
XX
PS   Example 1; Fig 3; 90pp; English.
XX
CC   The present invention describes an isolated, purified nucleic acid, which
CC   is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC   residues 331-455 of the sequence comprising 455 nucleotides given in
CC   AAF74905 where A in the wild type sequence at position 331 (corresponding
CC   to position -125) is replaced with C. (I) has antiarthritic,
CC   antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC   be used in gene therapy. (I) is useful in the study, diagnosis and
CC   treatment of inflammatory and autoimmune diseases, as well as diseases in
CC   which elevated expression of CD40L is a factor, e.g., rheumatoid
CC   arthritis. The present sequence represents a CD40L poly-A tract sequence
CC   which is used in an example from the present invention
XX
SQ   Sequence 29 BP; 23 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 29;
  Best Local Similarity   83.3%;  Pred. No. 2.5e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
                ||   ||||||| ||||||||||
Db          1 AAAAAAAAAAAACAAAAAAAAAA 24


RESULT 1777
AAF74907
ID   AAF74907 standard; DNA; 29 BP.
XX
AC   AAF74907;
XX
DT   23-MAY-2001  (first entry)
XX
DE   CD40L poly-A tract sequence SEQ ID NO:4.
XX
KW   Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW   diagnosis; antiarthritic; antirheumatic; immunosuppressive;
KW   antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200119844-A1.
```

```
XX
PD   22-MAR-2001.
XX
PF   13-SEP-2000; 2000WO-US024966.
XX
PR   13-SEP-1999;   99US-0153625P.
XX
PA   (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
PI   Crow MK,  Li Y;
XX
DR   WPI; 2001-244776/25.
XX
PT   New altered CD40L promoter for use in the study, diagnosis and treatment
PT   of a variety of inflammatory disorders and autoimmune diseases, such as
PT   rheumatoid arthritis.
XX
PS   Example 1; Fig 3; 90pp; English.
XX
CC   The present invention describes an isolated, purified nucleic acid, which
CC   is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC   residues 331-455 of the sequence comprising 455 nucleotides given in
CC   AAF74905 where A in the wild type sequence at position 331 (corresponding
CC   to position -125) is replaced with C. (I) has antiarthritic,
CC   antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC   be used in gene therapy. (I) is useful in the study, diagnosis and
CC   treatment of inflammatory and autoimmune diseases, as well as diseases in
CC   which elevated expression of CD40L is a factor, e.g., rheumatoid
CC   arthritis. The present sequence represents a CD40L poly-A tract sequence
CC   which is used in an example from the present invention
XX
SQ   Sequence 29 BP; 23 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 29;
  Best Local Similarity   83.3%;  Pred. No. 2.5e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
                ||   |||||||||||| ||||||
Db          1 AAAAAAAAAAAAAAAAACAAAAAA 24


RESULT 1778
AAF74935
ID   AAF74935 standard; DNA; 29 BP.
XX
AC   AAF74935;
XX
DT   23-MAY-2001  (first entry)
XX
DE   CD40L poly-A tract sequence SEQ ID NO:32.
XX
KW   Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW   diagnosis; antiarthritic; antirheumatic; immunosuppressive;
KW   antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200119844-A1.
XX
PD   22-MAR-2001.
XX
PF   13-SEP-2000; 2000WO-US024966.
XX
PR   13-SEP-1999;   99US-0153625P.
XX
PA   (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
PI   Crow MK,  Li Y;
XX
DR   WPI; 2001-244776/25.
XX
PT   New altered CD40L promoter for use in the study, diagnosis and treatment
PT   of a variety of inflammatory disorders and autoimmune diseases, such as
PT   rheumatoid arthritis.
XX
PS   Example 1; Fig 3; 90pp; English.
XX
CC   The present invention describes an isolated, purified nucleic acid, which
CC   is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC   residues 331-455 of the sequence comprising 455 nucleotides given in
CC   AAF74905 where A in the wild type sequence at position 331 (corresponding
CC   to position -125) is replaced with C. (I) has antiarthritic,
CC   antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC   be used in gene therapy. (I) is useful in the study, diagnosis and
CC   treatment of inflammatory and autoimmune diseases, as well as diseases in
CC   which elevated expression of CD40L is a factor, e.g., rheumatoid
CC   arthritis. The present sequence represents a CD40L poly-A tract sequence
CC   which is used in an example from the present invention
XX
SQ   Sequence 29 BP; 23 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 29;
  Best Local Similarity   83.3%;  Pred. No. 2.5e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
                ||   |||||||||||| ||||||
Db          1 AAAAAAAAAAAAAAAAACAAAAAA 24


RESULT 1779
AAF74921
ID   AAF74921 standard; DNA; 29 BP.
XX
AC   AAF74921;
XX
DT   23-MAY-2001  (first entry)
XX
DE   CD40L poly-A tract sequence SEQ ID NO:18.
XX
KW   Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW   diagnosis; antiarthritic; antirheumatic; immunosuppressive;
KW   antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200119844-A1.
XX
PD   22-MAR-2001.
XX
PF   13-SEP-2000; 2000WO-US024966.
XX
PR   13-SEP-1999;   99US-0153625P.
XX
PA   (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
PI   Crow MK,  Li Y;
XX
DR   WPI; 2001-244776/25.
XX
PT   New altered CD40L promoter for use in the study, diagnosis and treatment
PT   of a variety of inflammatory disorders and autoimmune diseases, such as
PT   rheumatoid arthritis.
XX
PS   Example 1; Fig 3; 90pp; English.
XX
CC   The present invention describes an isolated, purified nucleic acid, which
CC   is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC   residues 331-455 of the sequence comprising 455 nucleotides given in
CC   AAF74905 where A in the wild type sequence at position 331 (corresponding
CC   to position -125) is replaced with C. (I) has antiarthritic,
CC   antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC   be used in gene therapy. (I) is useful in the study, diagnosis and
CC   treatment of inflammatory and autoimmune diseases, as well as diseases in
CC   which elevated expression of CD40L is a factor, e.g., rheumatoid
```

```
CC   arthritis. The present sequence represents a CD40L poly-A tract sequence
CC   which is used in an example from the present invention
XX
SQ   Sequence 29 BP; 23 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 29;
  Best Local Similarity   83.3%;  Pred. No. 2.5e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
                ||   |||||||||||| ||||||
Db          1 AAAAAAAAAAAAAAAAACAAAAAA 24


RESULT 1780
AAF74928
ID   AAF74928 standard; DNA; 29 BP.
XX
AC   AAF74928;
XX
DT   23-MAY-2001  (first entry)
XX
DE   CD40L poly-A tract sequence SEQ ID NO:25.
XX
KW   Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW   diagnosis; antiarthritic; antirheumatic; immunosuppressive;
KW   antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200119844-A1.
XX
PD   22-MAR-2001.
XX
PF   13-SEP-2000; 2000WO-US024966.
XX
PR   13-SEP-1999;   99US-0153625P.
XX
PA   (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
PI   Crow MK,  Li Y;
XX
DR   WPI; 2001-244776/25.
XX
PT   New altered CD40L promoter for use in the study, diagnosis and treatment
PT   of a variety of inflammatory disorders and autoimmune diseases, such as
PT   rheumatoid arthritis.
XX
PS   Example 1; Fig 3; 90pp; English.
XX
CC   The present invention describes an isolated, purified nucleic acid, which
CC   is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC   residues 331-455 of the sequence comprising 455 nucleotides given in
CC   AAF74905 where A in the wild type sequence at position 331 (corresponding
CC   to position -125) is replaced with C. (I) has antiarthritic,
CC   antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC   be used in gene therapy. (I) is useful in the study, diagnosis and
CC   treatment of inflammatory and autoimmune diseases, as well as diseases in
CC   which elevated expression of CD40L is a factor, e.g., rheumatoid
CC   arthritis. The present sequence represents a CD40L poly-A tract sequence
CC   which is used in an example from the present invention
XX
SQ   Sequence 29 BP; 23 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 29;
  Best Local Similarity   83.3%;  Pred. No. 2.5e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
                ||   |||||||||||| ||||||
Db          1 AAAAAAAAAAAAAAAAACAAAAAA 24


RESULT 1781
ABA97621/c
ID   ABA97621 standard; DNA; 31 BP.
XX
AC   ABA97621;
XX
DT   11-APR-2002  (first entry)
XX
DE   Poly j nucleotide sequence.
XX
KW   ss; fluorochrome; nucleic acid probe; fluorescence.
XX
OS   Unidentified.
XX
PN   JP2001286300-A.
XX
PD   16-OCT-2001.
XX
PF   20-APR-2000; 2000JP-00120097.
XX
PR   20-APR-1999;   99JP-00111601.
PR   24-AUG-1999;   99JP-00236666.
PR   30-AUG-1999;   99JP-00242693.
PR   01-FEB-2000; 2000JP-00028896.
XX
PA   (BIOI-) BIOINDUSTRY KYOKAI SH.
PA   (KANK-) KANKYO ENG KK.
PA   (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.
XX
DR   WPI; 2002-134193/18.
XX
PT   Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT   the obtained data.
XX
PS   Example 5; Page 17; 34pp; Japanese.
XX
CC   This invention relates to a method for measuring nucleic acids using a
CC   nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC   decreases the fluorescence of the fluorochrome when hybridised with a
CC   target nucleic acid, the decrease in the fluorescence is measured. The
CC   method can be used for measuring a target nucleic acid
XX
SQ   Sequence 31 BP; 4 A; 1 C; 0 G; 26 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 31;
  Best Local Similarity   83.3%;  Pred. No. 2.7e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
                ||   ||||| ||||||||||||
Db         31 AAAAAAAAAAGAAAAAAAAAAAAA 8


RESULT 1782
AAQ75552/c
ID   AAQ75552 standard; DNA; 19 BP.
XX
AC   AAQ75552;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
```

```
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 19 BP; 2 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAA 2801
              || ||||||||||||||||
Db         19 TTAAAAAAAAAAAAAAAA 1


RESULT 1783
AAQ75556
ID   AAQ75556 standard; DNA; 19 BP.
XX
AC   AAQ75556;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 19 BP; 1 A; 1 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||  |
Db          1 TTTTTTTTTTTTTTTTCA 19


RESULT 1784
AAQ75553/c
ID   AAQ75553 standard; DNA; 19 BP.
XX
AC   AAQ75553;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 19 BP; 1 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              | ||||||||||||||||||
Db         19 ATAAAAAAAAAAAAAAAAA 1


RESULT 1785
AAQ75554/c
ID   AAQ75554 standard; DNA; 19 BP.
XX
AC   AAQ75554;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
```

```
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 19 BP; 1 A; 1 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2803
              | ||||||||||||||||||
Db         19 GTAAAAAAAAAAAAAAAAA 1


RESULT 1786
AAQ75557
ID   AAQ75557 standard; DNA; 19 BP.
XX
AC   AAQ75557;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 19 BP; 0 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTTCT 19


RESULT 1787
AAQ75549
ID   AAQ75549 standard; DNA; 19 BP.
XX
AC   AAQ75549;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 19 BP; 0 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTTGT 19
```

```
RESULT 1788
AAQ75549/c
ID   AAQ75549 standard; DNA; 19 BP.
XX
AC   AAQ75549;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 19 BP; 0 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              | ||||||||||||||||||
Db         19 ACAAAAAAAAAAAAAAAAA 1


RESULT 1789
AAQ75548
ID   AAQ75548 standard; DNA; 19 BP.
XX
AC   AAQ75548;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 19 BP; 1 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTGA 19


RESULT 1790
AAQ75548/c
ID   AAQ75548 standard; DNA; 19 BP.
XX
AC   AAQ75548;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 19 BP; 1 A; 0 C; 1 G; 17 T; 0 U; 0 Other;
```

```
  Query Match             0.6%;  Score 17.4;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAA 2802
              | ||||||||||||||||||
Db         19 TCAAAAAAAAAAAAAAAAA 1


RESULT 1791
AAQ75550/c
ID   AAQ75550 standard; DNA; 19 BP.
XX
AC   AAQ75550;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 19 BP; 0 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              | ||||||||||||||||||
Db         19 GCAAAAAAAAAAAAAAAAAA 1


RESULT 1792
ADE29541
ID   ADE29541 standard; RNA; 19 BP.
XX
AC   ADE29541;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Mitogen activated protein kinase siNA oligonucleotide SEQ ID NO:163.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition;
KW   mitogen-activated protein kinase; MAP kinase; MAPK; RNA interference;
KW   cytostatic; anorectic; antidiabetic; antiinflammatory; antiasthmatic;
KW   immunosuppressive; antibacterial; antirheumatic; antiarthritic;
KW   antipsoriatic; gastrointestinal; obesity; diabetes; tumour;
KW   inflammatory disease; asthma; septic shock; rheumatoid arthritis;
KW   psoriasis; inflammatory bowel disease; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003072590-A1.
XX
PD   04-SEP-2003.
XX
PF   28-JAN-2003; 2003WO-US002510.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI   Mcswiggen J,  Beigelman L,  Usman N,  Haeberli P,  Chowrira B;
XX
DR   WPI; 2003-689980/65.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of cancer, downregulates expression of mitogen-activated
PT   protein kinase genes.
XX
PS   Example 3; SEQ ID NO 163; 164pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of a mitogen-activated protein kinase
CC   (MAPK) genes by RNA interference. Also described: (1) a method for
CC   modulating expression of MAPK genes in cells, tissue explants or
CC   organisms by introduction of siNA; (2) kits for in vitro or in vivo
CC   delivery of siNA; (3) conjugates and/or complexes of siNA; and (4)
CC   vectors that express siNA and cells containing these vectors. MAPK siNAs
CC   have cytostatic, anorectic, antidiabetic, antiinflammatory,
CC   antiasthmatic, immunosuppressive, antibacterial, antirheumatic,
CC   antiarthritic, antipsoriatic and gastrointestinal activities. The MAPK
CC   siNAs can be used to modulate the expression of MAPK genes, in cells,
CC   tissue explants or organisms, e.g. for treating obesity; diabetes types I
CC   and II; a wide range of tumours, and inflammatory diseases (asthma,
CC   septic shock, rheumatoid arthritis, psoriasis and inflammatory bowel
CC   disease). They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents a MAPK siNA which is used
CC   in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 16 A; 1 C; 0 G; 0 T; 2 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAA 2801
              :: ||||||||||||||||
Db          1 UUCAAAAAAAAAAAAAAAA 19


RESULT 1793
ADE29541/c
ID   ADE29541 standard; RNA; 19 BP.
XX
AC   ADE29541;
XX
```

DT 29-JAN-2004 (first entry)
XX
DE Mitogen activated protein kinase siNA oligonucleotide SEQ ID NO:163.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition;
KW mitogen-activated protein kinase; MAP kinase; MAPK; RNA interference;
KW cytostatic; anorectic; antidiabetic; antiinflammatory; antiasthmatic;
KW immunosuppressive; antibacterial; antirheumatic; antiarthritic;
KW antipsoriatic; gastrointestinal; obesity; diabetes; tumour;
KW inflammatory disease; asthma; septic shock; rheumatoid arthritis;
KW psoriasis; inflammatory bowel disease; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003072590-A1.
XX
PD 04-SEP-2003.
XX
PF 28-JAN-2003; 2003WO-US002510.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI Mcswiggen J, Beigelman L, Usman N, Haeberli P, Chowrira B;
XX
DR WPI; 2003-689980/65.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of cancer, downregulates expression of mitogen-activated
PT protein kinase genes.
XX
PS Example 3; SEQ ID NO 163; 164pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of a mitogen-activated protein kinase
CC (MAPK) genes by RNA interference. Also described: (1) a method for
CC modulating expression of MAPK genes in cells, tissue explants or
CC organisms by introduction of siNA; (2) kits for in vitro or in vivo
CC delivery of siNA; (3) conjugates and/or complexes of siNA; and (4)
CC vectors that express siNA and cells containing these vectors. MAPK siNAs
CC have cytostatic, anorectic, antidiabetic, antiinflammatory,
CC antiasthmatic, immunosuppressive, antibacterial, antirheumatic,
CC antiarthritic, antipsoriatic and gastrointestinal activities. The MAPK
CC siNAs can be used to modulate the expression of MAPK genes, in cells,
CC tissue explants or organisms, e.g. for treating obesity; diabetes types I
CC and II; a wide range of tumours, and inflammatory diseases (asthma,
CC septic shock, rheumatoid arthritis, psoriasis and inflammatory bowel
CC disease). They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents a MAPK siNA which is used
CC in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 16 A; 1 C; 0 G; 0 T; 2 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2170 TTTTTTTTTTTTTTTTTAA 2188
||||||||||||||||| ||
Db 19 TTTTTTTTTTTTTTTTGAA 1

RESULT 1794

ADE29704
ID ADE29704 standard; RNA; 19 BP.
XX
AC ADE29704;
XX
DT 29-JAN-2004 (first entry)
XX
DE Mitogen activated protein kinase siNA oligonucleotide SEQ ID NO:326.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition;
KW mitogen-activated protein kinase; MAP kinase; MAPK; RNA interference;
KW cytostatic; anorectic; antidiabetic; antiinflammatory; antiasthmatic;
KW immunosuppressive; antibacterial; antirheumatic; antiarthritic;
KW antipsoriatic; gastrointestinal; obesity; diabetes; tumour;
KW inflammatory disease; asthma; septic shock; rheumatoid arthritis;
KW psoriasis; inflammatory bowel disease; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003072590-A1.
XX
PD 04-SEP-2003.
XX
PF 28-JAN-2003; 2003WO-US002510.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI Mcswiggen J, Beigelman L, Usman N, Haeberli P, Chowrira B;
XX
DR WPI; 2003-689980/65.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of cancer, downregulates expression of mitogen-activated
PT protein kinase genes.
XX
PS Example 3; SEQ ID NO 326; 164pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of a mitogen-activated protein kinase
CC (MAPK) genes by RNA interference. Also described: (1) a method for
CC modulating expression of MAPK genes in cells, tissue explants or
CC organisms by introduction of siNA; (2) kits for in vitro or in vivo
CC delivery of siNA; (3) conjugates and/or complexes of siNA; and (4)
CC vectors that express siNA and cells containing these vectors. MAPK siNAs
CC have cytostatic, anorectic, antidiabetic, antiinflammatory,
CC antiasthmatic, immunosuppressive, antibacterial, antirheumatic,
CC antiarthritic, antipsoriatic and gastrointestinal activities. The MAPK
CC siNAs can be used to modulate the expression of MAPK genes, in cells,
CC tissue explants or organisms, e.g. for treating obesity; diabetes types I
CC and II; a wide range of tumours, and inflammatory diseases (asthma,
CC septic shock, rheumatoid arthritis, psoriasis and inflammatory bowel
CC disease). They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents a MAPK siNA which is used
CC in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 2 A; 0 C; 1 G; 0 T; 16 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 19;
Best Local Similarity 10.5%; Pred. No. 1.1e+03;
Matches 2; Conservative 16; Mismatches 1; Indels 0; Gaps 0;

Qy 2170 TTTTTTTTTTTTTTTTTAA 2188

```
                  ::::::::::::::::: ||
Db          1 UUUUUUUUUUUUUUUUGAA 19


RESULT 1795
ADE29704/c
ID   ADE29704 standard; RNA; 19 BP.
XX
AC   ADE29704;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Mitogen activated protein kinase siNA oligonucleotide SEQ ID NO:326.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition;
KW   mitogen-activated protein kinase; MAP kinase; MAPK; RNA interference;
KW   cytostatic; anorectic; antidiabetic; antiinflammatory; antiasthmatic;
KW   immunosuppressive; antibacterial; antirheumatic; antiarthritic;
KW   antipsoriatic; gastrointestinal; obesity; diabetes; tumour;
KW   inflammatory disease; asthma; septic shock; rheumatoid arthritis;
KW   psoriasis; inflammatory bowel disease; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003072590-A1.
XX
PD   04-SEP-2003.
XX
PF   28-JAN-2003; 2003WO-US002510.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI   Mcswiggen J,  Beigelman L,  Usman N,  Haeberli P,  Chowrira B;
XX
DR   WPI; 2003-689980/65.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of cancer, downregulates expression of mitogen-activated
PT   protein kinase genes.
XX
PS   Example 3; SEQ ID NO 326; 164pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of a mitogen-activated protein kinase
CC   (MAPK) genes by RNA interference. Also described: (1) a method for
CC   modulating expression of MAPK genes in cells, tissue explants or
CC   organisms by introduction of siNA; (2) kits for in vitro or in vivo
CC   delivery of siNA; (3) conjugates and/or complexes of siNA; and (4)
CC   vectors that express siNA and cells containing these vectors. MAPK siNAs
CC   have cytostatic, anorectic, antidiabetic, antiinflammatory,
CC   antiasthmatic, immunosuppressive, antibacterial, antirheumatic,
CC   antiarthritic, antipsoriatic and gastrointestinal activities. The MAPK
CC   siNAs can be used to modulate the expression of MAPK genes, in cells,
CC   tissue explants or organisms, e.g. for treating obesity; diabetes types I
CC   and II; a wide range of tumours, and inflammatory diseases (asthma,
CC   septic shock, rheumatoid arthritis, psoriasis and inflammatory bowel
CC   disease). They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents a MAPK siNA which is used
CC   in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 2 A; 0 C; 1 G; 0 T; 16 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAA 2801
              || |||||||||||||||
Db         19 TTCAAAAAAAAAAAAAAA 1


RESULT 1796
AAQ75582/c
ID   AAQ75582 standard; DNA; 20 BP.
XX
AC   AAQ75582;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAA 2801
              || |||||||||||||||
Db         19 TTAAAAAAAAAAAAAAAA 1


RESULT 1797
AAQ75579/c
ID   AAQ75579 standard; DNA; 20 BP.
XX
AC   AAQ75579;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
```

```
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 2 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAA 2801
              || ||||||||||||||||
Db         19 TTAAAAAAAAAAAAAAAAA 1


RESULT 1798
AAQ75597
ID   AAQ75597 standard; DNA; 20 BP.
XX
AC   AAQ75597;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||  |
Db          1 TTTTTTTTTTTTTTTTTCA 19


RESULT 1799
AAQ75595
ID   AAQ75595 standard; DNA; 20 BP.
XX
AC   AAQ75595;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||  |
Db          1 TTTTTTTTTTTTTTTTTCA 19


RESULT 1800
AAA91207
```

```
ID   AAA91207 standard; DNA; 20 BP.
XX
AC   AAA91207;
XX
DT   08-MAY-2001  (first entry)
XX
DE   Antisense IGFBP-5 inhibitor #13.
XX
KW   Insulin-like growth factor binding protein-5; IGFBP-5; human;
KW   antisense oligonucleotide; hormone-regulated cancer; prostatic cancer;
KW   breast cancer; therapy; ss.
XX
OS   Homo sapiens.
XX
PN   WO200105435-A2.
XX
PD   25-JAN-2001.
XX
PF   19-JUL-2000; 2000WO-CA000853.
XX
PR   19-JUL-1999;   99US-0144495P.
XX
PA   (UYBR-) UNIV BRITISH COLUMBIA.
PA   (MIYA/) MIYAKE H.
XX
PI   Gleave M;
XX
DR   WPI; 2001-168448/17.
XX
PT   Composition for treating hormone-regulated cancer, e.g. breast and
PT   prostatic tumors, comprising an antisense oligonucleotide that inhibits
PT   expression of insulin like growth factor binding protein-5 by hormone-
PT   regulated tumor cells.
XX
PS   Disclosure; Page 34; 45pp; English.
XX
CC   This sequence represents an antisense oligonucleotide targeted against
CC   human insulin-like growth factor binding protein-5 (IGFBP-5). The
CC   invention relates to a composition for treatment of hormone-regulated
CC   cancer, comprising an antisense oligonucleotide (such as this sequence)
CC   which inhibits expression of IGFBP-5 by hormone-regulated tumour cells.
CC   The compositions is useful for delaying progression of hormone-regulated
CC   tumour cells such as prostatic cancer cells or breast cancer cells, to an
CC   androgen-independent state, by treating hormone sensitive tumour cells
CC   with the antisense sequence which inhibits expression of IGFBP-5 by the
CC   tumour cells. The composition can also be used for treating a hormone-
CC   responsive cancer in an individual, and administering the composition to
CC   the individual after initiation of hormone-withdrawal to induce apoptotic
CC   cell death of hormone-responsive tumour cells, and therefore delaying the
CC   progression of hormone-responsive cancer cells to a hormone-independent
CC   state in the individual. It can also be used for inhibiting or delaying
CC   metastatic boney progression of an IGF-1 sensitive tumour in a mammal, by
CC   administering the composition to inhibit the expression of IGFBP-5 by the
CC   hormone-responsive cancer cells, and therefore inhibiting or delaying
CC   metastatic boney progression of the tumour
XX
SQ   Sequence 20 BP; 3 A; 1 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTAA 2188
              ||||||||||||||||  ||
Db          1 TTTTTTTTTTTTTTTCAA 19


RESULT 1801
AAQ75566/c
ID   AAQ75566 standard; DNA; 20 BP.
XX
AC   AAQ75566;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAA 2802
              | ||||||||||||||||
Db         19 TCAAAAAAAAAAAAAAAAA 1


RESULT 1802
AAQ75569/c
ID   AAQ75569 standard; DNA; 20 BP.
XX
AC   AAQ75569;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
```

```
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 0 A; 0 C; 1 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              || ||||||||||||||||
Db         20 AACAAAAAAAAAAAAAAA 2


RESULT 1803
AAQ75584/c
ID   AAQ75584 standard; DNA; 20 BP.
XX
AC   AAQ75584;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 2 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              | ||||||||||||||||
Db         19 ATAAAAAAAAAAAAAAAA 1


RESULT 1804
AAQ75585/c
ID   AAQ75585 standard; DNA; 20 BP.
XX
AC   AAQ75585;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 1 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              || ||||||||||||||||
Db         20 AATAAAAAAAAAAAAAAA 2


RESULT 1805
AAQ75568/c
ID   AAQ75568 standard; DNA; 20 BP.
XX
AC   AAQ75568;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
```

```
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              | ||||||||||||||||
Db         19 ACAAAAAAAAAAAAAAAA 1


RESULT 1806
AAQ75570
ID   AAQ75570 standard; DNA; 20 BP.
XX
AC   AAQ75570;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTGT 19


RESULT 1807
AAQ75589/c
ID   AAQ75589 standard; DNA; 20 BP.
XX
AC   AAQ75589;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2803
              | ||||||||||||||||
Db         19 GTAAAAAAAAAAAAAAAA 1


RESULT 1808
AAQ75590/c
ID   AAQ75590 standard; DNA; 20 BP.
XX
AC   AAQ75590;
XX
DT   04-AUG-1995  (first entry)
```

```
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 1 A; 2 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2803
              | ||||||||||||||||||
Db         19 GTAAAAAAAAAAAAAAAAA 1


RESULT 1809
AAQ75602
ID   AAQ75602 standard; DNA; 20 BP.
XX
AC   AAQ75602;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 0 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2184
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTCT 19


RESULT 1810
ABZ85534
ID   ABZ85534 standard; DNA; 20 BP.
XX
AC   ABZ85534;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Claim 15; SEQ ID NO 776; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
```

CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 18 A; 0 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2804
||||||||||||||| ||||
Db 1 AAAAAAAAAAAAAAGAAAA 19

RESULT 1811
ABZ88938
ID ABZ88938 standard; DNA; 20 BP.
XX
AC ABZ88938;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4180; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 17 A; 1 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2784 TGAAAAAAAAAAAAAAAA 2802
| |||||||||||||||||
Db 2 TCAAAAAAAAAAAAAAAAA 20

RESULT 1812
ABZ88813/c
ID ABZ88813 standard; DNA; 20 BP.
XX
AC ABZ88813;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4055; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

```
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 16 A; 0 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTAACTT 2191
              ||||||||||||||||| ||
Db         20 TTTTTTTTTTTTTTAAATT 2

RESULT 1813
AAQ75583/c
ID   AAQ75583 standard; DNA; 20 BP.
XX
AC   AAQ75583;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              | ||||||||||||||||||

Db         19 ATAAAAAAAAAAAAAAAAA 1

RESULT 1814
AAQ75587/c
ID   AAQ75587 standard; DNA; 20 BP.
XX
AC   AAQ75587;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              | ||||||||||||||||||
Db         19 GTAAAAAAAAAAAAAAAAA 1

RESULT 1815
AAQ75599
ID   AAQ75599 standard; DNA; 20 BP.
XX
AC   AAQ75599;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
```

XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTT 2184
||||||||||||||||| |
Db 1 TTTTTTTTTTTTTTTTTCT 19

RESULT 1816
ABZ89703
ID ABZ89703 standard; DNA; 20 BP.
XX
AC ABZ89703;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4945; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 16 A; 0 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2783 TTGAAAAAAAAAAAAAAAA 2801
|| ||||||||||||||||
Db 2 TTTAAAAAAAAAAAAAAAA 20

RESULT 1817
AAQ75574/c
ID AAQ75574 standard; DNA; 20 BP.
XX
AC AAQ75574;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The

```
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 0 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2803
              | ||||||||||||||||||
Db         19 GCAAAAAAAAAAAAAAAAA 1


RESULT 1818
AAQ75563
ID   AAQ75563 standard; DNA; 20 BP.
XX
AC   AAQ75563;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 1 A; 0 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTGA 19


RESULT 1819
AAQ75563/c
ID   AAQ75563 standard; DNA; 20 BP.
XX
AC   AAQ75563;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 1 A; 0 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAA 2802
              | ||||||||||||||||||
Db         19 TCAAAAAAAAAAAAAAAAA 1


RESULT 1820
AAQ75565
ID   AAQ75565 standard; DNA; 20 BP.
XX
AC   AAQ75565;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
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XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTGA 19


RESULT 1821
AAQ75565/c
ID   AAQ75565 standard; DNA; 20 BP.
XX
AC   AAQ75565;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAA 2802
              | ||||||||||||||||
Db         19 TCAAAAAAAAAAAAAAAA 1


RESULT 1822
AAQ75573/c
ID   AAQ75573 standard; DNA; 20 BP.
XX
AC   AAQ75573;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2803
              | ||||||||||||||||
Db         19 GCAAAAAAAAAAAAAAAA 1


RESULT 1823
AAQ75567
ID   AAQ75567 standard; DNA; 20 BP.
XX
AC   AAQ75567;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
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PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2184
              ||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTGT 19


RESULT 1824
AAQ75567/c
ID   AAQ75567 standard; DNA; 20 BP.
XX
AC   AAQ75567;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              | ||||||||||||||||||
Db         19 ACAAAAAAAAAAAAAAAAA 1


RESULT 1825
AAQ75571/c
ID   AAQ75571 standard; DNA; 20 BP.
XX
AC   AAQ75571;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 0 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2803
              | ||||||||||||||||||
Db         19 GCAAAAAAAAAAAAAAAAA 1


RESULT 1826
AAF99943/c
ID   AAF99943 standard; DNA; 20 BP.
XX
AC   AAF99943;
XX
DT   12-JUL-2001  (first entry)
XX
DE   Synthetic oligonucleotide #9.
```

XX
KW Oligonucleotide purification; liquid chromatography;
KW hydrophobic protective group; deprotection; ds.
XX
OS Synthetic.
XX
PN JP2000342265-A.
XX
PD 12-DEC-2000.
XX
PF 02-JUN-1999; 99JP-00154974.
XX
PR 02-JUN-1999; 99JP-00154974.
XX
PA (TOAG) TOA GOSEI CHEM IND LTD.
XX
DR WPI; 2001-268251/28.
XX
PT A process for purification of oligonucleotides using liquid
PT chromatography.
XX
PS Example 1; Page 4; 13pp; Japanese.
XX
CC The present sequence is an oligonucleotide provided in a specification
CC relating to the simplified purification of oligonucleotides by liquid
CC chromatography. The process comprises: (a) pouring oligonucleotides
CC protected with a hydrophobic group and oligonucleotide with no protective
CC group into a liquid chromatography column packed with an acid and alkali
CC resistant packing agent, such as polystyrene resin; (b) pouring a mixed
CC developing solvent composed of a buffer made from a volatile salt and a
CC water soluble organic solvent at a suitable concentration gradient into
CC the column; (c) pouring an acid, particularly 6-16 v/v% acetic acid, into
CC the column to deprotect the oligonucleotides protected with the
CC hydrophobic group; (d) pouring a mixed developing solvent composed of a
CC buffer made from a volatile salt, particularly 0.05-0.5 N aqueous
CC ammonium hydrogencarbonate solution adjusted at pH 8-10, and a water
CC soluble organic solvent at a suitable concentration gradient to elute the
CC deprotected oligonucleotides; and (e) removal of the solvent and the salt
CC from the eluted oligonucleotides
XX
SQ Sequence 20 BP; 17 A; 1 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2169 TTTTTTTTTTTTTTTTTA 2187
||||||||| |||||||||
Db 19 TTTTTTTCTTTTTTTTA 1

RESULT 1827
ABA05917
ID ABA05917 standard; DNA; 20 BP.
XX
AC ABA05917;
XX
DT 05-MAR-2002 (first entry)
XX
DE Hepatitis B virus diagnostic PCR primer SEQ ID NO 7.
XX
KW Hepatitis B virus; HBV; infection; hepatocellular carcinoma; diagnosis;
KW PCR primer; ss.
XX
OS Hepatitis B virus.
XX
PN EP1152063-A1.
XX
PD 07-NOV-2001.
XX
PF 03-MAY-2000; 2000EP-00109436.
XX
PR 03-MAY-2000; 2000EP-00109436.
XX
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI Schroeder KH, Koike K;
XX
DR WPI; 2002-068256/10.
XX
PT Diagnosing hepatitis B virus (HBV) infection stages and determining the
PT risk for hepatocellular carcinoma, comprises identifying full length HBV
PT transcripts and truncated HBV transcripts in a serum sample.
XX
PS Example 1; Page 6; 25pp; English.
XX
CC The invention relates to diagnosis of hepatitis B virus (HBV) infection
CC stages comprising identification of full length HBV transcripts (I) and
CC truncated HBV transcripts (II) in a serum sample, where the ratio of I:II
CC is indicative of a particular infection stage. The method is useful for
CC diagnosing HBV infection stages and determining the risk for developing
CC hepatocellular carcinoma. The present sequence is that of a HBV
CC diagnostic PCR primer, useful for the invention
XX
SQ Sequence 20 BP; 1 A; 2 C; 1 G; 16 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2172 TTTTTTTTTTTTTTAACT 2190
|||||||||||||||| ||
Db 1 TTTTTTTTTTTTTTAGCT 19

RESULT 1828
ABZ88879/c
ID ABZ88879 standard; DNA; 20 BP.
XX
AC ABZ88879;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4121; 872pp; English.
XX

CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 16 A; 1 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2174 TTTTTTTTTTTTTAACTTT 2192
||||||||||||||| |||
Db 20 TTTTTTTTTTTTTAAGTTT 2

RESULT 1829
ABZ85669/c
ID ABZ85669 standard; DNA; 20 BP.
XX
AC ABZ85669;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Claim 15; SEQ ID NO 911; 872pp; English.
XX

CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 0 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAAAAAAAAA 2803
||||||||| ||||||||||
Db 19 GAAAAAAAGAAAAAAAAAA 1

RESULT 1830
ABZ90829
ID ABZ90829 standard; DNA; 20 BP.
XX
AC ABZ90829;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 6071; 872pp; English.
XX

```
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 8 A; 4 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1486 AACCCTGGAGAAAATGGAG 1504
              ||||||| ||||||||||||
Db          2 AACCCTGCAGAAAATGGAG 20


RESULT 1831
ABZ89301
ID   ABZ89301 standard; DNA; 20 BP.
XX
AC   ABZ89301;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 4543; 872pp; English.
XX
```

```
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 17 A; 2 C; 0 G; 1 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAA 2802
              | |||||||||||||||||
Db          2 TCAAAAAAAAAAAAAAAAA 20


RESULT 1832
ABZ89301/c
ID   ABZ89301 standard; DNA; 20 BP.
XX
AC   ABZ89301;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 4543; 872pp; English.
XX
```

```
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 17 A; 2 C; 0 G; 1 T; 0 U; 0 Other;

  Query Match              0.6%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTA 2187
                ||||||||||||||||| |
Db         20 TTTTTTTTTTTTTTTTTGA 2

RESULT 1833
AAQ75731/c
ID   AAQ75731 standard; DNA; 21 BP.
XX
AC   AAQ75731;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match              0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAA 2801
                || |||||||||||||||||
Db         19 TTAAAAAAAAAAAAAAAAA 1

RESULT 1834
AAQ75734/c
ID   AAQ75734 standard; DNA; 21 BP.
XX
AC   AAQ75734;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match              0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAA 2801
                || |||||||||||||||||
Db         19 TTAAAAAAAAAAAAAAAAA 1

RESULT 1835
AAQ75649/c
ID   AAQ75649 standard; DNA; 21 BP.
XX
AC   AAQ75649;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
```

```
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 0 C; 1 G; 20 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              ||| ||||||||||||||||
Db         21 AAACAAAAAAAAAAAAAA 3


RESULT 1836
AAQ75701/c
ID   AAQ75701 standard; DNA; 21 BP.
XX
AC   AAQ75701;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2803
              | ||||||||||||||||
Db         19 GTAAAAAAAAAAAAAAAA 1


RESULT 1837
AAF24290/c
ID   AAF24290 standard; DNA; 21 BP.
XX
AC   AAF24290;
XX
DT   03-APR-2001  (first entry)
XX
DE   Complementary nucleic acid detection method related sequence #5.
XX
KW   Complementary nucleic acid; gene analysis; polymorphism; variation;
KW   DNA chip; primer; ss.
XX
OS   Unidentified.
XX
PN   EP1065278-A2.
XX
PD   03-JAN-2001.
XX
PF   07-JUN-2000; 2000EP-00112235.
XX
PR   07-JUN-1999;   99JP-00159339.
XX
PA   (FUJF ) FUJI PHOTO FILM CO LTD.
XX
PI   Makino Y,  Abe Y,  Ogawa M,  Takagi M,  Takenaka S,  Yamashita K;
XX
DR   WPI; 2001-140003/15.
XX
PT   Determining complementarity of nucleotide fragment for gene analysis, by
PT   comparing flow of electric current from or to electroconductive substrate
PT   through DNA fragment, with reference obtained from its complement.
XX
PS   Example 1; Page 12; 28pp; English.
XX
CC   The present invention provides a method for analysing a nucleic acid
CC   strand to determine the degree of complementarity between two sequences.
CC   This involves the measurement of an electric current along the annealed
CC   strands compared to a standard. This is useful in the analysis of genetic
CC   polymorphisms and variation between genes
XX
SQ   Sequence 21 BP; 1 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              ||||||||| |||||||||
Db         21 AAAAAAAAATAAAAAAAAA 3
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RESULT 1838
ABX79794/c
ID   ABX79794 standard; cDNA; 21 BP.
XX
AC   ABX79794;
XX
DT   17-APR-2003  (first entry)
XX
DE   EST polymorphic DNA repeat polynucleotide #119.
XX
KW   EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
KW   polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
KW   Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
KW   Haw River syndrome; Huntington's disease; fragile-X syndrome;
KW   Fredreich's ataxis; myotonic dystrophy; hyperandrogenaemia;
KW   spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
XX
OS   Homo sapiens.
XX
PN   US6472154-B1.
XX
PD   29-OCT-2002.
XX
PF   31-DEC-1999;   99US-00475947.
XX
PR   31-DEC-1999;   99US-00475947.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Garner HR,  Wren JD,  Minna JD,  Fondon JW;
XX
DR   WPI; 2003-208818/20.
XX
PT   Identifying a candidate polymorphic repeat within a coding sequence, for
PT   understanding or treating genetic disease, comprises detecting tandem
PT   repeats in a target coding sequence and scoring the repeats for
PT   polymorphic probability.
XX
PS   Example; Col 495; 588pp; English.
XX
CC   The invention discloses a method for identifying a candidate polymorphic
CC   repeat within a coding sequence (expressed sequence tag, EST), which
CC   comprises detecting tandem repeats in a target coding sequence, scoring
CC   the repeats for polymorphic probability and generating a dataset
CC   correlating the repeats with polymorphic probability to identify a
CC   candidate polymorphic repeat. The computational methods (polymorphic
CC   marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
CC   useful for identifying and detecting candidate polymorphic repeats in
CC   human genes, which can be used to understand, treat or eliminate genetic
CC   diseases, predispositions or adverse drug-treatment reactions. Examples
CC   of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
CC   syndrome, Huntington's disease, fragile-X syndrome, Fredreich's ataxis,
CC   myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
CC   spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
CC   the polymorphic repeats identified for a search of human ESTs
XX
SQ   Sequence 21 BP; 1 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||| |||||||||
Db         21 AAAAAAAAATAAAAAAAAA 3


RESULT 1839
AAQ75752
ID   AAQ75752 standard; DNA; 21 BP.
XX
AC   AAQ75752;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||  |
Db          1 TTTTTTTTTTTTTTTTTCA 19


RESULT 1840
AAQ75719/c
ID   AAQ75719 standard; DNA; 21 BP.
XX
AC   AAQ75719;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
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PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAA 2801
                || ||||||||||||||||
Db         19 TTAAAAAAAAAAAAAAAAA 1


RESULT 1841
AAQ75722/c
ID   AAQ75722 standard; DNA; 21 BP.
XX
AC   AAQ75722;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAA 2801
                || ||||||||||||||||
Db         19 TTAAAAAAAAAAAAAAAAA 1


RESULT 1842
AAQ75751
ID   AAQ75751 standard; DNA; 21 BP.
XX
AC   AAQ75751;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTA 2187
                ||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTCA 19


RESULT 1843
AAQ75759
ID   AAQ75759 standard; DNA; 21 BP.
XX
AC   AAQ75759;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
```

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PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTCA 19


RESULT 1844
AAQ75720/c
ID   AAQ75720 standard; DNA; 21 BP.
XX
AC   AAQ75720;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 3 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAA 2801
              || |||||||||||||||
Db         19 TTAAAAAAAAAAAAAAAA 1


RESULT 1845
AAQ75651
ID   AAQ75651 standard; DNA; 21 BP.
XX
AC   AAQ75651;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2184
              ||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTGT 19


RESULT 1846
AAQ75702/c
ID   AAQ75702 standard; DNA; 21 BP.
XX
AC   AAQ75702;
XX
DT   04-AUG-1995  (first entry)
```

XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 3 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAAAAAAAA 2803
| ||||||||||||||||||
Db 19 GTAAAAAAAAAAAAAAAA 1

RESULT 1847
AAQ75675/c
ID AAQ75675 standard; DNA; 21 BP.
XX
AC AAQ75675;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2804
| ||||||||||||||||||
Db 19 ATAAAAAAAAAAAAAAAA 1

RESULT 1848
AAQ75643/c
ID AAQ75643 standard; DNA; 21 BP.
XX
AC AAQ75643;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 6; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2804
| ||||||||||||||||||

```
Db         19 ACAAAAAAAAAAAAAAAAA 1


RESULT 1849
AAQ75695/c
ID   AAQ75695 standard; DNA; 21 BP.
XX
AC   AAQ75695;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              | ||||||||||||||||||
Db         19 GTAAAAAAAAAAAAAAAAA 1


RESULT 1850
AAQ75646/c
ID   AAQ75646 standard; DNA; 21 BP.
XX
AC   AAQ75646;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
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CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              | ||||||||||||||||||
Db         19 ACAAAAAAAAAAAAAAAAA 1


RESULT 1851
AAQ75678/c
ID   AAQ75678 standard; DNA; 21 BP.
XX
AC   AAQ75678;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
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CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
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CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              | ||||||||||||||||||
Db         19 ATAAAAAAAAAAAAAAAAA 1


RESULT 1852
AAQ75779
ID   AAQ75779 standard; DNA; 21 BP.
XX
AC   AAQ75779;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTCT 19


RESULT 1853
AAQ75698/c
ID   AAQ75698 standard; DNA; 21 BP.
XX
AC   AAQ75698;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2803
              | ||||||||||||||||||
Db         19 GTAAAAAAAAAAAAAAAAA 1


RESULT 1854
AAQ75699/c
ID   AAQ75699 standard; DNA; 21 BP.
XX
AC   AAQ75699;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
```

```
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2803
              |||||||||||||||||
Db         19 GTAAAAAAAAAAAAAAAAA 1


RESULT 1855
AAQ75635/c
ID   AAQ75635 standard; DNA; 21 BP.
XX
AC   AAQ75635;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         19 TCAAAAAAAAAAAAAAAAA 1


RESULT 1856
AAQ75782
ID   AAQ75782 standard; DNA; 21 BP.
XX
AC   AAQ75782;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 3 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTCT 19


RESULT 1857
AAQ75679/c
ID   AAQ75679 standard; DNA; 21 BP.
XX
AC   AAQ75679;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
```

```
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              || ||||||||||||||||
Db         20 AATAAAAAAAAAAAAAAA 2

RESULT 1858
AAQ75638/c
ID   AAQ75638 standard; DNA; 21 BP.
XX
AC   AAQ75638;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAA 2802
              | ||||||||||||||||
Db         19 TCAAAAAAAAAAAAAAAA 1

RESULT 1859
AAQ75647/c
ID   AAQ75647 standard; DNA; 21 BP.
XX
AC   AAQ75647;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 0 C; 2 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              || ||||||||||||||||
Db         20 AACAAAAAAAAAAAAAAA 2

RESULT 1860
AAQ75654
ID   AAQ75654 standard; DNA; 21 BP.
XX
AC   AAQ75654;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
```

```
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||  |
Db          1 TTTTTTTTTTTTTTTTGT 19


RESULT 1861
AAQ75671/c
ID   AAQ75671 standard; DNA; 21 BP.
XX
AC   AAQ75671;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              | ||||||||||||||||||
Db         19 ATAAAAAAAAAAAAAAAAA 1


RESULT 1862
AAQ75674/c
ID   AAQ75674 standard; DNA; 21 BP.
XX
AC   AAQ75674;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              | ||||||||||||||||||
Db         19 ATAAAAAAAAAAAAAAAAA 1
```

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RESULT 1863
AAQ75687/c
ID   AAQ75687 standard; DNA; 21 BP.
XX
AC   AAQ75687;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              | ||||||||||||||||||
Db         19 GTAAAAAAAAAAAAAAAAAA 1


RESULT 1864
AAQ75690/c
ID   AAQ75690 standard; DNA; 21 BP.
XX
AC   AAQ75690;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              | ||||||||||||||||||
Db         19 GTAAAAAAAAAAAAAAAAAA 1


RESULT 1865
AAQ75767
ID   AAQ75767 standard; DNA; 21 BP.
XX
AC   AAQ75767;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
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```
SQ   Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2184
              ||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTTCT 19


RESULT 1866
AAQ75689/c
ID   AAQ75689 standard; DNA; 21 BP.
XX
AC   AAQ75689;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2803
              | |||||||||||||||||
Db         19 GTAAAAAAAAAAAAAAAAA 1


RESULT 1867
AAQ75673/c
ID   AAQ75673 standard; DNA; 21 BP.
XX
AC   AAQ75673;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              | |||||||||||||||||
Db         19 ATAAAAAAAAAAAAAAAAA 1


RESULT 1868
AAQ75770
ID   AAQ75770 standard; DNA; 21 BP.
XX
AC   AAQ75770;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
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XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2184
              ||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTCT 19


RESULT 1869
AAQ75626/c
ID   AAQ75626 standard; DNA; 21 BP.
XX
AC   AAQ75626;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAA 2802
              | |||||||||||||||||
Db         19 TCAAAAAAAAAAAAAAAAA 1


RESULT 1870
AAQ75669/c
ID   AAQ75669 standard; DNA; 21 BP.
XX
AC   AAQ75669;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2803
              | |||||||||||||||||
Db         19 GCAAAAAAAAAAAAAAAAA 1


RESULT 1871
AAQ75634/c
ID   AAQ75634 standard; DNA; 21 BP.
XX
AC   AAQ75634;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
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PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAA 2802
              | ||||||||||||||||||
Db         19 TCAAAAAAAAAAAAAAAAA 1


RESULT 1872
AAQ75665/c
ID   AAQ75665 standard; DNA; 21 BP.
XX
AC   AAQ75665;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              | ||||||||||||||||||
Db         19 GCAAAAAAAAAAAAAAAAA 1


RESULT 1873
AAQ75641/c
ID   AAQ75641 standard; DNA; 21 BP.
XX
AC   AAQ75641;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 0 C; 2 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              | ||||||||||||||||||
Db         19 ACAAAAAAAAAAAAAAAAA 1


RESULT 1874
AAQ75632/c
ID   AAQ75632 standard; DNA; 21 BP.
XX
AC   AAQ75632;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
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KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 6; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2784 TGAAAAAAAAAAAAAAAAA 2802
| ||||||||||||||||||
Db 19 TCAAAAAAAAAAAAAAAAA 1

RESULT 1875
AAQ75670/c
ID AAQ75670 standard; DNA; 21 BP.
XX
AC AAQ75670;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 3 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAAAAAAAAA 2803
| ||||||||||||||||||
Db 19 GCAAAAAAAAAAAAAAAAA 1

RESULT 1876
AAQ75657/c
ID AAQ75657 standard; DNA; 21 BP.
XX
AC AAQ75657;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 6; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAAAAAAAAA 2803
| ||||||||||||||||||
Db 19 GCAAAAAAAAAAAAAAAAA 1

RESULT 1877

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AAQ75631
ID   AAQ75631 standard; DNA; 21 BP.
XX
AC   AAQ75631;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTA 2187
                ||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTTGA 19


RESULT 1878
AAQ75631/c
ID   AAQ75631 standard; DNA; 21 BP.
XX
AC   AAQ75631;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAA 2802
              | |||||||||||||||||
Db         19 TCAAAAAAAAAAAAAAAAA 1


RESULT 1879
AAQ75639
ID   AAQ75639 standard; DNA; 21 BP.
XX
AC   AAQ75639;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 0 C; 3 G; 18 T; 0 U; 0 Other;
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  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||  |
Db          1 TTTTTTTTTTTTTTTTGT 19


RESULT 1880
AAQ75639/c
ID   AAQ75639 standard; DNA; 21 BP.
XX
AC   AAQ75639;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 0 C; 3 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              | ||||||||||||||||||
Db         19 ACAAAAAAAAAAAAAAAAA 1


RESULT 1881
AAQ75667/c
ID   AAQ75667 standard; DNA; 21 BP.
XX
AC   AAQ75667;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 2 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2803
              | ||||||||||||||||||
Db         19 GCAAAAAAAAAAAAAAAAA 1


RESULT 1882
AAQ75642
ID   AAQ75642 standard; DNA; 21 BP.
XX
AC   AAQ75642;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
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CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||  |
Db          1 TTTTTTTTTTTTTTTTGT 19


RESULT 1883
AAQ75642/c
ID   AAQ75642 standard; DNA; 21 BP.
XX
AC   AAQ75642;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              | ||||||||||||||||||
Db         19 ACAAAAAAAAAAAAAAAAA 1


RESULT 1884
AAQ75655/c
ID   AAQ75655 standard; DNA; 21 BP.
XX
AC   AAQ75655;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 1 C; 3 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2803
              | ||||||||||||||||||
Db         19 GCAAAAAAAAAAAAAAAAA 1


RESULT 1885
AAQ75663/c
ID   AAQ75663 standard; DNA; 21 BP.
XX
AC   AAQ75663;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
```

```
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              | ||||||||||||||||||
Db         19 GCAAAAAAAAAAAAAAAAA 1


RESULT 1886
AAQ75624
ID   AAQ75624 standard; DNA; 21 BP.
XX
AC   AAQ75624;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTGA 19


RESULT 1887
AAQ75624/c
ID   AAQ75624 standard; DNA; 21 BP.
XX
AC   AAQ75624;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAA 2802
              | ||||||||||||||||||
Db         19 TCAAAAAAAAAAAAAAAAA 1


RESULT 1888
AAQ75666/c
ID   AAQ75666 standard; DNA; 21 BP.
XX
AC   AAQ75666;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
```

```
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2803
              | ||||||||||||||||||
Db         19 GCAAAAAAAAAAAAAAAAA 1


RESULT 1889
AAQ75623
ID   AAQ75623 standard; DNA; 21 BP.
XX
AC   AAQ75623;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 0 C; 3 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||  |
Db          1 TTTTTTTTTTTTTTTTTGA 19


RESULT 1890
AAQ75623/c
ID   AAQ75623 standard; DNA; 21 BP.
XX
AC   AAQ75623;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 0 C; 3 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAA 2802
              | ||||||||||||||||||
Db         19 TCAAAAAAAAAAAAAAAAA 1


RESULT 1891
AAQ75658/c
ID   AAQ75658 standard; DNA; 21 BP.
```

```
XX
AC   AAQ75658;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 2 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2803
              | ||||||||||||||||||
Db         19 GCAAAAAAAAAAAAAAAAA 1


RESULT 1892
ADE80976
ID   ADE80976 standard; DNA; 21 BP.
XX
AC   ADE80976;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human papillomavirus L1 gene type-specific PCR primer SEQ ID NO:26.
XX
KW   detection; human papillomavirus; HPV; genotype;
KW   HPV genus-specific primer; HPV genus-specific probe; amplification;
KW   hybridisation; genotyping; L1 gene; PCR primer; ss.
XX
OS   Synthetic.
OS   Human papillomavirus.
XX
PN   WO2003076667-A1.
XX
PD   18-SEP-2003.
XX
PF   10-MAR-2003; 2003WO-HU000020.
XX
PR   14-MAR-2002; 2002HU-00000981.
XX
PA   (JENE/) JENEY C.
PA   (TAKA/) TAKACS T.
XX
PI   Jeney C,  Takacs T;
XX
DR   WPI; 2003-902774/82.
XX
PT   Use of amplification primer-mixture and human papillomavirus genus-
PT   specific hybridization probes, for detecting and genotyping human
PT   papillomavirus in biological samples.
XX
PS   Claim 2; SEQ ID NO 26; 61pp; English.
XX
CC   The present invention describes a method for detecting many human
CC   papillomavirus (HPV) genotypes from biological samples. The method
CC   comprises amplifying and hybridising the extracted nucleic acid molecules
CC   with HPV genus-specific primers and probes designed from HPV genomic
CC   regions. Amplification primer-mixtures, consensus primers, type-specific
CC   primers, hybridisation probes, and reagent kits of the present invention
CC   can be used for detecting and genotyping HPV. The primer mixture is
CC   useful for the amplification of the 3, 4, 6, 7, 9, 10, 11, 12, 13, 14,
CC   16, 18, 20, 24, 26, 28, 29, 30, 31, 32, 33, 34, 35, 36, 39, 39, 40, 41,
CC   42, 44, 45, 51, 52, 53, 54, 55, 56, 58, 49, 60, 61, 66, 67, 68, 72, 74 or
CC   77 genotypes of HPV. The HPV genomic regions are useful for designing HPV
CC   genus-specific and HPV genotype-specific hybridisation probes. The
CC   present sequence is used in the exemplification of the present invention.
XX
SQ   Sequence 21 BP; 8 A; 2 C; 4 G; 7 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2533 ATACAGGGTATTAAGAATT 2551
              ||||||||||| ||||||
Db          3 ATACAGGGTATTTAGAATT 21


RESULT 1893
AAT33702
ID   AAT33702 standard; DNA; 23 BP.
XX
AC   AAT33702;
XX
DT   19-MAY-1997  (first entry)
XX
DE   Primer #2 for tissue or cell derived RNA.
XX
KW   PCR; polymerase chain reaction; primer; amplify; reverse-transcription;
KW   molecular indexing; class IIS restriction enzyme; cancer; causative gene;
KW   viral infection; hereditary disease; agricultural gene; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1
FT                   /*tag= a
FT                   /note= "hydroxylated"
XX
PN   EP735144-A1.
XX
PD   02-OCT-1996.
XX
PF   26-MAR-1996;   96EP-00104817.
XX
PR   28-MAR-1995;   95JP-00069695.
PR   20-JUL-1995;   95JP-00184006.
PR   12-SEP-1995;   95JP-00234122.
XX
PA   (SHKJ ) RES DEV CORP JAPAN.
XX
PI   Kato K;
```

```
XX
DR   WPI; 1996-435619/44.
XX
PT   Molecular indexing of DNA - using restriction enzymes, PCR amplification
PT   and electrophoresis to analyse DNA fragments.
XX
PS   Claim 3; Page 14; 20pp; English.
XX
CC   AAT33701-T33703 represent amplification primers used in the reverse-
CC   transcription of tissue or cell derived mRNA, in the method of the
CC   invention. The method of the invention is a molecular indexing method,
CC   and comprises digesting the cDNA amplified by these sequences with a
CC   class IIS restriction enzyme. Each resultant cDNA fragment is then
CC   ligated to a biotinylated adaptor (selected from a pool of 64 adaptors
CC   cohesive to all possible overhangs), and digesting the products with two
CC   further class IIS restriction enzymes. These steps are repeated (but the
CC   enzyme used for the first step is different in each) to produce two
CC   further cDNA samples. The ligation samples are then recovered using
CC   streptavidin-coated paramagnetic beads, removing the strand complementary
CC   to an adaptor-primer. The adaptor primer and an anchored oligo-dT primer
CC   (such as this sequence) are then used to amplify the cDNA samples. The
CC   amplified products are separated, and the sizes of the fragments obtained
CC   is recorded. The method can be used for the analysis and diagnosis or
CC   diseases such as cancers or viral infections, for the search and
CC   isolation of the genes of physiologically active substances that are
CC   potential pharmaceuticals, or causative genes of hereditary diseases, as
CC   well as for the isolation of genes for improving agricultural products.
CC   Using this method, it is possible to classify (index) DNA into groups in
CC   a short period of time without duplication
XX
SQ   Sequence 23 BP; 1 A; 3 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 23;
  Best Local Similarity   94.7%;  Pred. No. 1.7e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTT 2183
              || ||||||||||||||||
Db          4 CTGTTTTTTTTTTTTTTT 22


RESULT 1894
AAT33702/c
ID   AAT33702 standard; DNA; 23 BP.
XX
AC   AAT33702;
XX
DT   19-MAY-1997  (first entry)
XX
DE   Primer #2 for tissue or cell derived RNA.
XX
KW   PCR; polymerase chain reaction; primer; amplify; reverse-transcription;
KW   molecular indexing; class IIS restriction enzyme; cancer; causative gene;
KW   viral infection; hereditary disease; agricultural gene; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1
FT                   /*tag=  a
FT                   /note= "hydroxylated"
XX
PN   EP735144-A1.
XX
PD   02-OCT-1996.
XX
PF   26-MAR-1996;   96EP-00104817.
XX
PR   28-MAR-1995;   95JP-00069695.
PR   20-JUL-1995;   95JP-00184006.
PR   12-SEP-1995;   95JP-00234122.
XX
PA   (SHKJ ) RES DEV CORP JAPAN.
XX
PI   Kato K;
XX
DR   WPI; 1996-435619/44.
XX
PT   Molecular indexing of DNA - using restriction enzymes, PCR amplification
PT   and electrophoresis to analyse DNA fragments.
XX
PS   Claim 3; Page 14; 20pp; English.
XX
CC   AAT33701-T33703 represent amplification primers used in the reverse-
CC   transcription of tissue or cell derived mRNA, in the method of the
CC   invention. The method of the invention is a molecular indexing method,
CC   and comprises digesting the cDNA amplified by these sequences with a
CC   class IIS restriction enzyme. Each resultant cDNA fragment is then
CC   ligated to a biotinylated adaptor (selected from a pool of 64 adaptors
CC   cohesive to all possible overhangs), and digesting the products with two
CC   further class IIS restriction enzymes. These steps are repeated (but the
CC   enzyme used for the first step is different in each) to produce two
CC   further cDNA samples. The ligation samples are then recovered using
CC   streptavidin-coated paramagnetic beads, removing the strand complementary
CC   to an adaptor-primer. The adaptor primer and an anchored oligo-dT primer
CC   (such as this sequence) are then used to amplify the cDNA samples. The
CC   amplified products are separated, and the sizes of the fragments obtained
CC   is recorded. The method can be used for the analysis and diagnosis or
CC   diseases such as cancers or viral infections, for the search and
CC   isolation of the genes of physiologically active substances that are
CC   potential pharmaceuticals, or causative genes of hereditary diseases, as
CC   well as for the isolation of genes for improving agricultural products.
CC   Using this method, it is possible to classify (index) DNA into groups in
CC   a short period of time without duplication
XX
SQ   Sequence 23 BP; 1 A; 3 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 23;
  Best Local Similarity   94.7%;  Pred. No. 1.7e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2803
              |||||||||||||||||
Db         23 GAAAAAAAAAAAAAAAACA 5


RESULT 1895
AAV61555
ID   AAV61555 standard; DNA; 23 BP.
XX
AC   AAV61555;
XX
DT   08-DEC-1998  (first entry)
XX
DE   Double-anchored oligo-dT primer, used to synthesise apolipoprotein cDNA.
XX
KW   Primer; PCR; amplification; RT-PCR; quantitate; amount ratio; liver;
KW   kidney; apolipoprotein; ATAC-PCR; Adaptor-tagged Competitive PCR;
KW   gene expression; internal standard; calibration curve; ss.
XX
OS   Synthetic.
OS   Mus sp.
XX
PN   EP870842-A2.
XX
PD   14-OCT-1998.
XX
PF   07-APR-1998;   98EP-00302726.
XX
PR   07-APR-1997;   97JP-00088495.
XX
PA   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI   Kato K;
XX
DR   WPI; 1998-523164/45.
```

```
XX
PT   Determination of gene expression levels - using combinations of different
PT   cDNA samples tagged with different PCR adaptors.
XX
PS   Example 2; Page 9; 22pp; English.
XX
CC   The present sequence represents a primer which was used to synthesise
CC   Apolipoprotein cDNA in a RT-PCR reaction. This primer as well as primers
CC   AAV61554 and AAV61556 were added to both mouse liver-derived and mouse
CC   kidney-derived total RNA to generate single-stranded cDNA. These primers
CC   were used in the method of the invention to determine the amount ratio
CC   between a cDNA coding for mouse liver-derived Apolipoprotein and a cDNA
CC   that codes for the mouse kidney-derived Apolipoprotein by using Adaptor-
CC   tagged Competitive PCR (ATAC-PCR). This method allows gene expression to
CC   be quantitatively determined, and because internal standards are not
CC   required to prepare a calibration curve, it is a quicker and less
CC   laborious process
XX
SQ   Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 23;
  Best Local Similarity   94.7%;  Pred. No. 1.7e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTT 2183
              || ||||||||||||||||
Db          4 CTGTTTTTTTTTTTTTTT 22


RESULT 1896
AAA07787/c
ID   AAA07787 standard; DNA; 23 BP.
XX
AC   AAA07787;
XX
DT   23-JUN-2000  (first entry)
XX
DE   Structure of a fragment of duplex A target strand.
XX
KW   Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW   viral infection; inflammatory response; cellular proliferation;
KW   psoriasis; duplex; ss.
XX
OS   Synthetic.
XX
PN   WO200011013-A1.
XX
PD   02-MAR-2000.
XX
PF   20-AUG-1999;   99WO-US019029.
XX
PR   22-AUG-1998;   98US-0097712P.
XX
PA   (UYNE-) UNIV NEBRASKA.
XX
PI   Gold B;
XX
DR   WPI; 2000-246530/21.
XX
PT   Modified nucleomonomers, used in physiologically stable, non-toxic
PT   oligomers used to inhibit expression of nucleic acids and in gene
PT   regulation, antisense technology and diagnostics.
XX
PS   Disclosure; Page 20; 42pp; English.
XX
CC   The invention provides modified nucleomonomers of specified formula and
CC   their pharmaceutically acceptable salts. The nucleomonomers are used as
CC   monomers in oligomers, which are used in pharmaceutical compositions to
CC   inhibit expression of nucleic acid molecules including DNA and RNA in
CC   cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC   infected cells. They are used in oligomers for gene regulation, antisense
CC   technology, diagnostic applications to detect target sequences in
CC   biological samples such as those containing pathogenic bacteria, fungi
CC   and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC   encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC   molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC   interleukins associated with pathological conditions such as inflammatory
CC   conditions, cardiovascular disorders, immune reactions, cancer, viral
CC   infections and bacterial infections (see AAA07786 for details of other
CC   uses for which the oligomers are suitable for). Oligomers comprising the
CC   nucleomonomers exhibit increased duplex DNA stability when hybridizing to
CC   target nucleic acid sequences, are physiologically stable, non-toxic and
CC   able to penetrate into cells while maintaining stringent base pair
CC   fidelity for target DNA sequences. The oligomers demonstrate significant
CC   single- or double-stranded target nucleic acid binding activity to form
CC   duplexes, triplexes or other forms of stable association
XX
SQ   Sequence 23 BP; 1 A; 2 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 23;
  Best Local Similarity   94.7%;  Pred. No. 1.7e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAA 2802
              ||| ||||||||||||||||
Db         23 TGAGAAAAAAAAAAAAAAA 5


RESULT 1897
AAA07786
ID   AAA07786 standard; DNA; 23 BP.
XX
AC   AAA07786;
XX
DT   23-JUN-2000  (first entry)
XX
DE   Structure of a fragment of duplex A target strand.
XX
KW   Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW   viral infection; inflammatory response; cellular proliferation;
KW   psoriasis; duplex; ss.
XX
OS   Synthetic.
XX
PN   WO200011013-A1.
XX
PD   02-MAR-2000.
XX
PF   20-AUG-1999;   99WO-US019029.
XX
PR   22-AUG-1998;   98US-0097712P.
XX
PA   (UYNE-) UNIV NEBRASKA.
XX
PI   Gold B;
XX
DR   WPI; 2000-246530/21.
XX
PT   Modified nucleomonomers, used in physiologically stable, non-toxic
PT   oligomers used to inhibit expression of nucleic acids and in gene
PT   regulation, antisense technology and diagnostics.
XX
PS   Disclosure; Page 20; 42pp; English.
XX
CC   The invention provides modified nucleomonomers of specified formula and
CC   their pharmaceutically acceptable salts. The nucleomonomers are used as
CC   monomers in oligomers, which are used in pharmaceutical compositions to
CC   inhibit expression of nucleic acid molecules including DNA and RNA in
CC   cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC   infected cells. They are used in oligomers for gene regulation, antisense
CC   technology, diagnostic applications to detect target sequences in
CC   biological samples such as those containing pathogenic bacteria, fungi
CC   and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC   encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC   molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC   interleukins associated with pathological conditions such as inflammatory
```

CC conditions, cardiovascular disorders, immune reactions, cancer, viral
CC infections and bacterial infections. The oligomers are suitable for use
CC in both in vivo and ex vivo therapeutic applications including treatment
CC of cells such as bone marrow or peripheral blood in conditions such as
CC leukemia or viral infections, genes as target for cancer treatments
CC including oncogenes such as ras, k-ras, bcl-2, c-myb, bcr, c-myc, c-abl
CC or overexpressed sequences such as mdm2, oncostatin M, interleukin 6
CC (Kaposi's sarcoma), HER-2 and translocations such as bcr/abl or RNAs
CC encoded by such genes, as well as viral gene sequences such as polymerase
CC or reverse transcriptase genes of cytomegalovirus, herpes simplex virus-1
CC or -2, HTLV-1, human immunodeficiency virus-1 or -2, hepatitis B virus,
CC human papilloma virus, varicella zoster virus, influenza virus or
CC rhinovirus. They can also be used to modulate inflammatory responses by
CC modulating expression of genes such as IL-1 receptor, IL-1, ICAM-1 or E-
CC selectin in mediating inflammation and modulation of cellular
CC proliferation in conditions such as arterial occlusion (restenosis) after
CC angioplasty by modulating the expression of growth or mitogenic factors
CC such as non-muscle myosin, myc, fos, PCNA, platelet-derived growth factor
CC or fibroblast growth factor or their receptors or cell proliferation
CC factor such as c-myb, other extracellular proliferation factors such as
CC transforming growth factor alpha, IL-6, approx.g-interferon, protein
CC kinase C for treatment of psoriasis or other conditions, and epithelial
CC growth factor, transforming growth factor or MHC alleges in autoimmune
CC disease. Oligomers comprising the nucleomonomers exhibit increased duplex
CC DNA stability when hybridizing to target nucleic acid sequences, are
CC physiologically stable, non-toxic and able to penetrate into cells while
CC maintaining stringent base pair fidelity for target DNA sequences. The
CC oligomers demonstrate significant single- or double-stranded target
CC nucleic acid binding activity to form duplexes, triplexes or other forms
CC of stable association
XX
SQ Sequence 23 BP; 18 A; 2 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 23;
Best Local Similarity 94.7%; Pred. No. 1.7e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       2784 TGAAAAAAAAAAAAAAAAA 2802
                ||| ||||||||||||||||
Db          1 TGAGAAAAAAAAAAAAAAA 19
```

RESULT 1898
AAA08408
ID AAA08408 standard; DNA; 23 BP.
XX
AC AAA08408;
XX
DT 13-JUL-2000 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO:2.
XX
KW Detection; primer; adapter; probe; hybridisation; gene cluster;
KW fractionation; ss.
XX
OS Synthetic.
XX
PN JP2000055914-A.
XX
PD 25-FEB-2000.
XX
PF 13-AUG-1998; 98JP-00228944.
XX
PR 13-AUG-1998; 98JP-00228944.
XX
PA (TAIS) TAISHO PHARM CO LTD.
XX
DR WPI; 2000-368733/32.
XX
PT Gene detection method involves hybridizing probe opposite to objective
PT gene out of fractional gene cluster.
XX
PS Example 1; Page 9; 11pp; Japanese.
XX
CC The present invention describes a gene detection method which comprises
CC fractionating using a probe opposite to the objective gene which is
CC hybridised out of fractioned gene cluster. The objective gene detected
CC belongs to the group of objective genes contained in the sample. The
CC method is used for gene detection by fractionation of cDNA by molecular
CC index method using specific primer. It provides high detection
CC sensitivity of objective gene. AAA08407 to AAA08414 represent
CC oligonucleotides used in the exemplification of the present invention
XX
SQ Sequence 23 BP; 1 A; 3 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 23;
Best Local Similarity 94.7%; Pred. No. 1.7e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       2165 CTTTTTTTTTTTTTTTTT 2183
                || ||||||||||||||||
Db          4 CTGTTTTTTTTTTTTTTT 22
```

RESULT 1899
AAA08408/c
ID AAA08408 standard; DNA; 23 BP.
XX
AC AAA08408;
XX
DT 13-JUL-2000 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO:2.
XX
KW Detection; primer; adapter; probe; hybridisation; gene cluster;
KW fractionation; ss.
XX
OS Synthetic.
XX
PN JP2000055914-A.
XX
PD 25-FEB-2000.
XX
PF 13-AUG-1998; 98JP-00228944.
XX
PR 13-AUG-1998; 98JP-00228944.
XX
PA (TAIS) TAISHO PHARM CO LTD.
XX
DR WPI; 2000-368733/32.
XX
PT Gene detection method involves hybridizing probe opposite to objective
PT gene out of fractional gene cluster.
XX
PS Example 1; Page 9; 11pp; Japanese.
XX
CC The present invention describes a gene detection method which comprises
CC fractionating using a probe opposite to the objective gene which is
CC hybridised out of fractioned gene cluster. The objective gene detected
CC belongs to the group of objective genes contained in the sample. The
CC method is used for gene detection by fractionation of cDNA by molecular
CC index method using specific primer. It provides high detection
CC sensitivity of objective gene. AAA08407 to AAA08414 represent
CC oligonucleotides used in the exemplification of the present invention
XX
SQ Sequence 23 BP; 1 A; 3 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 23;
Best Local Similarity 94.7%; Pred. No. 1.7e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       2785 GAAAAAAAAAAAAAAAAA 2803
                |||||||||||||||||  |
Db         23 GAAAAAAAAAAAAAAAACA 5
```

```
RESULT 1900
AAH24266/c
ID   AAH24266 standard; DNA; 24 BP.
XX
AC   AAH24266;
XX
DT   11-SEP-2001  (first entry)
XX
DE   Human phosphatase 79 RT-PCR primer, SEQ ID NO:4.
XX
KW   Phosphatase 79; human; BAC clone CTB-54D4-encoded protein homologue;
KW   recombinant production; malignant tumour; cancer; blood disease;
KW   HIV infection; human immunodeficiency virus; immune disorder;
KW   inflammatory condition; cytostatic; anti-HIV; antiinflammatory;
KW   immunomodulator; reverse transcription-PCR; RT-PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138385-A1.
XX
PD   31-MAY-2001.
XX
PF   20-NOV-2000; 2000WO-CN000459.
XX
PR   22-NOV-1999;   99CN-00124059.
XX
PA   (BIOR-) BIOROAD GENE DEV LTD SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2001-355903/37.
XX
PT   Human phosphatase 79 and encoded polynucleotide, applicable in diagnosis
PT   and treatment of malignant tumor, hemopathy, HIV infection, immunological
PT   diseases and various inflammation.
XX
PS   Example 3; Page 12; 38pp; Chinese.
XX
CC   The invention relates to human phosphatase 79 (AAB73700), nucleic acids
CC   encoding it (AAH24264), and a method for the recombinant production of
CC   human phosphatase 79. The present invention additionally discloses an
CC   agonist of phosphatase 79 for therapeutic use, and an antibody which
CC   specifically binds to human phosphatase 79. Human phosphatase 79, and
CC   nucleotides which encode it may be used for treating a variety of
CC   diseases, such as malignant tumours, blood diseases, HIV (human
CC   immunodeficiency virus) infection, immune disorders and inflammatory
CC   conditions. The protein may also be used to screen for modulators of its
CC   activity or for peptide fingerprinting identification. The polynucleotide
CC   can be used as a primer for nucleic acid amplification reaction or as a
CC   probe for hybridisation reactions, or in producing gene chips or
CC   microarrays. Sequences AAH24265-AAH24266 represent reverse transcription-
CC   PCR (RT-PCR) primers used in an exemplification of the invention to
CC   isolate human phosphatase 79 cDNA
XX
SQ   Sequence 24 BP; 2 A; 0 C; 0 G; 22 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 24;
  Best Local Similarity   94.7%;  Pred. No. 1.8e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||  |
Db         24 AAAAAAAAAAAAAAAAATA 6


RESULT 1901
AAH44623/c
ID   AAH44623 standard; DNA; 24 BP.
XX
AC   AAH44623;
XX
DT   16-NOV-2001  (first entry)
XX
DE   Human FD 17 PCR primer 2 SEQ ID NO:4.
XX
KW   Human; FD 17; cytostatic; virucidal; immunomodulatory; haemostatic;
KW   antiinflammatory; gene therapy; malignant tumour; haemopathy;
KW   human immunodeficiency virus infection; HIV infection;
KW   immunological disease; inflammation; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200164729-A1.
XX
PD   07-SEP-2001.
XX
PF   26-FEB-2001; 2001WO-CN000221.
XX
PR   02-MAR-2000; 2000CN-00111868.
XX
PA   (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2001-550164/61.
XX
PT   New human polypeptide FD 17 for diagnosing and treating malignant tumor,
PT   hemopathy, human immunodeficiency virus (HIV) infection, immunological
PT   diseases and inflammations.
XX
PS   Example 2; Page 11; 36pp; Chinese.
XX
CC   The present invention describes the human FD 17 protein (I). (I) has
CC   cytostatic, virucidal, immunomodulatory, antiinflammatory and haemostatic
CC   activities. The polynucleotide encoding (I) can be used in gene therapy.
CC   (I) and the polynucleotide encoding it are applicable in the diagnosis
CC   and treatment of malignant tumour, haemopathy, human immunodeficiency
CC   virus (HIV) infection, immunological diseases and various inflammations.
CC   The present sequence represents a PCR primer for human FD 17, which is
CC   used in an example from the present invention
XX
SQ   Sequence 24 BP; 0 A; 2 C; 1 G; 21 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 24;
  Best Local Similarity   94.7%;  Pred. No. 1.8e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||||  |||||
Db         23 AAAAAAAAAAAAAGAAAAA 5


RESULT 1902
ABK13715/c
ID   ABK13715 standard; DNA; 24 BP.
XX
AC   ABK13715;
XX
DT   23-APR-2002  (first entry)
XX
DE   RT-PCR primer #2 for human transcriptional activation subunit 14 cDNA.
XX
KW   Human; transcriptional activation subunit 14; malignant neoplasm;
KW   haematopathy; cytostatic; HIV infection; human immunodeficiency virus;
KW   immunological disease; inflammation; virucide; immunomodulatory;
KW   antiinflammatory; reverse transcriptase-PCR; RT-PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200194403-A1.
XX
PD   13-DEC-2001.
XX
PF   14-MAY-2001; 2001WO-CN000753.
XX
PR   16-MAY-2000; 2000CN-00115720.
```

XX
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-090139/12.
XX
PT Human transcriptional activation subunit 14 and encoding polynucleotide,
PT used in diagnosis and treatment of malignant tumors, hemopathy, human
PT immunodeficiency virus infection, immunological diseases and
PT inflammation.
XX
PS Example 2; Page 17; 36pp; Chinese.
XX
CC The present invention relates to the isolation of human transcriptional
CC activation subunit 14, and the polynucleotide encoding it. Also described
CC is the process for preparing the protein by DNA recombination and the
CC application of the polypeptide and polynucleotide in treating various
CC diseases such as malignant neoplasms, haematopathy, human
CC immunodeficiency virus (HIV) infection, immunological diseases, and
CC various inflammations. Antagonists against the polypeptide can also be
CC used in treating such diseases. The present sequence for reverse
CC transcriptase (RT)-PCR primer #2 is used with RT-PCR primer #1 (ABK13714)
CC for isolating cDNA encoding human transcriptional activation subunit 14
XX
SQ Sequence 24 BP; 0 A; 2 C; 2 G; 20 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 24;
Best Local Similarity 94.7%; Pred. No. 1.8e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2804
||||||||||||| |||||
Db 22 AAAAAAAAAAAAAGAAAAA 4

RESULT 1903
AAL47515/c
ID AAL47515 standard; DNA; 24 BP.
XX
AC AAL47515;
XX
DT 13-SEP-2002 (first entry)
XX
DE Human cyclophilin-40-12-54 coding sequence PCR primer #2.
XX
KW Human; cyclophilin-40-12.54; immunopathy; cancer; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN CN1331162-A.
XX
PD 16-JAN-2002.
XX
PF 28-JUN-2000; 2000CN-00116823.
XX
PR 28-JUN-2000; 2000CN-00116823.
XX
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-305482/35.
XX
PT Polypeptide-human cyclophilin-40-12.54 and polynucleotide for coding it.
XX
PS Example 2; Page 17 (Disclosure); 33pp; Chinese.
XX
CC The present invention provides the protein and coding sequences of human
CC cyclophilin-40-12.54. The sequences can be used in the treatment of
CC immunopathy and cancer. The present sequence is a PCR primer for the
CC coding sequence of the invention
XX
SQ Sequence 24 BP; 2 A; 1 C; 2 G; 19 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 24;
Best Local Similarity 94.7%; Pred. No. 1.8e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2804
||||||||||| |||||||
Db 19 AAAAAAAAAAAGAAAAAAA 1

RESULT 1904
AAH76998/c
ID AAH76998 standard; DNA; 24 BP.
XX
AC AAH76998;
XX
DT 15-DEC-2001 (first entry)
XX
DE Human amyloid precursor protein 9 RT-PCR primer, SEQ ID NO:4.
XX
KW Human; amyloid precursor protein 9; recombinant production;
KW malignant tumour; cancer; blood disease; HIV infection;
KW human immunodeficiency virus; immune disorder; inflammatory condition;
KW cytostatic; anti-HIV; antiinflammatory; immunomodulator;
KW reverse transcription-PCR; RT-PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200174878-A1.
XX
PD 11-OCT-2001.
XX
PF 23-MAR-2001; 2001WO-CN000391.
XX
PR 24-MAR-2000; 2000CN-00115106.
XX
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2001-626386/72.
XX
PT New human amyloid precursor protein 9 and encoded polynucleotide,
PT applicable in diagnosis and treatment of cancer, hemopathy, human
PT immunodeficiency virus infection, immunological diseases and various
PT inflammations.
XX
PS Example 2; Page 16; 37pp; Chinese.
XX
CC The invention relates to human amyloid precursor protein 9 (AAG66809),
CC nucleic acids encoding it (AAH76996), and a method for the recombinant
CC production of amyloid precursor protein 9. The protein has a molecular
CC weight of 9 kD. The present invention additionally discloses an
CC antagonist of amyloid precursor protein 9 for therapeutic use, and an
CC antibody which specifically binds to amyloid precursor protein 9. Amyloid
CC precursor protein 9, and nucleotides which encode it may be used for
CC treating a variety of diseases, such as malignant tumours, blood
CC diseases, HIV (human immunodeficiency virus) infection, immune disorders
CC and inflammatory conditions. The protein may also be used to screen for
CC modulators of its activity or for peptide fingerprinting identification.
CC The polynucleotide can be used as a primer for nucleic acid amplification
CC reactions or as a probe for hybridisation reactions, or in producing gene
CC chips or microarrays. Sequences AAH76997-AAH76998 represent reverse
CC transcription-PCR (RT-PCR) primers used in an exemplification of the
CC invention to isolate human amyloid precursor protein 9 cDNA
XX
SQ Sequence 24 BP; 1 A; 1 C; 4 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 24;
Best Local Similarity 94.7%; Pred. No. 1.8e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              | ||||||||||||||||||
Db         19 GTAAAAAAAAAAAAAAAAAA 1


RESULT 1905
AAC96267/c
ID   AAC96267 standard; DNA; 25 BP.
XX
AC   AAC96267;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DPA1 gene PCR primer #24.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 48; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 4 A; 0 C; 3 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 25;
  Best Local Similarity   94.7%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAA 2799
              |||| ||||||||||||||
Db         19 AATTCAAAAAAAAAAAAAA 1


RESULT 1906
AAF74925
ID   AAF74925 standard; DNA; 25 BP.
XX
AC   AAF74925;
XX
DT   23-MAY-2001  (first entry)
XX
DE   CD40L poly-A tract sequence SEQ ID NO:22.
XX
KW   Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW   diagnosis; antiarthritic; antirheumatic; immunosuppressive;
KW   antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200119844-A1.
XX
PD   22-MAR-2001.
XX
PF   13-SEP-2000; 2000WO-US024966.
XX
PR   13-SEP-1999;   99US-0153625P.
XX
PA   (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
PI   Crow MK,  Li Y;
XX
DR   WPI; 2001-244776/25.
XX
PT   New altered CD40L promoter for use in the study, diagnosis and treatment
PT   of a variety of inflammatory disorders and autoimmune diseases, such as
PT   rheumatoid arthritis.
XX
PS   Example 1; Fig 3; 90pp; English.
XX
CC   The present invention describes an isolated, purified nucleic acid, which
CC   is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC   residues 331-455 of the sequence comprising 455 nucleotides given in
CC   AAF74905 where A in the wild type sequence at position 331 (corresponding
CC   to position -125) is replaced with C. (I) has antiarthritic,
CC   antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC   be used in gene therapy. (I) is useful in the study, diagnosis and
CC   treatment of inflammatory and autoimmune diseases, as well as diseases in
CC   which elevated expression of CD40L is a factor, e.g., rheumatoid
CC   arthritis. The present sequence represents a CD40L poly-A tract sequence
CC   which is used in an example from the present invention
XX
SQ   Sequence 25 BP; 19 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 25;
  Best Local Similarity   94.7%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||||||||| ||||
Db          1 AAAAAAAAAAAAAAACAAAA 19


RESULT 1907
AAF74930
ID   AAF74930 standard; DNA; 25 BP.
XX
AC   AAF74930;
XX
DT   23-MAY-2001  (first entry)
XX
DE   CD40L poly-A tract sequence SEQ ID NO:27.
XX
KW   Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW   diagnosis; antiarthritic; antirheumatic; immunosuppressive;
KW   antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200119844-A1.
XX
PD   22-MAR-2001.
XX
PF   13-SEP-2000; 2000WO-US024966.
XX
PR   13-SEP-1999;   99US-0153625P.
XX
PA   (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
```

PI Crow MK, Li Y;
XX
DR WPI; 2001-244776/25.
XX
PT New altered CD40L promoter for use in the study, diagnosis and treatment
PT of a variety of inflammatory disorders and autoimmune diseases, such as
PT rheumatoid arthritis.
XX
PS Example 1; Fig 3; 90pp; English.
XX
CC The present invention describes an isolated, purified nucleic acid, which
CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC residues 331-455 of the sequence comprising 455 nucleotides given in
CC AAF74905 where A in the wild type sequence at position 331 (corresponding
CC to position -125) is replaced with C. (I) has antiarthritic,
CC antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC be used in gene therapy. (I) is useful in the study, diagnosis and
CC treatment of inflammatory and autoimmune diseases, as well as diseases in
CC which elevated expression of CD40L is a factor, e.g., rheumatoid
CC arthritis. The present sequence represents a CD40L poly-A tract sequence
CC which is used in an example from the present invention
XX
SQ Sequence 25 BP; 19 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 25;
Best Local Similarity 94.7%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||| |||||
Db 1 AAAAAAAAAAAAACAAAAA 19

RESULT 1908
AAH38315/c
ID AAH38315 standard; DNA; 25 BP.
XX
AC AAH38315;
XX
DT 14-AUG-2001 (first entry)
XX
DE SNP specific SNPE primer SEQ ID 1111.
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW inflammation; forensic investigation; paternity analysis; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200129262-A2.
XX
PD 26-APR-2001.
XX
PF 13-OCT-2000; 2000WO-US028436.
XX
PR 15-OCT-1999; 99US-0160096P.
XX
PA (ORCH-) ORCHID BIOSCIENCES INC.
XX
PI Picoult-Newburg L, Pohl M;
XX
DR WPI; 2001-290930/30.
XX
PT New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample.
XX
PS Claim 1; Page 55; 83pp; English.
XX
CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a single nucleotide
CC primer extension (SNPE) primer specific for a human SNP containing DNA
CC sequence
XX
SQ Sequence 25 BP; 2 A; 2 C; 2 G; 19 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 25;
Best Local Similarity 94.7%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||| ||||||||||
Db 25 AAAAAAACAAAAAAAAAAA 7

RESULT 1909
AAC95727
ID AAC95727 standard; DNA; 25 BP.
XX
AC AAC95727;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA DQA1 gene PCR primer #24.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 39; 66pp; English.
XX
CC The present invention provides a method for identifying a set of

```
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 3 A; 5 C; 1 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 25;
  Best Local Similarity   94.7%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAACTTT 2192
              ||||||||||||||||||  |
Db          1 TTTTTTTTTTTTTAACTCT 19


RESULT 1910
AAC96201/c
ID   AAC96201 standard; DNA; 25 BP.
XX
AC   AAC96201;
XX
DT   26-FEB-2001  (first entry)
XX
DE   16s rRNA gene PCR primer #168.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 47; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 1 A; 3 C; 3 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 25;
  Best Local Similarity   94.7%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAA 2800
              | ||||||||||||||||||
Db         19 ACTGAAAAAAAAAAAAAAA 1


RESULT 1911
AAC96718
ID   AAC96718 standard; DNA; 25 BP.
XX
AC   AAC96718;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA HLA-A gene PCR primer #95.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 56; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 1 A; 5 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 25;
  Best Local Similarity   94.7%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAACTTT 2192
              ||||||||||||| |||||
Db          1 TTTTTTTTTTTTTCACTTT 19


RESULT 1912
AAH39903
ID   AAH39903 standard; DNA; 25 BP.
XX
AC   AAH39903;
XX
DT   14-AUG-2001  (first entry)
XX
DE   SNP specific SNPE primer SEQ ID 2699.
XX
KW   Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW   SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
KW   Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW   polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW   acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW   inflammation; forensic investigation; paternity analysis; primer; ss.
```

XX
OS Homo sapiens.
XX
PN WO200129262-A2.
XX
PD 26-APR-2001.
XX
PF 13-OCT-2000; 2000WO-US028436.
XX
PR 15-OCT-1999; 99US-0160096P.
XX
PA (ORCH-) ORCHID BIOSCIENCES INC.
XX
PI Picoult-Newburg L, Pohl M;
XX
DR WPI; 2001-290930/30.
XX
PT New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample.
XX
PS Claim 1; Page 63; 83pp; English.
XX
CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a single nucleotide
CC primer extension (SNPE) primer specific for a human SNP containing DNA
CC sequence
XX
SQ Sequence 25 BP; 19 A; 3 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 25;
Best Local Similarity 94.7%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||| |||||||
Db 1 AAAAAAAAAAAGAAAAAAA 19

RESULT 1913
AAH39903/c
ID AAH39903 standard; DNA; 25 BP.
XX
AC AAH39903;
XX
DT 14-AUG-2001 (first entry)
XX
DE SNP specific SNPE primer SEQ ID 2699.
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW inflammation; forensic investigation; paternity analysis; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200129262-A2.
XX
PD 26-APR-2001.
XX
PF 13-OCT-2000; 2000WO-US028436.
XX
PR 15-OCT-1999; 99US-0160096P.
XX
PA (ORCH-) ORCHID BIOSCIENCES INC.
XX
PI Picoult-Newburg L, Pohl M;
XX
DR WPI; 2001-290930/30.
XX
PT New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample.
XX
PS Claim 1; Page 63; 83pp; English.
XX
CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a single nucleotide
CC primer extension (SNPE) primer specific for a human SNP containing DNA
CC sequence
XX
SQ Sequence 25 BP; 19 A; 3 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 25;
Best Local Similarity 94.7%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTT 2184
||||||| ||||||||||||
Db 19 TTTTTTTCTTTTTTTTTTT 1

RESULT 1914
AAC90736/c
ID AAC90736 standard; DNA; 25 BP.
XX
AC AAC90736;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human secretory protein TGC-715 PCR primer SEQ ID NO:51.
XX
KW Human; secretory protein; cancer; immune disease; infectious disease;
KW lung function disorder; liver function disorder; antiinflammatory;

KW gastrointestinal disorder; cytostatic; haematopoietic; anticoagulant;
KW immunomodulatory; hepatotropic; cell proliferation-stimulant;
KW cell migratory agent; cell differentiation-inducer; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200071581-A1.
XX
PD 30-NOV-2000.
XX
PF 19-MAY-2000; 2000WO-JP003221.
XX
PR 20-MAY-1999; 99JP-00140229.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Itoh Y, Mogi S, Tanaka H, Ohkubo S, Ogi K;
XX
DR WPI; 2001-032023/04.
XX
PT Novel secretory protein and its salt with e.g. anti-cancer, anti-
PT inflammatory and hematopoietic, effects, applicable as drugs in remedies
PT and preventives to treat diseases like cancer and immune diseases.
XX
PS Example 11; Page 70; 122pp; Japanese.
XX
CC AAC90701 to AAC90715 encode the human secretory proteins given in
CC AAB36661 to AAB36675. The proteins can have cytostatic, anti-
CC inflammatory, haematopoietic, anti-coagulant, immunomodulatory and
CC hepatotropic activities, and can be used as cell migratory agents, cell
CC proliferation- stimulants and cell differentiation-inducers. The proteins
CC are useful in the treatment and prevention of diseases such as cancer,
CC lung function disorder, liver function disorder, gastrointestinal
CC disorder and immune diseases. AAC90716 to AAC90755 represent PCR primers
CC which are used in the exemplification of the present invention
XX
SQ Sequence 25 BP; 1 A; 7 C; 10 G; 7 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 25;
Best Local Similarity 94.7%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 454 AGGCAGCCAGCAGCAGGCC 472
|||||||||||||||||||
Db 25 AAGCAGCCAGCAGCAGGCC 7

RESULT 1915
ADB04567
ID ADB04567 standard; DNA; 25 BP.
XX
AC ADB04567;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ7 scanning oligonucleotide SEQ ID 5553.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
DR WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS Example 8; SEQ ID NO 5553; 103pp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 25 BP; 2 A; 1 C; 4 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 25;
Best Local Similarity 94.7%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2163 TCCTTTTTTTTTTTTTTTT 2181
|||||||||||||||||||
Db 7 TTCTTTTTTTTTTTTTTTT 25

RESULT 1916
ADB04567/c
ID ADB04567 standard; DNA; 25 BP.
XX
AC ADB04567;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ7 scanning oligonucleotide SEQ ID 5553.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
DR WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,

```
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 5553; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 25 BP; 2 A; 1 C; 4 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 25;
  Best Local Similarity   94.7%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              ||||||||||||||||| ||
Db         25 AAAAAAAAAAAAAAAAGAA 7


RESULT 1917
ADB04568
ID   ADB04568 standard; DNA; 25 BP.
XX
AC   ADB04568;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ7 scanning oligonucleotide SEQ ID 5554.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 5554; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 25 BP; 2 A; 1 C; 4 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 25;
  Best Local Similarity   94.7%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTT 2181
              | ||||||||||||||||||
Db          6 TTCTTTTTTTTTTTTTTTT 24


RESULT 1918
ADB04568/c
ID   ADB04568 standard; DNA; 25 BP.
XX
AC   ADB04568;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ7 scanning oligonucleotide SEQ ID 5554.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 5554; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
```

```
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 25 BP; 2 A; 1 C; 4 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 25;
  Best Local Similarity   94.7%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||| ||
Db         24 AAAAAAAAAAAAAAAAGAA 6


RESULT 1919
AAF16616
ID   AAF16616 standard; DNA; 26 BP.
XX
AC   AAF16616;
XX
DT   13-MAR-2001  (first entry)
XX
DE   Gastric acid production inhibiting oligonucleotide SEQ ID NO: 103.
XX
KW   Gastric acid disturbance; gastric reflux; gastritis; dyspepsia;
KW   stomach ulcer; duodenal ulcer; Helicobacter pylori; antisense;
KW   DNA-RNA hybrid; ss.
XX
OS   Homo sapiens.
XX
PN   WO200071164-A1.
XX
PD   30-NOV-2000.
XX
PF   24-MAY-2000; 2000WO-AU000498.
XX
PR   24-MAY-1999;   99AU-00000510.
XX
PA   (TACH/) TACHAS G.
XX
PI   Tachas G;
XX
DR   WPI; 2001-025093/03.
XX
PT   Treating gastric acid disturbance by administering an oligonucleotide
PT   which modulates the activity of a polypeptide involved in gastric acid
PT   production or secretion.
XX
PS   Example 3; Page 150; 164pp; English.
XX
CC   The present invention provides oligonucleotides, and methods for their
CC   use, which are useful in modulating the action of proteins involved in
CC   gastric acid production. The target protein is preferably the histamine
CC   H2 receptor or one of the proteins which form part of the gastric proton
CC   pump. The sequences and methods of the invention are useful in the
CC   treatment of gastric reflux, gastritis, dyspepsia, stomach ulcers,
CC   duodenal ulcers and other gastric acid disturbances, most of which are
CC   caused by Helicobacter pylori
XX
SQ   Sequence 26 BP; 23 A; 0 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 26;
  Best Local Similarity   94.7%;  Pred. No. 2.2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||| |||||||
Db          1 AAAAAAAAAAGAAAAAAA 19


RESULT 1920
AAF74913
ID   AAF74913 standard; DNA; 26 BP.
XX
AC   AAF74913;
XX
DT   23-MAY-2001  (first entry)
XX
DE   CD40L poly-A tract sequence SEQ ID NO:10.
XX
KW   Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW   diagnosis; antiarthritic; antirheumatic; immunosuppressive;
KW   antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200119844-A1.
XX
PD   22-MAR-2001.
XX
PF   13-SEP-2000; 2000WO-US024966.
XX
PR   13-SEP-1999;   99US-0153625P.
XX
PA   (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
PI   Crow MK,  Li Y;
XX
DR   WPI; 2001-244776/25.
XX
PT   New altered CD40L promoter for use in the study, diagnosis and treatment
PT   of a variety of inflammatory disorders and autoimmune diseases, such as
PT   rheumatoid arthritis.
XX
PS   Example 1; Fig 3; 90pp; English.
XX
CC   The present invention describes an isolated, purified nucleic acid, which
CC   is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC   residues 331-455 of the sequence comprising 455 nucleotides given in
CC   AAF74905 where A in the wild type sequence at position 331 (corresponding
CC   to position -125) is replaced with C. (I) has antiarthritic,
CC   antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC   be used in gene therapy. (I) is useful in the study, diagnosis and
CC   treatment of inflammatory and autoimmune diseases, as well as diseases in
CC   which elevated expression of CD40L is a factor, e.g., rheumatoid
CC   arthritis. The present sequence represents a CD40L poly-A tract sequence
CC   which is used in an example from the present invention
XX
SQ   Sequence 26 BP; 20 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 26;
  Best Local Similarity   94.7%;  Pred. No. 2.2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||||| ||||
Db          1 AAAAAAAAAAAAAACAAAA 19


RESULT 1921
AAF74926
ID   AAF74926 standard; DNA; 27 BP.
XX
AC   AAF74926;
XX
DT   23-MAY-2001  (first entry)
XX
DE   CD40L poly-A tract sequence SEQ ID NO:23.
XX
KW   Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW   diagnosis; antiarthritic; antirheumatic; immunosuppressive;
KW   antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
OS   Homo sapiens.
XX
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```
PN   WO200119844-A1.
XX
PD   22-MAR-2001.
XX
PF   13-SEP-2000; 2000WO-US024966.
XX
PR   13-SEP-1999;   99US-0153625P.
XX
PA   (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
PI   Crow MK,  Li Y;
XX
DR   WPI; 2001-244776/25.
XX
PT   New altered CD40L promoter for use in the study, diagnosis and treatment
PT   of a variety of inflammatory disorders and autoimmune diseases, such as
PT   rheumatoid arthritis.
XX
PS   Example 1; Fig 3; 90pp; English.
XX
CC   The present invention describes an isolated, purified nucleic acid, which
CC   is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC   residues 331-455 of the sequence comprising 455 nucleotides given in
CC   AAF74905 where A in the wild type sequence at position 331 (corresponding
CC   to position -125) is replaced with C. (I) has antiarthritic,
CC   antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC   be used in gene therapy. (I) is useful in the study, diagnosis and
CC   treatment of inflammatory and autoimmune diseases, as well as diseases in
CC   which elevated expression of CD40L is a factor, e.g., rheumatoid
CC   arthritis. The present sequence represents a CD40L poly-A tract sequence
CC   which is used in an example from the present invention
XX
SQ   Sequence 27 BP; 21 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 27;
  Best Local Similarity   94.7%;  Pred. No. 2.3e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||||||||||| |||
Db          1 AAAAAAAAAAAAAAAACAAA 19


RESULT 1922
AAF74932
ID   AAF74932 standard; DNA; 27 BP.
XX
AC   AAF74932;
XX
DT   23-MAY-2001  (first entry)
XX
DE   CD40L poly-A tract sequence SEQ ID NO:29.
XX
KW   Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW   diagnosis; antiarthritic; antirheumatic; immunosuppressive;
KW   antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200119844-A1.
XX
PD   22-MAR-2001.
XX
PF   13-SEP-2000; 2000WO-US024966.
XX
PR   13-SEP-1999;   99US-0153625P.
XX
PA   (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
PI   Crow MK,  Li Y;
XX
DR   WPI; 2001-244776/25.
XX
PT   New altered CD40L promoter for use in the study, diagnosis and treatment
PT   of a variety of inflammatory disorders and autoimmune diseases, such as
PT   rheumatoid arthritis.
XX
PS   Example 1; Fig 3; 90pp; English.
XX
CC   The present invention describes an isolated, purified nucleic acid, which
CC   is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC   residues 331-455 of the sequence comprising 455 nucleotides given in
CC   AAF74905 where A in the wild type sequence at position 331 (corresponding
CC   to position -125) is replaced with C. (I) has antiarthritic,
CC   antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC   be used in gene therapy. (I) is useful in the study, diagnosis and
CC   treatment of inflammatory and autoimmune diseases, as well as diseases in
CC   which elevated expression of CD40L is a factor, e.g., rheumatoid
CC   arthritis. The present sequence represents a CD40L poly-A tract sequence
CC   which is used in an example from the present invention
XX
SQ   Sequence 27 BP; 21 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 27;
  Best Local Similarity   94.7%;  Pred. No. 2.3e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||||||||||| |||
Db          1 AAAAAAAAAAAAAAAACAAA 19


RESULT 1923
AAF74931
ID   AAF74931 standard; DNA; 27 BP.
XX
AC   AAF74931;
XX
DT   23-MAY-2001  (first entry)
XX
DE   CD40L poly-A tract sequence SEQ ID NO:28.
XX
KW   Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW   diagnosis; antiarthritic; antirheumatic; immunosuppressive;
KW   antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200119844-A1.
XX
PD   22-MAR-2001.
XX
PF   13-SEP-2000; 2000WO-US024966.
XX
PR   13-SEP-1999;   99US-0153625P.
XX
PA   (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
PI   Crow MK,  Li Y;
XX
DR   WPI; 2001-244776/25.
XX
PT   New altered CD40L promoter for use in the study, diagnosis and treatment
PT   of a variety of inflammatory disorders and autoimmune diseases, such as
PT   rheumatoid arthritis.
XX
PS   Example 1; Fig 3; 90pp; English.
XX
CC   The present invention describes an isolated, purified nucleic acid, which
CC   is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC   residues 331-455 of the sequence comprising 455 nucleotides given in
CC   AAF74905 where A in the wild type sequence at position 331 (corresponding
CC   to position -125) is replaced with C. (I) has antiarthritic,
CC   antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC   be used in gene therapy. (I) is useful in the study, diagnosis and
CC   treatment of inflammatory and autoimmune diseases, as well as diseases in
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```
CC   which elevated expression of CD40L is a factor, e.g., rheumatoid
CC   arthritis. The present sequence represents a CD40L poly-A tract sequence
CC   which is used in an example from the present invention
XX
SQ   Sequence 27 BP; 21 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 27;
  Best Local Similarity   94.7%;  Pred. No. 2.3e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||| |||
Db          1 AAAAAAAAAAAAAAAACAAA 19


RESULT 1924
AAF74934
ID   AAF74934 standard; DNA; 27 BP.
XX
AC   AAF74934;
XX
DT   23-MAY-2001  (first entry)
XX
DE   CD40L poly-A tract sequence SEQ ID NO:31.
XX
KW   Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW   diagnosis; antiarthritic; antirheumatic; immunosuppressive;
KW   antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200119844-A1.
XX
PD   22-MAR-2001.
XX
PF   13-SEP-2000; 2000WO-US024966.
XX
PR   13-SEP-1999;   99US-0153625P.
XX
PA   (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
PI   Crow MK,  Li Y;
XX
DR   WPI; 2001-244776/25.
XX
PT   New altered CD40L promoter for use in the study, diagnosis and treatment
PT   of a variety of inflammatory disorders and autoimmune diseases, such as
PT   rheumatoid arthritis.
XX
PS   Example 1; Fig 3; 90pp; English.
XX
CC   The present invention describes an isolated, purified nucleic acid, which
CC   is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC   residues 331-455 of the sequence comprising 455 nucleotides given in
CC   AAF74905 where A in the wild type sequence at position 331 (corresponding
CC   to position -125) is replaced with C. (I) has antiarthritic,
CC   antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC   be used in gene therapy. (I) is useful in the study, diagnosis and
CC   treatment of inflammatory and autoimmune diseases, as well as diseases in
CC   which elevated expression of CD40L is a factor, e.g., rheumatoid
CC   arthritis. The present sequence represents a CD40L poly-A tract sequence
CC   which is used in an example from the present invention
XX
SQ   Sequence 27 BP; 21 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 27;
  Best Local Similarity   94.7%;  Pred. No. 2.3e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||| |||
Db          1 AAAAAAAAAAAAAAAACAAA 19


RESULT 1925
AAQ05023/c
ID   AAQ05023 standard; DNA; 27 BP.
XX
AC   AAQ05023;
XX
DT   25-MAR-2003  (revised)
DT   31-OCT-1990  (first entry)
XX
DE   Sequence binding to and inhibiting the Beta-globin gene.
XX
KW   C-myc; cancer; HIV-I; AIDS; collagenase; Alzheimers disease; EGF;
KW   epidermal growth factor; GSTpi; HMGCoA; thallasemia;
KW   Herpes simplex virus; nerve growth factor receptor; globin; ss.
XX
OS   Synthetic.
XX
PN   EP375408-A.
XX
PD   27-JUN-1990.
XX
PF   20-DEC-1989;   89EP-00313391.
XX
PR   20-DEC-1988;   88US-00287359.
XX
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (HOGA/) HOGAN M E.
XX
PI   Hogan ME,  Kessler DJ;
XX
DR   WPI; 1990-195509/26.
XX
PT   Synthetic oligo-nucleotide(s) which bind target duplex DNA - forming co-
PT   linear triplex to control transcription process in gene-specific fashion.
XX
PS   Claim 47; Page 31; 40pp; English.
XX
CC   Sequence forms triplex with the double stranded target sequence with G
CC   binding to G-C and T to A-T. The strand runs 3' to 5' in an antiparallel
CC   orientation and when targeted to a specific sequence will deactivate it.
CC   This allows for growth inhibition in cancerous cells; manipulation of
CC   cellular structural protein content; inhibition of IL-2 chain receptor;
CC   disbursing plaque formation in Alzheimer's disease; inhibiting EGF gene;
CC   modulating cholestrol synthesis through the HMGCoA gene; suppressing NGF
CC   gene expression; arresting HSV-I replication and suppressing Beta- globin
CC   expression in thallassaemia and sicle cell anaemia patients. (Updated on
CC   25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA
CC   field.)
XX
SQ   Sequence 27 BP; 0 A; 0 C; 6 G; 21 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 27;
  Best Local Similarity   94.7%;  Pred. No. 2.3e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||| ||||||||
Db         27 AAAAAAAAAACAAAAAAAA 9


RESULT 1926
AAQ36361/c
ID   AAQ36361 standard; DNA; 27 BP.
XX
AC   AAQ36361;
XX
DT   25-MAR-2003  (revised)
DT   07-JUN-1993  (first entry)
XX
DE   GL6par, targetted to human beta globin sequence.
XX
KW   Heamoglobin; beta thalassemia; sickle cell anaemia; delta protein;
```

```
KW   triplex; target; duplex; promoter; coding domain; 3'-5'; ss.
XX
OS   Synthetic.
XX
PN   US5176996-A.
XX
PD   05-JAN-1993.
XX
PF   22-DEC-1989;   89US-00453532.
XX
PR   20-DEC-1988;   88US-00287359.
XX
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PI   Hogan ME,  Kessler DJ;
XX
DR   WPI; 1993-035718/04.
XX
PT   Synthetic oligo-nucleotide(s), prodn. useful e.g. for HIV-1 inhibition -
PT   which bind to target sequence in duplex DNA forming colinear triplex by
PT   binding to major groove.
XX
PS   Example 13; Col 35; 29pp; English.
XX
CC   The beta globin gene encodes on of the proteins comprising human adult
CC   haemoglobin. Mutation in this gene is responsible for beta thalassemia
CC   and sickle cell anaemia. Expression of the gene may be prevented by the
CC   formation of a triplex between the duplex target DNA sequence and an anti
CC   parallel or parallel synthetic oligonucleotide. The triplex
CC   oligonucleotides are designed to inhibit the beta globin gene in
CC   thallassemics and in patients with sickle cell anaemia, to be replaced by
CC   the naturally occurring delta protein. Two classes of triplex
CC   oligonucleotides may be used, targetted against the 5' enhancer or the
CC   promoter/coding domain, in this case from base 874 to 900 (numbering is
CC   relative to the principal mRNA start site). A suitable parallel
CC   oligonucleotide is GL6par (3'-5'). See also AAQ36219-362. (Updated on 25-
CC   MAR-2003 to correct PF field.)
XX
SQ   Sequence 27 BP; 0 A; 0 C; 6 G; 21 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 27;
  Best Local Similarity   94.7%;  Pred. No. 2.3e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||||| ||||||||
Db         27 AAAAAAAAAACAAAAAAAA 9


RESULT 1927
AAF74920
ID   AAF74920 standard; DNA; 28 BP.
XX
AC   AAF74920;
XX
DT   23-MAY-2001  (first entry)
XX
DE   CD40L poly-A tract sequence SEQ ID NO:17.
XX
KW   Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW   diagnosis; antiarthritic; antirheumatic; immunosuppressive;
KW   antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200119844-A1.
XX
PD   22-MAR-2001.
XX
PF   13-SEP-2000; 2000WO-US024966.
XX
PR   13-SEP-1999;   99US-0153625P.
XX
PA   (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
PI   Crow MK,  Li Y;
XX
DR   WPI; 2001-244776/25.
XX
PT   New altered CD40L promoter for use in the study, diagnosis and treatment
PT   of a variety of inflammatory disorders and autoimmune diseases, such as
PT   rheumatoid arthritis.
XX
PS   Example 1; Fig 3; 90pp; English.
XX
CC   The present invention describes an isolated, purified nucleic acid, which
CC   is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC   residues 331-455 of the sequence comprising 455 nucleotides given in
CC   AAF74905 where A in the wild type sequence at position 331 (corresponding
CC   to position -125) is replaced with C. (I) has antiarthritic,
CC   antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC   be used in gene therapy. (I) is useful in the study, diagnosis and
CC   treatment of inflammatory and autoimmune diseases, as well as diseases in
CC   which elevated expression of CD40L is a factor, e.g., rheumatoid
CC   arthritis. The present sequence represents a CD40L poly-A tract sequence
CC   which is used in an example from the present invention
XX
SQ   Sequence 28 BP; 22 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 28;
  Best Local Similarity   94.7%;  Pred. No. 2.5e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||||||||||| ||
Db          1 AAAAAAAAAAAAAAAAACAA 19


RESULT 1928
AAF74906
ID   AAF74906 standard; DNA; 28 BP.
XX
AC   AAF74906;
XX
DT   23-MAY-2001  (first entry)
XX
DE   CD40L poly-A tract sequence SEQ ID NO:3.
XX
KW   Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW   diagnosis; antiarthritic; antirheumatic; immunosuppressive;
KW   antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200119844-A1.
XX
PD   22-MAR-2001.
XX
PF   13-SEP-2000; 2000WO-US024966.
XX
PR   13-SEP-1999;   99US-0153625P.
XX
PA   (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
PI   Crow MK,  Li Y;
XX
DR   WPI; 2001-244776/25.
XX
PT   New altered CD40L promoter for use in the study, diagnosis and treatment
PT   of a variety of inflammatory disorders and autoimmune diseases, such as
PT   rheumatoid arthritis.
XX
PS   Example 1; Fig 3; 90pp; English.
XX
CC   The present invention describes an isolated, purified nucleic acid, which
CC   is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
```

```
CC   residues 331-455 of the sequence comprising 455 nucleotides given in
CC   AAF74905 where A in the wild type sequence at position 331 (corresponding
CC   to position -125) is replaced with C. (I) has antiarthritic,
CC   antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC   be used in gene therapy. (I) is useful in the study, diagnosis and
CC   treatment of inflammatory and autoimmune diseases, as well as diseases in
CC   which elevated expression of CD40L is a factor, e.g., rheumatoid
CC   arthritis. The present sequence represents a CD40L poly-A tract sequence
CC   which is used in an example from the present invention
XX
SQ   Sequence 28 BP; 22 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 28;
  Best Local Similarity   94.7%;  Pred. No. 2.5e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              ||||||||||||||||| ||
Db          1 AAAAAAAAAAAAAAAACAA 19


RESULT 1929
AAF74916
ID   AAF74916 standard; DNA; 28 BP.
XX
AC   AAF74916;
XX
DT   23-MAY-2001  (first entry)
XX
DE   CD40L poly-A tract sequence SEQ ID NO:13.
XX
KW   Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW   diagnosis; antiarthritic; antirheumatic; immunosuppressive;
KW   antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200119844-A1.
XX
PD   22-MAR-2001.
XX
PF   13-SEP-2000; 2000WO-US024966.
XX
PR   13-SEP-1999;   99US-0153625P.
XX
PA   (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
PI   Crow MK,  Li Y;
XX
DR   WPI; 2001-244776/25.
XX
PT   New altered CD40L promoter for use in the study, diagnosis and treatment
PT   of a variety of inflammatory disorders and autoimmune diseases, such as
PT   rheumatoid arthritis.
XX
PS   Example 1; Fig 3; 90pp; English.
XX
CC   The present invention describes an isolated, purified nucleic acid, which
CC   is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC   residues 331-455 of the sequence comprising 455 nucleotides given in
CC   AAF74905 where A in the wild type sequence at position 331 (corresponding
CC   to position -125) is replaced with C. (I) has antiarthritic,
CC   antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC   be used in gene therapy. (I) is useful in the study, diagnosis and
CC   treatment of inflammatory and autoimmune diseases, as well as diseases in
CC   which elevated expression of CD40L is a factor, e.g., rheumatoid
CC   arthritis. The present sequence represents a CD40L poly-A tract sequence
CC   which is used in an example from the present invention
XX
SQ   Sequence 28 BP; 22 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 28;
  Best Local Similarity   94.7%;  Pred. No. 2.5e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              ||||||||||||||||| ||
Db          1 AAAAAAAAAAAAAAAACAA 19


RESULT 1930
AAF74927
ID   AAF74927 standard; DNA; 28 BP.
XX
AC   AAF74927;
XX
DT   23-MAY-2001  (first entry)
XX
DE   CD40L poly-A tract sequence SEQ ID NO:24.
XX
KW   Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW   diagnosis; antiarthritic; antirheumatic; immunosuppressive;
KW   antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200119844-A1.
XX
PD   22-MAR-2001.
XX
PF   13-SEP-2000; 2000WO-US024966.
XX
PR   13-SEP-1999;   99US-0153625P.
XX
PA   (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
PI   Crow MK,  Li Y;
XX
DR   WPI; 2001-244776/25.
XX
PT   New altered CD40L promoter for use in the study, diagnosis and treatment
PT   of a variety of inflammatory disorders and autoimmune diseases, such as
PT   rheumatoid arthritis.
XX
PS   Example 1; Fig 3; 90pp; English.
XX
CC   The present invention describes an isolated, purified nucleic acid, which
CC   is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC   residues 331-455 of the sequence comprising 455 nucleotides given in
CC   AAF74905 where A in the wild type sequence at position 331 (corresponding
CC   to position -125) is replaced with C. (I) has antiarthritic,
CC   antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC   be used in gene therapy. (I) is useful in the study, diagnosis and
CC   treatment of inflammatory and autoimmune diseases, as well as diseases in
CC   which elevated expression of CD40L is a factor, e.g., rheumatoid
CC   arthritis. The present sequence represents a CD40L poly-A tract sequence
CC   which is used in an example from the present invention
XX
SQ   Sequence 28 BP; 22 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 28;
  Best Local Similarity   94.7%;  Pred. No. 2.5e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              ||||||||||||||||| ||
Db          1 AAAAAAAAAAAAAAAACAA 19


RESULT 1931
AAQ52308/c
ID   AAQ52308 standard; cDNA; 28 BP.
XX
AC   AAQ52308;
XX
DT   25-MAR-2003  (revised)
```

```
DT   03-JUN-1994  (first entry)
XX
DE   FKBP12C PCR primer VX10801.
XX
KW   Transplant rejection; monitoring; FK506 immunosuppressant therapy;
KW   tissue specific; polymerase chain reaction; ss.
XX
OS   Synthetic.
XX
PN   WO9323548-A2.
XX
PD   25-NOV-1993.
XX
PF   20-MAY-1993;   93WO-US004916.
XX
PR   20-MAY-1992;   92US-00886611.
XX
PA   (VERT-) VERTEX PHARM INC.
XX
PI   Peattie DA;
XX
DR   WPI; 1993-386579/48.
XX
PT   New cDNA for tissue specific FK506 binding proteins - and detection of
PT   its mRNA to monitor transplant rejection and effect or FK506
PT   immunosuppressant therapy.
XX
PS   Example 4; Page 36; 54pp; English.
XX
CC   The sequence is that of a PCR primer VX10801 which was used to amplify
CC   DNA specific to FKBP12C. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 28 BP; 5 A; 1 C; 4 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 28;
  Best Local Similarity   94.7%;  Pred. No. 2.5e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAA 2800
                ||| ||||||||||||||||
Db         19 ATTCAAAAAAAAAAAAAA 1


RESULT 1932
AAQ36362/c
ID   AAQ36362 standard; DNA; 28 BP.
XX
AC   AAQ36362;
XX
DT   25-MAR-2003  (revised)
DT   07-JUN-1993  (first entry)
XX
DE   GL6anti, targetted to human beta globin sequence.
XX
KW   Heamoglobin; beta thalassemia; sickle cell anaemia; delta protein;
KW   triplex; target; duplex; promoter; coding domain; ss.
XX
OS   Synthetic.
XX
PN   US5176996-A.
XX
PD   05-JAN-1993.
XX
PF   22-DEC-1989;   89US-00453532.
XX
PR   20-DEC-1988;   88US-00287359.
XX
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PI   Hogan ME,  Kessler DJ;
XX
DR   WPI; 1993-035718/04.
XX
PT   Synthetic oligo-nucleotide(s), prodn. useful e.g. for HIV-1 inhibition -
PT   which bind to target sequence in duplex DNA forming colinear triplex by
PT   binding to major groove.
XX
PS   Example 13; Col 36; 29pp; English.
XX
CC   The beta globin gene encodes on of the proteins comprising human adult
CC   haemoglobin. . Mutation in this gene is responsible for beta thalassemia
CC   and sickle cell anaemia. Expression of the gene may be prevented by the
CC   formation of a triplex between the duplex target DNA sequence and an anti
CC   parallel or parallel synthetic oligonucleotide. The triplex
CC   oligonucleotides are designed to inhibit the beta globin gene in
CC   thallassemics and in patients with sickle cell anaemia, to be replaced by
CC   the naturally occurring delta protein. Two classes of triplex
CC   oligonucleotides may be used, targetted against the 5' enhancer or the
CC   promoter/coding domain, in this case from base 874 to 900 (numbering is
CC   relative to the principal mRNA start site). A suitable antiparallel
CC   oligonucleotide is GL6anti. See also AAQ36219-361. (Updated on 25-MAR-
CC   2003 to correct PF field.)
XX
SQ   Sequence 28 BP; 0 A; 0 C; 6 G; 22 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 28;
  Best Local Similarity   94.7%;  Pred. No. 2.5e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
                ||||||||||| |||||||
Db         28 AAAAAAAAAAACAAAAAAA 10


RESULT 1933
AAT70113
ID   AAT70113 standard; DNA; 28 BP.
XX
AC   AAT70113;
XX
DT   24-SEP-1997  (first entry)
XX
DE   PolyAB primer 2.
XX
KW   primer; polymerase chain reaction; cDNA library; anchored end; PCSUB;
KW   lock-docking; screening; PCR-based cDNA subtractive cloning; ss.
XX
OS   Synthetic.
XX
PN   WO9640998-A1.
XX
PD   19-DEC-1996.
XX
PF   05-JUN-1996;   96WO-US008582.
XX
PR   07-JUN-1995;   95US-00481687.
XX
PA   (PION-) PIONEER HI-BRED INT INC.
XX
PI   Wang X,  Duvick JP,  Briggs SP;
XX
DR   WPI; 1997-087067/08.
XX
PT   Method for prodn. of cDNA libraries with anchored ends - useful for
PT   subtractive cloning of sequences of interest.
XX
PS   Claim 1; Page 28; 56pp; English.
XX
CC   The invention provides a PCR-based method for generating a full-length
CC   cDNA library with anchored ends. The method uses lock-docking primers
CC   (AAT70106-11), where one primer, poly TV (V = G,C or A) locks over the
CC   polyA tail of eukaryotic mRNA producing first strand synthesis and a
CC   second primer, polyGH (H = A, C or T) locks onto the polyC tail added by
CC   terminal deoxynucleotidyl transferase (TdT). In the final step, AAT70112-
CC   17 (polyAB and polyCD primers; B = G, T or C; D = G, A or T) are used to
CC   amplify the first strand and produce a cDNA library with anchored ends.
```

CC cDNA libraries produced may be used to identify new (unique) nucleotide
CC sequences from PCSUB (PCR-based cDNA subtractive) libraries. The new
CC method produces discreet sized PCR products which would not necessarily
CC require further subcloning/screening. The method also produces full-
CC length cDNA's obtainable from the libraries as opposed to specific cDNA
CC clones, as produced by previously known methods. Other methods such as
CC PCR and RACE require a knowledge of the target sequence to be amplified,
CC by using the PCSUB method no previous knowledge is necessary
XX
SQ Sequence 28 BP; 18 A; 4 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 28;
Best Local Similarity 94.7%; Pred. No. 2.5e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAAAAAAAA 2803
Db 9 GCAAAAAAAAAAAAAAAAA 27

RESULT 1934
ADA26181/c
ID ADA26181 standard; DNA; 30 BP.
XX
AC ADA26181;
XX
DT 20-NOV-2003 (first entry)
XX
DE Rice semi-dwarf (sd-1) DNA fragment SEQ ID NO:26.
XX
KW genotype; plant; rice; semi-dwarf; sd-1; polymorphism; detection;
KW characteristic; single nucleotide polymorphism; SNP; genotyping;
KW chromosome 1; gene; ds.
XX
OS Synthetic.
OS Oryza sativa.
XX
PN WO2003070934-A1.
XX
PD 28-AUG-2003.
XX
PF 07-FEB-2003; 2003WO-JP001317.
XX
PR 25-FEB-2002; 2002JP-00048115.
XX
PA (PLAN-) PLANT GENOME CENT CO LTD.
XX
PI Minobe Y, Monna L, Kitazawa N, Yoshino R, Suzuki J;
XX
DR WPI; 2003-697617/66.
XX
PT Judging the genotype of a region around a plant sd-1 gene with
PT polymorphism-obtained markers isolated by positional cloning, useful in
PT genotyping for examination of semi-dwarf character of rice.
XX
PS Disclosure; Page 15; 104pp; Japanese.
XX
CC The present invention describes a method for judging the genotype of a
CC region around a plant semi-dwarf (sd-1) gene in which polymorphisms are
CC present, by detecting the polymorphisms. Also described: (1) examining
CC semi-dwarf characteristics of a plant using the judgment method with
CC detection of polymorphisms; (2) oligonucleotides for amplifying sd-1 DNA
CC regions, which are primers for judging the genotype of a region around a
CC plant sd-1 gene; (3) reagents for judging the genotype of a region around
CC a plant sd-1 gene containing these oligonucleotides; and (4) reagents for
CC examining the semi-dwarf character of a plant containing the
CC oligonucleotides. The method is for judging the genotype of a region
CC around a plant sd-1 gene, which is applicable in genotyping by (d)CAPS
CC ((derived) cleaved amplified polymorphic sequence) for examination of the
CC semi-dwarf character of rice to identify desirable strains e.g. with high
CC crop yield, pest resistance and resistance to flooded water. The method
CC is easy and quick, in which a seedling is required for studying single
CC nucleotide polymorphisms (SNPs) for genotyping, without needing
CC cultivation of seedling to fully-grown plant for judging heterozygote and
CC distinguishing morphology. The present sequence represents a rice sd-1
CC DNA fragment, which is given in the exemplification of the present
CC invention. Rice sd-1 is located on chromosome 1.
XX
SQ Sequence 30 BP; 0 A; 3 C; 0 G; 27 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.7e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2804
Db 30 AAAAAAAAAAAAGAAAAAA 12

RESULT 1935
ABL56893/c
ID ABL56893 standard; DNA; 30 BP.
XX
AC ABL56893;
XX
DT 26-JUL-2002 (first entry)
XX
DE Synthetic deoxyribooligonucleotide poly f.
XX
KW Concentration; quantification; mutation detection; polymorphic;
KW polymerase chain reaction; PCR; ss.
XX
OS Synthetic.
XX
PN EP1046717-A2.
XX
PD 25-OCT-2000.
XX
PF 20-APR-2000; 2000EP-00108643.
XX
PR 20-APR-1999; 99JP-00111601.
XX
PA (NIBI-) JAPAN BIOINDUSTRY ASSOC.
PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
PA (KANK-) KANKYO ENG CO LTD.
XX
PI Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;
PI Koyama O, Furusho K;
XX
DR WPI; 2000-657765/64.
XX
PT Determining the concentration of a target nucleic acid, useful e.g. for
PT detecting genetic mutations, comprises using a fluorescently labeled
PT probe in which emission is reduced by binding to the target nucleic acid.
XX
PS Example 5; Page 21; 55pp; English.
XX
CC The invention relates to the determination of the concentration of a
CC nucleic acid target, using a fluorescently labeled probe which produces
CC reduced fluorescence emission when hybridised to the target nucleic acid.
CC The method comprises measuring the reduction in emission caused by
CC hybridisation. The new method is particularly used to quantify target
CC nucleic acids by a real-time polymerase chain reaction, e.g. for
CC quantifying microbial cells in co-cultures or symbiotic systems, for
CC detecting gene mutations or polymorphisms, and for analysing melting
CC curves of target nucleic acids to determine a Tm value. Methods of the
CC invention allow target nucleic acids to be quantified quickly, easily and
CC accurately. Particularly there is no need to remove unbound probe, and no
CC materials are introduced that inhibit amplification by Taq polymerase (so
CC conventional PCR conditions can be used). The specificity of PCR is kept
CC high (amplification of primer dimers is delayed), and the limit of
CC quantitation is reduced. Complex probes are not needed, and amplification
CC can be monitored in real time. The working graph for data analysis
CC (automatically generated by a computer) has a higher correlation
CC coefficient than conventional graphs so more accurate quantitation is
CC possible. The current sequence represents a synthetic

```
CC   deoxyribooligonucleotide that was used for investigating the base
CC   selectivity of a target nucleic acid
XX
SQ   Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.7e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||||| ||||
Db         30 AAAAAAAAAAAAAAGAAAA 12


RESULT 1936
ABA97617/c
ID   ABA97617 standard; DNA; 30 BP.
XX
AC   ABA97617;
XX
DT   11-APR-2002  (first entry)
XX
DE   Poly f nucleotide sequence.
XX
KW   ss; fluorochrome; nucleic acid probe; fluorescence.
XX
OS   Unidentified.
XX
PN   JP2001286300-A.
XX
PD   16-OCT-2001.
XX
PF   20-APR-2000; 2000JP-00120097.
XX
PR   20-APR-1999;   99JP-00111601.
PR   24-AUG-1999;   99JP-00236666.
PR   30-AUG-1999;   99JP-00242693.
PR   01-FEB-2000; 2000JP-00028896.
XX
PA   (BIOI-) BIOINDUSTRY KYOKAI SH.
PA   (KANK-) KANKYO ENG KK.
PA   (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.
XX
DR   WPI; 2002-134193/18.
XX
PT   Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT   the obtained data.
XX
PS   Example 5; Page 17; 34pp; Japanese.
XX
CC   This invention relates to a method for measuring nucleic acids using a
CC   nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC   decreases the fluorescence of the fluorochrome when hybridised with a
CC   target nucleic acid, the decrease in the fluorescence is measured. The
CC   method can be used for measuring a target nucleic acid
XX
SQ   Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.7e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||||| ||||
Db         30 AAAAAAAAAAAAAAGAAAA 12


RESULT 1937
ABL95890/c
ID   ABL95890 standard; DNA; 30 BP.
XX
AC   ABL95890;
XX
DT   19-JUN-2002  (first entry)
XX
DE   Probe poly f for assaying nucleic acids.
XX
KW   Probe; polymorphism detection; mutation detection; disease diagnosis;
KW   microbial identification; ss.
XX
OS   Unidentified.
XX
PN   WO200208414-A1.
XX
PD   31-JAN-2002.
XX
PF   27-JUN-2001; 2001WO-IB001147.
XX
PR   27-JUN-2000; 2000JP-00193133.
PR   03-AUG-2000; 2000JP-00236115.
PR   26-SEP-2000; 2000JP-00292483.
XX
PA   (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA   (KANK-) KANKYO ENG CO LTD.
XX
PI   Kurane R,  Kanagawa T,  Kamagata Y,  Torimura M,  Kurata S,  Yamada K;
PI   Yokomaku T;
XX
DR   WPI; 2002-195876/25.
XX
PT   Fluorescently-labeled nucleic acid probes for assaying nucleic acids and
PT   their polymorphism and mutation, particularly useful in science and
PT   medicine for e.g. analytical applications, disease diagnosis and
PT   microbial identification.
XX
PS   Example 12; Page 60; 152pp; Japanese.
XX
CC   The present invention relates to nucleic acid probes, which are useful
CC   for assaying nucleic acids by hybridising with a target nucleic acid, in
CC   which a single-stranded oligonucleotide is labelled with a fluorescent
CC   substance and a quencher in a manner that the fluorescence intensity of
CC   the hybridisation reaction system is increased after completion of the
CC   hybridisation but no stem loop structure is formed. The probes are useful
CC   for assaying nucleic acids and their polymorphism and mutation,
CC   particularly useful for e.g. analytical applications, disease diagnosis
CC   and microbial identification. The present sequence was used to illustrate
CC   the invention
XX
SQ   Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.7e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||||| ||||
Db         30 AAAAAAAAAAAAAAGAAAA 12


RESULT 1938
ABL56894/c
ID   ABL56894 standard; DNA; 30 BP.
XX
AC   ABL56894;
XX
DT   26-JUL-2002  (first entry)
XX
DE   Synthetic deoxyribooligonucleotide poly g.
XX
KW   Concentration; quantification; mutation detection; polymorphic;
KW   polymerase chain reaction; PCR; ss.
XX
OS   Synthetic.
XX
PN   EP1046717-A2.
XX
```

PD 25-OCT-2000.
XX
PF 20-APR-2000; 2000EP-00108643.
XX
PR 20-APR-1999; 99JP-00111601.
XX
PA (NIBI-) JAPAN BIOINDUSTRY ASSOC.
PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
PA (KANK-) KANKYO ENG CO LTD.
XX
PI Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;
PI Koyama O, Furusho K;
XX
DR WPI; 2000-657765/64.
XX
PT Determining the concentration of a target nucleic acid, useful e.g. for
PT detecting genetic mutations, comprises using a fluorescently labeled
PT probe in which emission is reduced by binding to the target nucleic acid.
XX
PS Example 5; Page 21; 55pp; English.
XX
CC The invention relates to the determination of the concentration of a
CC nucleic acid target, using a fluorescently labeled probe which produces
CC reduced fluorescence emission when hybridised to the target nucleic acid.
CC The method comprises measuring the reduction in emission caused by
CC hybridisation. The new method is particularly used to quantify target
CC nucleic acids by a real-time polymerase chain reaction, e.g. for
CC quantifying microbial cells in co-cultures or symbiotic systems, for
CC detecting gene mutations or polymorphisms, and for analysing melting
CC curves of target nucleic acids to determine a Tm value. Methods of the
CC invention allow target nucleic acids to be quantified quickly, easily and
CC accurately. Particularly there is no need to remove unbound probe, and no
CC materials are introduced that inhibit amplification by Taq polymerase (so
CC conventional PCR conditions can be used). The specificity of PCR is kept
CC high (amplification of primer dimers is delayed), and the limit of
CC quantitation is reduced. Complex probes are not needed, and amplification
CC can be monitored in real time. The working graph for data analysis
CC (automatically generated by a computer) has a higher correlation
CC coefficient than conventional graphs so more accurate quantitation is
CC possible. The current sequence represents a synthetic
CC deoxyribooligonucleotide that was used for investigating the base
CC selectivity of a target nucleic acid
XX
SQ Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.7e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2804
|||||||||||| |||||
Db 30 AAAAAAAAAAAAAGAAAAA 12

RESULT 1939
ABL56895/c
ID ABL56895 standard; DNA; 30 BP.
XX
AC ABL56895;
XX
DT 26-JUL-2002 (first entry)
XX
DE Synthetic deoxyribooligonucleotide poly h.
XX
KW Concentration; quantification; mutation detection; polymorphic;
KW polymerase chain reaction; PCR; ss.
XX
OS Synthetic.
XX
PN EP1046717-A2.
XX
PD 25-OCT-2000.
XX
PF 20-APR-2000; 2000EP-00108643.
XX
PR 20-APR-1999; 99JP-00111601.
XX
PA (NIBI-) JAPAN BIOINDUSTRY ASSOC.
PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
PA (KANK-) KANKYO ENG CO LTD.
XX
PI Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;
PI Koyama O, Furusho K;
XX
DR WPI; 2000-657765/64.
XX
PT Determining the concentration of a target nucleic acid, useful e.g. for
PT detecting genetic mutations, comprises using a fluorescently labeled
PT probe in which emission is reduced by binding to the target nucleic acid.
XX
PS Example 5; Page 21; 55pp; English.
XX
CC The invention relates to the determination of the concentration of a
CC nucleic acid target, using a fluorescently labeled probe which produces
CC reduced fluorescence emission when hybridised to the target nucleic acid.
CC The method comprises measuring the reduction in emission caused by
CC hybridisation. The new method is particularly used to quantify target
CC nucleic acids by a real-time polymerase chain reaction, e.g. for
CC quantifying microbial cells in co-cultures or symbiotic systems, for
CC detecting gene mutations or polymorphisms, and for analysing melting
CC curves of target nucleic acids to determine a Tm value. Methods of the
CC invention allow target nucleic acids to be quantified quickly, easily and
CC accurately. Particularly there is no need to remove unbound probe, and no
CC materials are introduced that inhibit amplification by Taq polymerase (so
CC conventional PCR conditions can be used). The specificity of PCR is kept
CC high (amplification of primer dimers is delayed), and the limit of
CC quantitation is reduced. Complex probes are not needed, and amplification
CC can be monitored in real time. The working graph for data analysis
CC (automatically generated by a computer) has a higher correlation
CC coefficient than conventional graphs so more accurate quantitation is
CC possible. The current sequence represents a synthetic
CC deoxyribooligonucleotide that was used for investigating the base
CC selectivity of a target nucleic acid
XX
SQ Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.7e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2804
|||||||||||| |||||
Db 30 AAAAAAAAAAAAAGAAAAA 12

RESULT 1940
ABA97619/c
ID ABA97619 standard; DNA; 30 BP.
XX
AC ABA97619;
XX
DT 11-APR-2002 (first entry)
XX
DE Poly h nucleotide sequence.
XX
KW ss; fluorochrome; nucleic acid probe; fluorescence.
XX
OS Unidentified.
XX
PN JP2001286300-A.
XX
PD 16-OCT-2001.
XX
PF 20-APR-2000; 2000JP-00120097.
XX
PR 20-APR-1999; 99JP-00111601.

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PR   24-AUG-1999;   99JP-00236666.
PR   30-AUG-1999;   99JP-00242693.
PR   01-FEB-2000; 2000JP-00028896.
XX
PA   (BIOI-) BIOINDUSTRY KYOKAI SH.
PA   (KANK-) KANKYO ENG KK.
PA   (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.
XX
DR   WPI; 2002-134193/18.
XX
PT   Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT   the obtained data.
XX
PS   Example 5; Page 17; 34pp; Japanese.
XX
CC   This invention relates to a method for measuring nucleic acids using a
CC   nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC   decreases the fluorescence of the fluorochrome when hybridised with a
CC   target nucleic acid, the decrease in the fluorescence is measured. The
CC   method can be used for measuring a target nucleic acid
XX
SQ   Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.7e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
                ||||||||||||| ||||||
Db         30 AAAAAAAAAAAAGAAAAAA 12


RESULT 1941
ABA97618/c
ID   ABA97618 standard; DNA; 30 BP.
XX
AC   ABA97618;
XX
DT   11-APR-2002  (first entry)
XX
DE   Poly g nucleotide sequence.
XX
KW   ss; fluorochrome; nucleic acid probe; fluorescence.
XX
OS   Unidentified.
XX
PN   JP2001286300-A.
XX
PD   16-OCT-2001.
XX
PF   20-APR-2000; 2000JP-00120097.
XX
PR   20-APR-1999;   99JP-00111601.
PR   24-AUG-1999;   99JP-00236666.
PR   30-AUG-1999;   99JP-00242693.
PR   01-FEB-2000; 2000JP-00028896.
XX
PA   (BIOI-) BIOINDUSTRY KYOKAI SH.
PA   (KANK-) KANKYO ENG KK.
PA   (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.
XX
DR   WPI; 2002-134193/18.
XX
PT   Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT   the obtained data.
XX
PS   Example 5; Page 17; 34pp; Japanese.
XX
CC   This invention relates to a method for measuring nucleic acids using a
CC   nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC   decreases the fluorescence of the fluorochrome when hybridised with a
CC   target nucleic acid, the decrease in the fluorescence is measured. The
CC   method can be used for measuring a target nucleic acid
XX
SQ   Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.7e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
                ||||||||||||| ||||||
Db         30 AAAAAAAAAAAAGAAAAAA 12


RESULT 1942
ABL95891/c
ID   ABL95891 standard; DNA; 30 BP.
XX
AC   ABL95891;
XX
DT   19-JUN-2002  (first entry)
XX
DE   Probe poly g for assaying nucleic acids.
XX
KW   Probe; polymorphism detection; mutation detection; disease diagnosis;
KW   microbial identification; ss.
XX
OS   Unidentified.
XX
PN   WO200208414-A1.
XX
PD   31-JAN-2002.
XX
PF   27-JUN-2001; 2001WO-IB001147.
XX
PR   27-JUN-2000; 2000JP-00193133.
PR   03-AUG-2000; 2000JP-00236115.
PR   26-SEP-2000; 2000JP-00292483.
XX
PA   (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA   (KANK-) KANKYO ENG CO LTD.
XX
PI   Kurane R,  Kanagawa T,  Kamagata Y,  Torimura M,  Kurata S,  Yamada K;
PI   Yokomaku T;
XX
DR   WPI; 2002-195876/25.
XX
PT   Fluorescently-labeled nucleic acid probes for assaying nucleic acids and
PT   their polymorphism and mutation, particularly useful in science and
PT   medicine for e.g. analytical applications, disease diagnosis and
PT   microbial identification.
XX
PS   Example 12; Page 60; 152pp; Japanese.
XX
CC   The present invention relates to nucleic acid probes, which are useful
CC   for assaying nucleic acids by hybridising with a target nucleic acid, in
CC   which a single-stranded oligonucleotide is labelled with a fluorescent
CC   substance and a quencher in a manner that the fluorescence intensity of
CC   the hybridisation reaction system is increased after completion of the
CC   hybridisation but no stem loop structure is formed. The probes are useful
CC   for assaying nucleic acids and their polymorphism and mutation,
CC   particularly useful for e.g. analytical applications, disease diagnosis
CC   and microbial identification. The present sequence was used to illustrate
CC   the invention
XX
SQ   Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.7e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
                ||||||||||||| ||||||
Db         30 AAAAAAAAAAAAGAAAAAA 12
```

```
RESULT 1943
ABL95892/c
ID   ABL95892 standard; DNA; 30 BP.
XX
AC   ABL95892;
XX
DT   19-JUN-2002  (first entry)
XX
DE   Probe poly h for assaying nucleic acids.
XX
KW   Probe; polymorphism detection; mutation detection; disease diagnosis;
KW   microbial identification; ss.
XX
OS   Unidentified.
XX
PN   WO200208414-A1.
XX
PD   31-JAN-2002.
XX
PF   27-JUN-2001; 2001WO-IB001147.
XX
PR   27-JUN-2000; 2000JP-00193133.
PR   03-AUG-2000; 2000JP-00236115.
PR   26-SEP-2000; 2000JP-00292483.
XX
PA   (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
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PI   Kurane R,  Kanagawa T,  Kamagata Y,  Torimura M,  Kurata S,  Yamada K;
PI   Yokomaku T;
XX
DR   WPI; 2002-195876/25.
XX
PT   Fluorescently-labeled nucleic acid probes for assaying nucleic acids and
PT   their polymorphism and mutation, particularly useful in science and
PT   medicine for e.g. analytical applications, disease diagnosis and
PT   microbial identification.
XX
PS   Example 12; Page 60; 152pp; Japanese.
XX
CC   The present invention relates to nucleic acid probes, which are useful
CC   for assaying nucleic acids by hybridising with a target nucleic acid, in
CC   which a single-stranded oligonucleotide is labelled with a fluorescent
CC   substance and a quencher in a manner that the fluorescence intensity of
CC   the hybridisation reaction system is increased after completion of the
CC   hybridisation but no stem loop structure is formed. The probes are useful
CC   for assaying nucleic acids and their polymorphism and mutation,
CC   particularly useful for e.g. analytical applications, disease diagnosis
CC   and microbial identification. The present sequence was used to illustrate
CC   the invention
XX
SQ   Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.7e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||| ||||||
Db         30 AAAAAAAAAAAAGAAAAAA 12


RESULT 1944
ABL56888/c
ID   ABL56888 standard; DNA; 30 BP.
XX
AC   ABL56888;
XX
DT   26-JUL-2002  (first entry)
XX
DE   Synthetic deoxyribooligonucleotide poly a.
XX
KW   Concentration; quantification; mutation detection; polymorphic;
KW   polymerase chain reaction; PCR; ss.
XX
OS   Synthetic.
XX
PN   EP1046717-A2.
XX
PD   25-OCT-2000.
XX
PF   20-APR-2000; 2000EP-00108643.
XX
PR   20-APR-1999;   99JP-00111601.
XX
PA   (NIBI-) JAPAN BIOINDUSTRY ASSOC.
PA   (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.
PA   (KANK-) KANKYO ENG CO LTD.
XX
PI   Kurane R,  Kanagawa T,  Kamagata Y,  Kurata S,  Yamada K,  Yokomaku T;
PI   Koyama O,  Furusho K;
XX
DR   WPI; 2000-657765/64.
XX
PT   Determining the concentration of a target nucleic acid, useful e.g. for
PT   detecting genetic mutations, comprises using a fluorescently labeled
PT   probe in which emission is reduced by binding to the target nucleic acid.
XX
PS   Example 5; Page 21; 55pp; English.
XX
CC   The invention relates to the determination of the concentration of a
CC   nucleic acid target, using a fluorescently labeled probe which produces
CC   reduced fluorescence emission when hybridised to the target nucleic acid.
CC   The method comprises measuring the reduction in emission caused by
CC   hybridisation. The new method is particularly used to quantify target
CC   nucleic acids by a real-time polymerase chain reaction, e.g. for
CC   quantifying microbial cells in co-cultures or symbiotic systems, for
CC   detecting gene mutations or polymorphisms, and for analysing melting
CC   curves of target nucleic acids to determine a Tm value. Methods of the
CC   invention allow target nucleic acids to be quantified quickly, easily and
CC   accurately. Particularly there is no need to remove unbound probe, and no
CC   materials are introduced that inhibit amplification by Taq polymerase (so
CC   conventional PCR conditions can be used). The specificity of PCR is kept
CC   high (amplification of primer dimers is delayed), and the limit of
CC   quantitation is reduced. Complex probes are not needed, and amplification
CC   can be monitored in real time. The working graph for data analysis
CC   (automatically generated by a computer) has a higher correlation
CC   coefficient than conventional graphs so more accurate quantitation is
CC   possible. The current sequence represents a synthetic
CC   deoxyribooligonucleotide that was used for investigating the base
CC   selectivity of a target nucleic acid
XX
SQ   Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.7e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||||| ||||
Db         30 AAAAAAAAAAAAAACAAAA 12


RESULT 1945
ABA97612/c
ID   ABA97612 standard; DNA; 30 BP.
XX
AC   ABA97612;
XX
DT   11-APR-2002  (first entry)
XX
DE   Poly a nucleotide sequence.
XX
KW   ss; fluorochrome; nucleic acid probe; fluorescence.
XX
```

```
OS   Unidentified.
XX
PN   JP2001286300-A.
XX
PD   16-OCT-2001.
XX
PF   20-APR-2000; 2000JP-00120097.
XX
PR   20-APR-1999;   99JP-00111601.
PR   24-AUG-1999;   99JP-00236666.
PR   30-AUG-1999;   99JP-00242693.
PR   01-FEB-2000; 2000JP-00028896.
XX
PA   (BIOI-) BIOINDUSTRY KYOKAI SH.
PA   (KANK-) KANKYO ENG KK.
PA   (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.
XX
DR   WPI; 2002-134193/18.
XX
PT   Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT   the obtained data.
XX
PS   Example 5; Page 17; 34pp; Japanese.
XX
CC   This invention relates to a method for measuring nucleic acids using a
CC   nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC   decreases the fluorescence of the fluorochrome when hybridised with a
CC   target nucleic acid, the decrease in the fluorescence is measured. The
CC   method can be used for measuring a target nucleic acid
XX
SQ   Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.7e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
                ||||||||||||||| ||||
Db         30 AAAAAAAAAAAAAACAAAA 12


RESULT 1946
ABL95885/c
ID   ABL95885 standard; DNA; 30 BP.
XX
AC   ABL95885;
XX
DT   19-JUN-2002  (first entry)
XX
DE   Probe poly a for assaying nucleic acids.
XX
KW   Probe; polymorphism detection; mutation detection; disease diagnosis;
KW   microbial identification; ss.
XX
OS   Unidentified.
XX
PN   WO200208414-A1.
XX
PD   31-JAN-2002.
XX
PF   27-JUN-2001; 2001WO-IB001147.
XX
PR   27-JUN-2000; 2000JP-00193133.
PR   03-AUG-2000; 2000JP-00236115.
PR   26-SEP-2000; 2000JP-00292483.
XX
PA   (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA   (KANK-) KANKYO ENG CO LTD.
XX
PI   Kurane R,  Kanagawa T,  Kamagata Y,  Torimura M,  Kurata S,  Yamada K;
PI   Yokomaku T;
XX
DR   WPI; 2002-195876/25.
XX
PT   Fluorescently-labeled nucleic acid probes for assaying nucleic acids and
PT   their polymorphism and mutation, particularly useful in science and
PT   medicine for e.g. analytical applications, disease diagnosis and
PT   microbial identification.
XX
PS   Example 12; Page 60; 152pp; Japanese.
XX
CC   The present invention relates to nucleic acid probes, which are useful
CC   for assaying nucleic acids by hybridising with a target nucleic acid, in
CC   which a single-stranded oligonucleotide is labelled with a fluorescent
CC   substance and a quencher in a manner that the fluorescence intensity of
CC   the hybridisation reaction system is increased after completion of the
CC   hybridisation but no stem loop structure is formed. The probes are useful
CC   for assaying nucleic acids and their polymorphism and mutation,
CC   particularly useful for e.g. analytical applications, disease diagnosis
CC   and microbial identification. The present sequence was used to illustrate
CC   the invention
XX
SQ   Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.7e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
                ||||||||||||||| ||||
Db         30 AAAAAAAAAAAAAACAAAA 12


RESULT 1947
ABL56892/c
ID   ABL56892 standard; DNA; 30 BP.
XX
AC   ABL56892;
XX
DT   26-JUL-2002  (first entry)
XX
DE   Synthetic deoxyribooligonucleotide poly e.
XX
KW   Concentration; quantification; mutation detection; polymorphic;
KW   polymerase chain reaction; PCR; ss.
XX
OS   Synthetic.
XX
PN   EP1046717-A2.
XX
PD   25-OCT-2000.
XX
PF   20-APR-2000; 2000EP-00108643.
XX
PR   20-APR-1999;   99JP-00111601.
XX
PA   (NIBI-) JAPAN BIOINDUSTRY ASSOC.
PA   (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.
PA   (KANK-) KANKYO ENG CO LTD.
XX
PI   Kurane R,  Kanagawa T,  Kamagata Y,  Kurata S,  Yamada K,  Yokomaku T;
PI   Koyama O,  Furusho K;
XX
DR   WPI; 2000-657765/64.
XX
PT   Determining the concentration of a target nucleic acid, useful e.g. for
PT   detecting genetic mutations, comprises using a fluorescently labeled
PT   probe in which emission is reduced by binding to the target nucleic acid.
XX
PS   Example 5; Page 21; 55pp; English.
XX
CC   The invention relates to the determination of the concentration of a
CC   nucleic acid target, using a fluorescently labeled probe which produces
CC   reduced fluorescence emission when hybridised to the target nucleic acid.
CC   The method comprises measuring the reduction in emission caused by
CC   hybridisation. The new method is particularly used to quantify target
```

CC nucleic acids by a real-time polymerase chain reaction, e.g. for
CC quantifying microbial cells in co-cultures or symbiotic systems, for
CC detecting gene mutations or polymorphisms, and for analysing melting
CC curves of target nucleic acids to determine a Tm value. Methods of the
CC invention allow target nucleic acids to be quantified quickly, easily and
CC accurately. Particularly there is no need to remove unbound probe, and no
CC materials are introduced that inhibit amplification by Taq polymerase (so
CC conventional PCR conditions can be used). The specificity of PCR is kept
CC high (amplification of primer dimers is delayed), and the limit of
CC quantitation is reduced. Complex probes are not needed, and amplification
CC can be monitored in real time. The working graph for data analysis
CC (automatically generated by a computer) has a higher correlation
CC coefficient than conventional graphs so more accurate quantitation is
CC possible. The current sequence represents a synthetic
CC deoxyribooligonucleotide that was used for investigating the base
CC selectivity of a target nucleic acid
XX
SQ Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.7e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2804
||||||||||| ||||||||
Db 30 AAAAAAAAAACAAAAAAAA 12

RESULT 1948
ABL56896/c
ID ABL56896 standard; DNA; 30 BP.
XX
AC ABL56896;
XX
DT 26-JUL-2002 (first entry)
XX
DE Synthetic deoxyribooligonucleotide poly i.
XX
KW Concentration; quantification; mutation detection; polymorphic;
KW polymerase chain reaction; PCR; ss.
XX
OS Synthetic.
XX
PN EP1046717-A2.
XX
PD 25-OCT-2000.
XX
PF 20-APR-2000; 2000EP-00108643.
XX
PR 20-APR-1999; 99JP-00111601.
XX
PA (NIBI-) JAPAN BIOINDUSTRY ASSOC.
PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
PA (KANK-) KANKYO ENG CO LTD.
XX
PI Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;
PI Koyama O, Furusho K;
XX
DR WPI; 2000-657765/64.
XX
PT Determining the concentration of a target nucleic acid, useful e.g. for
PT detecting genetic mutations, comprises using a fluorescently labeled
PT probe in which emission is reduced by binding to the target nucleic acid.
XX
PS Example 5; Page 21; 55pp; English.
XX
CC The invention relates to the determination of the concentration of a
CC nucleic acid target, using a fluorescently labeled probe which produces
CC reduced fluorescence emission when hybridised to the target nucleic acid.
CC The method comprises measuring the reduction in emission caused by
CC hybridisation. The new method is particularly used to quantify target
CC nucleic acids by a real-time polymerase chain reaction, e.g. for
CC quantifying microbial cells in co-cultures or symbiotic systems, for
CC detecting gene mutations or polymorphisms, and for analysing melting
CC curves of target nucleic acids to determine a Tm value. Methods of the
CC invention allow target nucleic acids to be quantified quickly, easily and
CC accurately. Particularly there is no need to remove unbound probe, and no
CC materials are introduced that inhibit amplification by Taq polymerase (so
CC conventional PCR conditions can be used). The specificity of PCR is kept
CC high (amplification of primer dimers is delayed), and the limit of
CC quantitation is reduced. Complex probes are not needed, and amplification
CC can be monitored in real time. The working graph for data analysis
CC (automatically generated by a computer) has a higher correlation
CC coefficient than conventional graphs so more accurate quantitation is
CC possible. The current sequence represents a synthetic
CC deoxyribooligonucleotide that was used for investigating the base
CC selectivity of a target nucleic acid
XX
SQ Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.7e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2804
|||||||||| |||||||
Db 30 AAAAAAAAAAGAAAAAAA 12

RESULT 1949
ABL56890/c
ID ABL56890 standard; DNA; 30 BP.
XX
AC ABL56890;
XX
DT 26-JUL-2002 (first entry)
XX
DE Synthetic deoxyribooligonucleotide poly c.
XX
KW Concentration; quantification; mutation detection; polymorphic;
KW polymerase chain reaction; PCR; ss.
XX
OS Synthetic.
XX
PN EP1046717-A2.
XX
PD 25-OCT-2000.
XX
PF 20-APR-2000; 2000EP-00108643.
XX
PR 20-APR-1999; 99JP-00111601.
XX
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PA (KANK-) KANKYO ENG CO LTD.
XX
PI Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;
PI Koyama O, Furusho K;
XX
DR WPI; 2000-657765/64.
XX
PT Determining the concentration of a target nucleic acid, useful e.g. for
PT detecting genetic mutations, comprises using a fluorescently labeled
PT probe in which emission is reduced by binding to the target nucleic acid.
XX
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XX
CC The invention relates to the determination of the concentration of a
CC nucleic acid target, using a fluorescently labeled probe which produces
CC reduced fluorescence emission when hybridised to the target nucleic acid.
CC The method comprises measuring the reduction in emission caused by
CC hybridisation. The new method is particularly used to quantify target
CC nucleic acids by a real-time polymerase chain reaction, e.g. for
CC quantifying microbial cells in co-cultures or symbiotic systems, for
CC detecting gene mutations or polymorphisms, and for analysing melting
CC curves of target nucleic acids to determine a Tm value. Methods of the

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CC accurately. Particularly there is no need to remove unbound probe, and no
CC materials are introduced that inhibit amplification by Taq polymerase (so
CC conventional PCR conditions can be used). The specificity of PCR is kept
CC high (amplification of primer dimers is delayed), and the limit of
CC quantitation is reduced. Complex probes are not needed, and amplification
CC can be monitored in real time. The working graph for data analysis
CC (automatically generated by a computer) has a higher correlation
CC coefficient than conventional graphs so more accurate quantitation is
CC possible. The current sequence represents a synthetic
CC deoxyribooligonucleotide that was used for investigating the base
CC selectivity of a target nucleic acid
XX
SQ Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.7e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2804
||||||||||||| ||||||
Db 30 AAAAAAAAAAAACAAAAAA 12

RESULT 1950
ABL56891/c
ID ABL56891 standard; DNA; 30 BP.
XX
AC ABL56891;
XX
DT 26-JUL-2002 (first entry)
XX
DE Synthetic deoxyribooligonucleotide poly d.
XX
KW Concentration; quantification; mutation detection; polymorphic;
KW polymerase chain reaction; PCR; ss.
XX
OS Synthetic.
XX
PN EP1046717-A2.
XX
PD 25-OCT-2000.
XX
PF 20-APR-2000; 2000EP-00108643.
XX
PR 20-APR-1999; 99JP-00111601.
XX
PA (NIBI-) JAPAN BIOINDUSTRY ASSOC.
PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
PA (KANK-) KANKYO ENG CO LTD.
XX
PI Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;
PI Koyama O, Furusho K;
XX
DR WPI; 2000-657765/64.
XX
PT Determining the concentration of a target nucleic acid, useful e.g. for
PT detecting genetic mutations, comprises using a fluorescently labeled
PT probe in which emission is reduced by binding to the target nucleic acid.
XX
PS Example 5; Page 21; 55pp; English.
XX
CC The invention relates to the determination of the concentration of a
CC nucleic acid target, using a fluorescently labeled probe which produces
CC reduced fluorescence emission when hybridised to the target nucleic acid.
CC The method comprises measuring the reduction in emission caused by
CC hybridisation. The new method is particularly used to quantify target
CC nucleic acids by a real-time polymerase chain reaction, e.g. for
CC quantifying microbial cells in co-cultures or symbiotic systems, for
CC detecting gene mutations or polymorphisms, and for analysing melting
CC curves of target nucleic acids to determine a Tm value. Methods of the
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CC accurately. Particularly there is no need to remove unbound probe, and no
CC materials are introduced that inhibit amplification by Taq polymerase (so
CC conventional PCR conditions can be used). The specificity of PCR is kept
CC high (amplification of primer dimers is delayed), and the limit of
CC quantitation is reduced. Complex probes are not needed, and amplification
CC can be monitored in real time. The working graph for data analysis
CC (automatically generated by a computer) has a higher correlation
CC coefficient than conventional graphs so more accurate quantitation is
CC possible. The current sequence represents a synthetic
CC deoxyribooligonucleotide that was used for investigating the base
CC selectivity of a target nucleic acid
XX
SQ Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.7e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2804
||||||||||||| ||||||
Db 30 AAAAAAAAAAAACAAAAAA 12

RESULT 1951
ABL56897/c
ID ABL56897 standard; DNA; 30 BP.
XX
AC ABL56897;
XX
DT 26-JUL-2002 (first entry)
XX
DE Synthetic deoxyribooligonucleotide poly j.
XX
KW Concentration; quantification; mutation detection; polymorphic;
KW polymerase chain reaction; PCR; ss.
XX
OS Synthetic.
XX
PN EP1046717-A2.
XX
PD 25-OCT-2000.
XX
PF 20-APR-2000; 2000EP-00108643.
XX
PR 20-APR-1999; 99JP-00111601.
XX
PA (NIBI-) JAPAN BIOINDUSTRY ASSOC.
PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
PA (KANK-) KANKYO ENG CO LTD.
XX
PI Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;
PI Koyama O, Furusho K;
XX
DR WPI; 2000-657765/64.
XX
PT Determining the concentration of a target nucleic acid, useful e.g. for
PT detecting genetic mutations, comprises using a fluorescently labeled
PT probe in which emission is reduced by binding to the target nucleic acid.
XX
PS Example 5; Page 21; 55pp; English.
XX
CC The invention relates to the determination of the concentration of a
CC nucleic acid target, using a fluorescently labeled probe which produces
CC reduced fluorescence emission when hybridised to the target nucleic acid.
CC The method comprises measuring the reduction in emission caused by
CC hybridisation. The new method is particularly used to quantify target
CC nucleic acids by a real-time polymerase chain reaction, e.g. for
CC quantifying microbial cells in co-cultures or symbiotic systems, for
CC detecting gene mutations or polymorphisms, and for analysing melting
CC curves of target nucleic acids to determine a Tm value. Methods of the
CC invention allow target nucleic acids to be quantified quickly, easily and
CC accurately. Particularly there is no need to remove unbound probe, and no
CC materials are introduced that inhibit amplification by Taq polymerase (so
CC conventional PCR conditions can be used). The specificity of PCR is kept

CC high (amplification of primer dimers is delayed), and the limit of
CC quantitation is reduced. Complex probes are not needed, and amplification
CC can be monitored in real time. The working graph for data analysis
CC (automatically generated by a computer) has a higher correlation
CC coefficient than conventional graphs so more accurate quantitation is
CC possible. The current sequence represents a synthetic
CC deoxyribooligonucleotide that was used for investigating the base
CC selectivity of a target nucleic acid
XX
SQ Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.7e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2804
||||||||||| ||||||||
Db 30 AAAAAAAAAAGAAAAAAA 12

RESULT 1952
ABL56889/c
ID ABL56889 standard; DNA; 30 BP.
XX
AC ABL56889;
XX
DT 26-JUL-2002 (first entry)
XX
DE Synthetic deoxyribooligonucleotide poly b.
XX
KW Concentration; quantification; mutation detection; polymorphic;
KW polymerase chain reaction; PCR; ss.
XX
OS Synthetic.
XX
PN EP1046717-A2.
XX
PD 25-OCT-2000.
XX
PF 20-APR-2000; 2000EP-00108643.
XX
PR 20-APR-1999; 99JP-00111601.
XX
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CC possible. The current sequence represents a synthetic
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CC selectivity of a target nucleic acid
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Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.7e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2804
||||||||||||| |||||
Db 30 AAAAAAAAAAAAACAAAAA 12

RESULT 1953
ABA97613/c
ID ABA97613 standard; DNA; 30 BP.
XX
AC ABA97613;
XX
DT 11-APR-2002 (first entry)
XX
DE Poly b nucleotide sequence.
XX
KW ss; fluorochrome; nucleic acid probe; fluorescence.
XX
OS Unidentified.
XX
PN JP2001286300-A.
XX
PD 16-OCT-2001.
XX
PF 20-APR-2000; 2000JP-00120097.
XX
PR 20-APR-1999; 99JP-00111601.
PR 24-AUG-1999; 99JP-00236666.
PR 30-AUG-1999; 99JP-00242693.
PR 01-FEB-2000; 2000JP-00028896.
XX
PA (BIOI-) BIOINDUSTRY KYOKAI SH.
PA (KANK-) KANKYO ENG KK.
PA (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.
XX
DR WPI; 2002-134193/18.
XX
PT Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT the obtained data.
XX
PS Example 5; Page 17; 34pp; Japanese.
XX
CC This invention relates to a method for measuring nucleic acids using a
CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC decreases the fluorescence of the fluorochrome when hybridised with a
CC target nucleic acid, the decrease in the fluorescence is measured. The
CC method can be used for measuring a target nucleic acid
XX
SQ Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.7e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2804
||||||||||||| |||||
Db 30 AAAAAAAAAAAAACAAAAA 12

RESULT 1954
ABA97620/c

```
ID   ABA97620 standard; DNA; 30 BP.
XX
AC   ABA97620;
XX
DT   11-APR-2002  (first entry)
XX
DE   Poly i nucleotide sequence.
XX
KW   ss; fluorochrome; nucleic acid probe; fluorescence.
XX
OS   Unidentified.
XX
PN   JP2001286300-A.
XX
PD   16-OCT-2001.
XX
PF   20-APR-2000; 2000JP-00120097.
XX
PR   20-APR-1999;   99JP-00111601.
PR   24-AUG-1999;   99JP-00236666.
PR   30-AUG-1999;   99JP-00242693.
PR   01-FEB-2000; 2000JP-00028896.
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DR   WPI; 2002-134193/18.
XX
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PT   the obtained data.
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CC   nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC   decreases the fluorescence of the fluorochrome when hybridised with a
CC   target nucleic acid, the decrease in the fluorescence is measured. The
CC   method can be used for measuring a target nucleic acid
XX
SQ   Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.7e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
                ||||||||||| |||||||
Db         30 AAAAAAAAAAAGAAAAAAA 12


RESULT 1955
ABA97614/c
ID   ABA97614 standard; DNA; 30 BP.
XX
AC   ABA97614;
XX
DT   11-APR-2002  (first entry)
XX
DE   Poly c nucleotide sequence.
XX
KW   ss; fluorochrome; nucleic acid probe; fluorescence.
XX
OS   Unidentified.
XX
PN   JP2001286300-A.
XX
PD   16-OCT-2001.
XX
PF   20-APR-2000; 2000JP-00120097.
XX
PR   20-APR-1999;   99JP-00111601.
PR   24-AUG-1999;   99JP-00236666.
PR   30-AUG-1999;   99JP-00242693.
PR   01-FEB-2000; 2000JP-00028896.
XX
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PA   (KANK-) KANKYO ENG KK.
PA   (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.
XX
DR   WPI; 2002-134193/18.
XX
PT   Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT   the obtained data.
XX
PS   Example 5; Page 17; 34pp; Japanese.
XX
CC   This invention relates to a method for measuring nucleic acids using a
CC   nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC   decreases the fluorescence of the fluorochrome when hybridised with a
CC   target nucleic acid, the decrease in the fluorescence is measured. The
CC   method can be used for measuring a target nucleic acid
XX
SQ   Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.7e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
                ||||||||||| |||||||
Db         30 AAAAAAAAAAAACAAAAAA 12


RESULT 1956
ABA97615/c
ID   ABA97615 standard; DNA; 30 BP.
XX
AC   ABA97615;
XX
DT   11-APR-2002  (first entry)
XX
DE   Poly d nucleotide sequence.
XX
KW   ss; fluorochrome; nucleic acid probe; fluorescence.
XX
OS   Unidentified.
XX
PN   JP2001286300-A.
XX
PD   16-OCT-2001.
XX
PF   20-APR-2000; 2000JP-00120097.
XX
PR   20-APR-1999;   99JP-00111601.
PR   24-AUG-1999;   99JP-00236666.
PR   30-AUG-1999;   99JP-00242693.
PR   01-FEB-2000; 2000JP-00028896.
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XX
DR   WPI; 2002-134193/18.
XX
PT   Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT   the obtained data.
XX
PS   Example 5; Page 17; 34pp; Japanese.
XX
CC   This invention relates to a method for measuring nucleic acids using a
CC   nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC   decreases the fluorescence of the fluorochrome when hybridised with a
CC   target nucleic acid, the decrease in the fluorescence is measured. The
CC   method can be used for measuring a target nucleic acid
XX
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```
SQ   Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.7e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||  |||||||
Db         30 AAAAAAAAAAACAAAAAAA 12


RESULT 1957
ABA97616/c
ID   ABA97616 standard; DNA; 30 BP.
XX
AC   ABA97616;
XX
DT   11-APR-2002  (first entry)
XX
DE   Poly e nucleotide sequence.
XX
KW   ss; fluorochrome; nucleic acid probe; fluorescence.
XX
OS   Unidentified.
XX
PN   JP2001286300-A.
XX
PD   16-OCT-2001.
XX
PF   20-APR-2000; 2000JP-00120097.
XX
PR   20-APR-1999;   99JP-00111601.
PR   24-AUG-1999;   99JP-00236666.
PR   30-AUG-1999;   99JP-00242693.
PR   01-FEB-2000; 2000JP-00028896.
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XX
DR   WPI; 2002-134193/18.
XX
PT   Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT   the obtained data.
XX
PS   Example 5; Page 17; 34pp; Japanese.
XX
CC   This invention relates to a method for measuring nucleic acids using a
CC   nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC   decreases the fluorescence of the fluorochrome when hybridised with a
CC   target nucleic acid, the decrease in the fluorescence is measured. The
CC   method can be used for measuring a target nucleic acid
XX
SQ   Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.7e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              ||||||||||  ||||||||
Db         30 AAAAAAAAAACAAAAAAA 12


RESULT 1958
ABL95886/c
ID   ABL95886 standard; DNA; 30 BP.
XX
AC   ABL95886;
XX
DT   19-JUN-2002  (first entry)
XX
DE   Probe poly b for assaying nucleic acids.
XX
KW   Probe; polymorphism detection; mutation detection; disease diagnosis;
KW   microbial identification; ss.
XX
OS   Unidentified.
XX
PN   WO200208414-A1.
XX
PD   31-JAN-2002.
XX
PF   27-JUN-2001; 2001WO-IB001147.
XX
PR   27-JUN-2000; 2000JP-00193133.
PR   03-AUG-2000; 2000JP-00236115.
PR   26-SEP-2000; 2000JP-00292483.
XX
PA   (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA   (KANK-) KANKYO ENG CO LTD.
XX
PI   Kurane R,  Kanagawa T,  Kamagata Y,  Torimura M,  Kurata S,  Yamada K;
PI   Yokomaku T;
XX
DR   WPI; 2002-195876/25.
XX
PT   Fluorescently-labeled nucleic acid probes for assaying nucleic acids and
PT   their polymorphism and mutation, particularly useful in science and
PT   medicine for e.g. analytical applications, disease diagnosis and
PT   microbial identification.
XX
PS   Example 12; Page 60; 152pp; Japanese.
XX
CC   The present invention relates to nucleic acid probes, which are useful
CC   for assaying nucleic acids by hybridising with a target nucleic acid, in
CC   which a single-stranded oligonucleotide is labelled with a fluorescent
CC   substance and a quencher in a manner that the fluorescence intensity of
CC   the hybridisation reaction system is increased after completion of the
CC   hybridisation but no stem loop structure is formed. The probes are useful
CC   for assaying nucleic acids and their polymorphism and mutation,
CC   particularly useful for e.g. analytical applications, disease diagnosis
CC   and microbial identification. The present sequence was used to illustrate
CC   the invention
XX
SQ   Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.7e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              ||||||||||||| |||||
Db         30 AAAAAAAAAAAAACAAAAA 12


RESULT 1959
ABL95887/c
ID   ABL95887 standard; DNA; 30 BP.
XX
AC   ABL95887;
XX
DT   19-JUN-2002  (first entry)
XX
DE   Probe poly c for assaying nucleic acids.
XX
KW   Probe; polymorphism detection; mutation detection; disease diagnosis;
KW   microbial identification; ss.
XX
OS   Unidentified.
XX
PN   WO200208414-A1.
XX
PD   31-JAN-2002.
XX
PF   27-JUN-2001; 2001WO-IB001147.
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XX
PR   27-JUN-2000; 2000JP-00193133.
PR   03-AUG-2000; 2000JP-00236115.
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CC   substance and a quencher in a manner that the fluorescence intensity of
CC   the hybridisation reaction system is increased after completion of the
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  Best Local Similarity   94.7%;  Pred. No. 2.7e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
                ||||||||||||| ||||||
Db         30 AAAAAAAAAAAACAAAAAA 12


RESULT 1960
ABL95894/c
ID   ABL95894 standard; DNA; 30 BP.
XX
AC   ABL95894;
XX
DT   19-JUN-2002  (first entry)
XX
DE   Probe poly j for assaying nucleic acids.
XX
KW   Probe; polymorphism detection; mutation detection; disease diagnosis;
KW   microbial identification; ss.
XX
OS   Unidentified.
XX
PN   WO200208414-A1.
XX
PD   31-JAN-2002.
XX
PF   27-JUN-2001; 2001WO-IB001147.
XX
PR   27-JUN-2000; 2000JP-00193133.
PR   03-AUG-2000; 2000JP-00236115.
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DR   WPI; 2002-195876/25.
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PT   their polymorphism and mutation, particularly useful in science and
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CC   the hybridisation reaction system is increased after completion of the
CC   hybridisation but no stem loop structure is formed. The probes are useful
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XX
SQ   Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.7e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
                ||||||||||| ||||||||
Db         30 AAAAAAAAAAGAAAAAAAA 12


RESULT 1961
ABL95888/c
ID   ABL95888 standard; DNA; 30 BP.
XX
AC   ABL95888;
XX
DT   19-JUN-2002  (first entry)
XX
DE   Probe poly d for assaying nucleic acids.
XX
KW   Probe; polymorphism detection; mutation detection; disease diagnosis;
KW   microbial identification; ss.
XX
OS   Unidentified.
XX
PN   WO200208414-A1.
XX
PD   31-JAN-2002.
XX
PF   27-JUN-2001; 2001WO-IB001147.
XX
PR   27-JUN-2000; 2000JP-00193133.
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CC   substance and a quencher in a manner that the fluorescence intensity of
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  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.7e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||  |||||||
Db         30 AAAAAAAAAAACAAAAAAA 12


RESULT 1962
ABL95889/c
ID   ABL95889 standard; DNA; 30 BP.
XX
AC   ABL95889;
XX
DT   19-JUN-2002  (first entry)
XX
DE   Probe poly e for assaying nucleic acids.
XX
KW   Probe; polymorphism detection; mutation detection; disease diagnosis;
KW   microbial identification; ss.
XX
OS   Unidentified.
XX
PN   WO200208414-A1.
XX
PD   31-JAN-2002.
XX
PF   27-JUN-2001; 2001WO-IB001147.
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PR   27-JUN-2000; 2000JP-00193133.
PR   03-AUG-2000; 2000JP-00236115.
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CC   the hybridisation reaction system is increased after completion of the
CC   hybridisation but no stem loop structure is formed. The probes are useful
CC   for assaying nucleic acids and their polymorphism and mutation,
CC   particularly useful for e.g. analytical applications, disease diagnosis
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CC   the invention
XX
SQ   Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.7e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||  |||||||
Db         30 AAAAAAAAAACAAAAAAA 12


RESULT 1963
ABL95893/c
ID   ABL95893 standard; DNA; 30 BP.
XX
AC   ABL95893;
XX
DT   19-JUN-2002  (first entry)
XX
DE   Probe poly I for assaying nucleic acids.
XX
KW   Probe; polymorphism detection; mutation detection; disease diagnosis;
KW   microbial identification; ss.
XX
OS   Unidentified.
XX
PN   WO200208414-A1.
XX
PD   31-JAN-2002.
XX
PF   27-JUN-2001; 2001WO-IB001147.
XX
PR   27-JUN-2000; 2000JP-00193133.
PR   03-AUG-2000; 2000JP-00236115.
PR   26-SEP-2000; 2000JP-00292483.
XX
PA   (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA   (KANK-) KANKYO ENG CO LTD.
XX
PI   Kurane R,  Kanagawa T,  Kamagata Y,  Torimura M,  Kurata S,  Yamada K;
PI   Yokomaku T;
XX
DR   WPI; 2002-195876/25.
XX
PT   Fluorescently-labeled nucleic acid probes for assaying nucleic acids and
PT   their polymorphism and mutation, particularly useful in science and
PT   medicine for e.g. analytical applications, disease diagnosis and
PT   microbial identification.
XX
PS   Example 12; Page 60; 152pp; Japanese.
XX
CC   The present invention relates to nucleic acid probes, which are useful
CC   for assaying nucleic acids by hybridising with a target nucleic acid, in
CC   which a single-stranded oligonucleotide is labelled with a fluorescent
CC   substance and a quencher in a manner that the fluorescence intensity of
CC   the hybridisation reaction system is increased after completion of the
CC   hybridisation but no stem loop structure is formed. The probes are useful
CC   for assaying nucleic acids and their polymorphism and mutation,
CC   particularly useful for e.g. analytical applications, disease diagnosis
CC   and microbial identification. The present sequence was used to illustrate
CC   the invention
XX
SQ   Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.7e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||  |||||||
Db         30 AAAAAAAAAAAGAAAAAAA 12


RESULT 1964
AAT94431
```

```
ID   AAT94431 standard; mRNA; 19 BP.
XX
AC   AAT94431;
XX
DT   02-MAR-1998  (first entry)
XX
DE   Template mRNA poly-A tail SEQ ID NO:1 from WO9729211.
XX
KW   Primer; detection; characterisation; mRNA; restriction display PCR;
KW   synthesis; cDNA; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9729211-A1.
XX
PD   14-AUG-1997.
XX
PF   07-FEB-1997;   97WO-US002009.
XX
PR   09-FEB-1996;   96US-0011379P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Weinstein JN,  Boulamwini J;
XX
DR   WPI; 1997-415362/38.
XX
PT   Detection and characterisation of mRNA by restriction display PCR -
PT   comprising synthesis of cDNA, digestion with a restriction endonuclease,
PT   ligation to an adaptor DNA and PCR amplification.
XX
PS   Disclosure; Page 24; 40pp; English.
XX
CC   A method has been improved for detecting and characterising mRNA
CC   molecules which includes synthesising a double stranded (ds) cDNA from
CC   isolated mRNA, digesting the ds cDNA with a restriction endonuclease to
CC   produce cDNA fragments in which at least one end of the cDNA fragments
CC   has a sequence capable of hybridising to an adaptor DNA sequence. The
CC   improvement comprises: (a) hybridising adaptor DNA sequences to at least
CC   one end of the cDNA fragments; (b) ligating the adaptor DNA sequences to
CC   the cDNA fragments; (c) amplifying the cDNA fragments having ligated
CC   adaptor DNA sequences by a PCR using primers that hybridise to the ends
CC   of the cDNA fragments, where the primers have at least one nucleotide at
CC   the 3' end that specifically hybridises to a subset of cDNA molecules;
CC   and (d) detecting the presence of the resulting amplified cDNA fragments.
CC   The present sequence represent a template poly-A tail used in the present
CC   specification. The method designate restriction display PCR can be used
CC   for characterising cells based on their mRNA content, for representing
CC   expressed genes, and for discovery of therapeutics that alter cellular
CC   gene expression. The method is also useful for characterising cells of a
CC   variety of types and under a variety of physiological conditions. The
CC   method is also useful for identifying cells or tissue from particular
CC   individuals or species based on the fingerprint obtained from the mRNA
CC   content of isolated cells or tissue and comparing it to cells or tissue
CC   from a known source
XX
SQ   Sequence 19 BP; 17 A; 0 C; 0 G; 0 T; 0 U; 2 Other;

  Query Match              0.6%;  Score 17.2;  DB 1;  Length 19;
  Best Local Similarity   94.4%;  Pred. No. 1.2e+03;
  Matches   17;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2802
              :|||||||||||||||||
Db          2 BAAAAAAAAAAAAAAAA 19


RESULT 1965
AAT94431/c
ID   AAT94431 standard; mRNA; 19 BP.
XX
AC   AAT94431;
XX
DT   02-MAR-1998  (first entry)
XX
DE   Template mRNA poly-A tail SEQ ID NO:1 from WO9729211.
XX
KW   Primer; detection; characterisation; mRNA; restriction display PCR;
KW   synthesis; cDNA; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9729211-A1.
XX
PD   14-AUG-1997.
XX
PF   07-FEB-1997;   97WO-US002009.
XX
PR   09-FEB-1996;   96US-0011379P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Weinstein JN,  Boulamwini J;
XX
DR   WPI; 1997-415362/38.
XX
PT   Detection and characterisation of mRNA by restriction display PCR -
PT   comprising synthesis of cDNA, digestion with a restriction endonuclease,
PT   ligation to an adaptor DNA and PCR amplification.
XX
PS   Disclosure; Page 24; 40pp; English.
XX
CC   A method has been improved for detecting and characterising mRNA
CC   molecules which includes synthesising a double stranded (ds) cDNA from
CC   isolated mRNA, digesting the ds cDNA with a restriction endonuclease to
CC   produce cDNA fragments in which at least one end of the cDNA fragments
CC   has a sequence capable of hybridising to an adaptor DNA sequence. The
CC   improvement comprises: (a) hybridising adaptor DNA sequences to at least
CC   one end of the cDNA fragments; (b) ligating the adaptor DNA sequences to
CC   the cDNA fragments; (c) amplifying the cDNA fragments having ligated
CC   adaptor DNA sequences by a PCR using primers that hybridise to the ends
CC   of the cDNA fragments, where the primers have at least one nucleotide at
CC   the 3' end that specifically hybridises to a subset of cDNA molecules;
CC   and (d) detecting the presence of the resulting amplified cDNA fragments.
CC   The present sequence represent a template poly-A tail used in the present
CC   specification. The method designate restriction display PCR can be used
CC   for characterising cells based on their mRNA content, for representing
CC   expressed genes, and for discovery of therapeutics that alter cellular
CC   gene expression. The method is also useful for characterising cells of a
CC   variety of types and under a variety of physiological conditions. The
CC   method is also useful for identifying cells or tissue from particular
CC   individuals or species based on the fingerprint obtained from the mRNA
CC   content of isolated cells or tissue and comparing it to cells or tissue
CC   from a known source
XX
SQ   Sequence 19 BP; 17 A; 0 C; 0 G; 0 T; 0 U; 2 Other;

  Query Match              0.6%;  Score 17.2;  DB 1;  Length 19;
  Best Local Similarity   94.4%;  Pred. No. 1.2e+03;
  Matches   17;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||:
Db         19 TTTTTTTTTTTTTTTTV 2


RESULT 1966
AAX18390
ID   AAX18390 standard; DNA; 19 BP.
XX
AC   AAX18390;
XX
DT   11-MAY-1999  (first entry)
XX
```

```
DE   RT-PCR primer of the invention SEQ ID 31.
XX
KW   RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS   Synthetic.
XX
PN   JP11032765-A.
XX
PD   09-FEB-1999.
XX
PF   18-JUL-1997;   97JP-00208312.
XX
PR   18-JUL-1997;   97JP-00208312.
XX
PA   (TAKI ) TAKARA SHUZO CO LTD.
XX
DR   WPI; 1999-183822/16.
XX
PT   Peptides having at least two new nucleotides - useful as primers in RT-
PT   PCR.
XX
PS   Example 1; Page 12; 19pp; Japanese.
XX
CC   This sequence represents a primer of the invention. The invention relates
CC   to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC   -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC   a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC   natural number indicating the repetition of alpha; beta, delta = V or N;
CC   V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC   thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC   repetition of gamma, in which thymine expressed by gamma is composed of
CC   1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC   useful as primers for RT-PCR and determination of base sequences. The new
CC   sequences allow for reproductive and highly efficient analysis of gene
CC   sequences
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 2 Other;

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 19;
  Best Local Similarity   94.4%;  Pred. No. 1.2e+03;
  Matches   17;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||:
Db          1 TTTTTTTTTTTTTTTTV 18


RESULT 1967
AAX18390/c
ID   AAX18390 standard; DNA; 19 BP.
XX
AC   AAX18390;
XX
DT   11-MAY-1999  (first entry)
XX
DE   RT-PCR primer of the invention SEQ ID 31.
XX
KW   RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS   Synthetic.
XX
PN   JP11032765-A.
XX
PD   09-FEB-1999.
XX
PF   18-JUL-1997;   97JP-00208312.
XX
PR   18-JUL-1997;   97JP-00208312.
XX
PA   (TAKI ) TAKARA SHUZO CO LTD.
XX
DR   WPI; 1999-183822/16.
XX
PT   Peptides having at least two new nucleotides - useful as primers in RT-
PT   PCR.
XX
PS   Example 1; Page 12; 19pp; Japanese.
XX
CC   This sequence represents a primer of the invention. The invention relates
CC   to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC   -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC   a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC   natural number indicating the repetition of alpha; beta, delta = V or N;
CC   V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC   thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC   repetition of gamma, in which thymine expressed by gamma is composed of
CC   1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC   useful as primers for RT-PCR and determination of base sequences. The new
CC   sequences allow for reproductive and highly efficient analysis of gene
CC   sequences
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 2 Other;

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 19;
  Best Local Similarity   94.4%;  Pred. No. 1.2e+03;
  Matches   17;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2802
              :|||||||||||||||||
Db         18 BAAAAAAAAAAAAAAAA 1


RESULT 1968
ABV74140
ID   ABV74140 standard; DNA; 22 BP.
XX
AC   ABV74140;
XX
DT   23-JAN-2003  (first entry)
XX
DE   Oligonucleotide used in cDNA library array.
XX
KW   G-protein coupled receptor; odourant; receptor; olfaction; array;
KW   microarray; anosmia; attractant; arometic; pesticide; PCR; primer; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "5' polylinker"
XX
PN   WO200277200-A2.
XX
PD   03-OCT-2002.
XX
PF   26-MAR-2002; 2002WO-US009559.
XX
PR   27-MAR-2001; 2001US-0279168P.
PR   31-JAN-2002; 2002US-0353392P.
XX
PA   (INSC-) INSCENT INC.
XX
PI   Woods D,  Dimitratos S;
XX
DR   WPI; 2003-029930/02.
XX
PT   Identifying nucleic acid encoding novel sex-linked-tissue-linked
PT   receptors, useful for isolating odorant binding proteins or pesticide
PT   alternatives, by analyzing sequences from a male- and female-specific
PT   nucleic acid library.
XX
PS   Disclosure; Fig 5; 83pp; English.
XX
CC   The present sequence is that of an oligonucleotide used in a method
```

```
CC   designed to rapidly array and normalize a complex cDNA library obtained
CC   from a target species. Clones are arrayed into multi-well plates. Each
CC   well contains 16 oligonucleotides with a 5' polylinker, a poly-T run
CC   capable of binding cDNAs by their poly-A tail and a unique 3' sequence,
CC   which allows an anchored oligonucleotide in each well to selectively
CC   hybridise only to those cDNA clones with a complementary 5' end. The
CC   unique 3' key sequences are designed to give a comprehensive level of
CC   degeneracy since they are diverse and numerous enough to ensure that
CC   every possible cDNA sequence can be bound by an individual, specific
CC   oligonucleotide in a single well. The cDNA library is heated to denature
CC   the clones into single stranded DNA, and an aliquot is added to every
CC   well. The anchored oligonucleotide serves as the 3' primer in PCR, and
CC   the common 5' region present in every cDNA clone serves as the 5' priming
CC   site. Denaturing and washing leave anchored cDNA in each well. The
CC   library is now arrayed and normalised. The method was used to identify
CC   and isolate clones encoding G-protein coupled receptors, especially
CC   odourant receptors, and active effectors involved in the olfactory
CC   pathway of invertebrates and vertebrates, e.g. odourant binding proteins,
CC   or other olfactory or neuronal proteins. The identified receptors and
CC   proteins are useful for identifying compounds that reduce a target
CC   animal's sensitivity to odours, for manufacturing compounds or devices
CC   that mask odours, or trapping invertebrates with odourants.
CC   Semiochemicals (e.g. arometics or pheromone mimetics) can be developed
CC   with desirable effects on specific species, for the development of pest
CC   monitoring systems or non-toxic, species-specific pesticide alternatives,
CC   for controlling insect feeding and breeding behaviour, detecting the
CC   presence of small air-borne molecules, etc
XX
SQ   Sequence 22 BP; 2 A; 1 C; 3 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 22;
  Best Local Similarity   86.4%;  Pred. No. 1.6e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTAACTTTG 2193
                ||||||||||||||| || | |
Db          1 TTTTTTTTTTTTTTTGACATGG 22


RESULT 1969
AAT33703
ID   AAT33703 standard; DNA; 23 BP.
XX
AC   AAT33703;
XX
DT   19-MAY-1997  (first entry)
XX
DE   Primer #3 for tissue or cell derived RNA.
XX
KW   PCR; polymerase chain reaction; primer; amplify; reverse-transcription;
KW   molecular indexing; class IIS restriction enzyme; cancer; causative gene;
KW   viral infection; hereditary disease; agricultural gene; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1
FT                   /*tag= a
FT                   /note= "hydroxylated"
XX
PN   EP735144-A1.
XX
PD   02-OCT-1996.
XX
PF   26-MAR-1996;   96EP-00104817.
XX
PR   28-MAR-1995;   95JP-00069695.
PR   20-JUL-1995;   95JP-00184006.
PR   12-SEP-1995;   95JP-00234122.
XX
PA   (SHKJ ) RES DEV CORP JAPAN.
XX
PI   Kato K;
XX
DR   WPI; 1996-435619/44.
XX
PT   Molecular indexing of DNA - using restriction enzymes, PCR amplification
PT   and electrophoresis to analyse DNA fragments.
XX
PS   Claim 3; Page 14; 20pp; English.
XX
CC   AAT33701-T33703 represent amplification primers used in the reverse-
CC   transcription of tissue or cell derived mRNA, in the method of the
CC   invention. The method of the invention is a molecular indexing method,
CC   and comprises digesting the cDNA amplified by these sequences with a
CC   class IIS restriction enzyme. Each resultant cDNA fragment is then
CC   ligated to a biotinylated adaptor (selected from a pool of 64 adaptors
CC   cohesive to all possible overhangs), and digesting the products with two
CC   further class IIS restriction enzymes. These steps are repeated (but the
CC   enzyme used for the first step is different in each) to produce two
CC   further cDNA samples. The ligation samples are then recovered using
CC   streptavidin-coated paramagnetic beads, removing the strand complementary
CC   to an adaptor-primer. The adaptor primer and an anchored oligo-dT primer
CC   (such as this sequence) are then used to amplify the cDNA samples. The
CC   amplified products are separated, and the sizes of the fragments obtained
CC   is recorded. The method can be used for the analysis and diagnosis or
CC   diseases such as cancers or viral infections, for the search and
CC   isolation of the genes of physiologically active substances that are
CC   potential pharmaceuticals, or causative genes of hereditary diseases, as
CC   well as for the isolation of genes for improving agricultural products.
CC   Using this method, it is possible to classify (index) DNA into groups in
CC   a short period of time without duplication
XX
SQ   Sequence 23 BP; 1 A; 2 C; 3 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 23;
  Best Local Similarity   86.4%;  Pred. No. 1.8e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTTTTTT 2183
                |||   ||||||||||||||||
Db          1 CTCGAGTTTTTTTTTTTTTTT 22


RESULT 1970
AAV61556
ID   AAV61556 standard; DNA; 23 BP.
XX
AC   AAV61556;
XX
DT   08-DEC-1998  (first entry)
XX
DE   Double-anchored oligo-dT primer, used to synthesise apolipoprotein cDNA.
XX
KW   Primer; PCR; amplification; RT-PCR; quantitate; amount ratio; liver;
KW   kidney; apolipoprotein; ATAC-PCR; Adaptor-tagged Competitive PCR;
KW   gene expression; internal standard; calibration curve; ss.
XX
OS   Synthetic.
OS   Mus sp.
XX
PN   EP870842-A2.
XX
PD   14-OCT-1998.
XX
PF   07-APR-1998;   98EP-00302726.
XX
PR   07-APR-1997;   97JP-00088495.
XX
PA   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI   Kato K;
XX
DR   WPI; 1998-523164/45.
XX
PT   Determination of gene expression levels - using combinations of different
```

PT cDNA samples tagged with different PCR adaptors.
XX
PS Example 2; Page 9; 22pp; English.
XX
CC The present sequence represents a primer which was used to synthesise
CC Apolipoprotein cDNA in a RT-PCR reaction. This primer as well as primers
CC AAV61554 and AAV61555 were added to both mouse liver-derived and mouse
CC kidney-derived total RNA to generate single-stranded cDNA. These primers
CC were used in the method of the invention to determine the amount ratio
CC between a cDNA coding for mouse liver-derived Apolipoprotein and a cDNA
CC that codes for the mouse kidney-derived Apolipoprotein by using Adaptor-
CC tagged Competitive PCR (ATAC-PCR). This method allows gene expression to
CC be quantitatively determined, and because internal standards are not
CC required to prepare a calibration curve, it is a quicker and less
CC laborious process
XX
SQ Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.2; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2162 CTCCTTTTTTTTTTTTTTTTT 2183
||| |||||||||||||||
Db 1 CTCGAGTTTTTTTTTTTTTTT 22

RESULT 1971
AAA08409
ID AAA08409 standard; DNA; 23 BP.
XX
AC AAA08409;
XX
DT 13-JUL-2000 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO:3.
XX
KW Detection; primer; adapter; probe; hybridisation; gene cluster;
KW fractionation; ss.
XX
OS Synthetic.
XX
PN JP2000055914-A.
XX
PD 25-FEB-2000.
XX
PF 13-AUG-1998; 98JP-00228944.
XX
PR 13-AUG-1998; 98JP-00228944.
XX
PA (TAIS) TAISHO PHARM CO LTD.
XX
DR WPI; 2000-368733/32.
XX
PT Gene detection method involves hybridizing probe opposite to objective
PT gene out of fractional gene cluster.
XX
PS Example 1; Page 9; 11pp; Japanese.
XX
CC The present invention describes a gene detection method which comprises
CC fractionating using a probe opposite to the objective gene which is
CC hybridised out of fractioned gene cluster. The objective gene detected
CC belongs to the group of objective genes contained in the sample. The
CC method is used for gene detection by fractionation of cDNA by molecular
CC index method using specific primer. It provides high detection
CC sensitivity of objective gene. AAA08407 to AAA08414 represent
CC oligonucleotides used in the exemplification of the present invention
XX
SQ Sequence 23 BP; 1 A; 2 C; 3 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.2; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2162 CTCCTTTTTTTTTTTTTTTTT 2183
||| |||||||||||||||
Db 1 CTCGAGTTTTTTTTTTTTTTT 22

RESULT 1972
AAS04989/c
ID AAS04989 standard; DNA; 23 BP.
XX
AC AAS04989;
XX
DT 07-SEP-2001 (first entry)
XX
DE Neurofibromatosis (NF1) genomic DNA sequencing primer #41.
XX
KW Neurofibromatosis type 1; NF1; peripheral blood lymphocyte; PBL; EBV; ss;
KW Epstein-Barr virus; B-lymphoblastoid cell; phytohaemagglutinin; PHA;
KW frame shift mutation; mis-sense mutation; silent mutation; PCR primer;
KW sequencing primer.
XX
OS Homo sapiens.
XX
PN WO200129251-A2.
XX
PD 26-APR-2001.
XX
PF 18-OCT-2000; 2000WO-EP010255.
XX
PR 18-OCT-1999; 99EP-00870216.
PR 05-JUN-2000; 2000EP-00870122.
XX
PA (UYGE-) UNIV GENT.
XX
PI Messiaen L, Callens T;
XX
DR WPI; 2001-300341/31.
XX
PT Mutation analysis of NF1 gene by treating EBV transformed lymphoblastoid
PT cell lines formed with lymphocytes of patient with protein synthesis
PT inhibitor, and obtaining peptides by translating amplified RNA from cell
PT line.
XX
PS Claim 9; Page 60; 102pp; English.
XX
CC The sequences represent neurofibromatosis type 1 (NF1) cDNA fragments and
CC PCR primers and sequencing primers for use in mutation analysis of NF1. A
CC method for mutation analysis of the NF1 gene involves isolating
CC peripheral blood lymphocytes (PBL) of a patient, establishing Epstein-
CC Barr virus (EBV) transformed B-lymphoblastoid cell line with isolated
CC PBL, or short-term culturing of PBL by phytohaemagglutinin (PHA)
CC stimulation, treating the cell line or short-term culture with protein
CC synthesis inhibitor and immediately extracting RNA from the cultures. The
CC RNA is then amplified and peptide fragments are obtained by in vitro
CC transcription/translation of amplified fragments. Mutation analysis of
CC NF1 is used for detection of frame shift, mis-sense and silent mutations
CC in various exons of the gene. This is useful in screening for NF1
CC mutations in young children who are often oligosymptomatic. Efficacy of a
CC drug or agent can be identified by a screening process in which
CC modulation is monitored in vitro using cell systems in which the
CC defective NF1 gene is expressed. The sequences can be used to design
CC drugs which modulate NF1 activity, by using knowledge of the structure of
CC the NF1 protein and of specific defects of the various NF1 mutant
CC proteins. The method allows for reliable analysis of mutations that are
CC difficult to detect due to unstable or wrong-spliced transcripts
XX
SQ Sequence 23 BP; 7 A; 4 C; 3 G; 9 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.2; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2750 GATACGTGTATAATAAAAGTAT 2771

```
                    |||||||| ||| || |||||||
Db          23 GATACGTGCATATTACAAGTAT 2

RESULT 1973
ABV74138/c
ID   ABV74138 standard; DNA; 23 BP.
XX
AC   ABV74138;
XX
DT   23-JAN-2003  (first entry)
XX
DE   5' End of cDNA library clone.
XX
KW   G-protein coupled receptor; odourant; receptor; olfaction; array;
KW   microarray; anosmia; attractant; arometic; pesticide; mosquito; ss.
XX
OS   Aedes aegypti.
XX
PN   WO200277200-A2.
XX
PD   03-OCT-2002.
XX
PF   26-MAR-2002; 2002WO-US009559.
XX
PR   27-MAR-2001; 2001US-0279168P.
PR   31-JAN-2002; 2002US-0353392P.
XX
PA   (INSC-) INSCENT INC.
XX
PI   Woods D,  Dimitratos S;
XX
DR   WPI; 2003-029930/02.
XX
PT   Identifying nucleic acid encoding novel sex-linked-tissue-linked
PT   receptors, useful for isolating odorant binding proteins or pesticide
PT   alternatives, by analyzing sequences from a male- and female-specific
PT   nucleic acid library.
XX
PS   Disclosure; Fig 5; 83pp; English.
XX
CC   The present sequence is that of the 5' end of a cDNA clone isolated from
CC   a mosquito antenna cDNA library. The clone was isolated using a method
CC   designed to rapidly array and normalize a complex cDNA library obtained
CC   from a target species. Clones are arrayed into multi-well plates. Each
CC   well contains 16 oligonucleotides (see ABV74137) with a 5' polylinker, a
CC   poly-T run capable of binding cDNAs by their poly-A tail and a unique 3'
CC   sequence, which allows an anchored oligonucleotide in each well to
CC   selectively hybridise only to those cDNA clones with a complementary 5'
CC   end. The unique 3' key sequences are designed to give a comprehensive
CC   level of degeneracy since they are diverse and numerous enough to ensure
CC   that every possible cDNA sequence can be bound by an individual, specific
CC   oligonucleotide in a single well. The cDNA library is heated to denature
CC   the clones into single stranded DNA, and an aliquot is added to every
CC   well. The anchored oligonucleotide serves as the 3' primer in PCR, and
CC   the common 5' region present in every cDNA clone serves as the 5' priming
CC   site. Denaturing and washing leave anchored cDNA in each well. The
CC   library is now arrayed and normalised. The method was used to identify
CC   and isolate clones encoding G-protein coupled receptors, especially
CC   odourant receptors, and active effectors involved in the olfactory
CC   pathway of invertebrates and vertebrates, e.g. odourant binding proteins,
CC   or other olfactory or neuronal proteins. The identified receptors and
CC   proteins are useful for identifying compounds that reduce a target
CC   animal's sensitivity to odours, for manufacturing compounds or devices
CC   that mask odours, or trapping invertebrates with odourants.
CC   Semiochemicals (e.g. arometics or pheromone mimetics) can be developed
CC   with desirable effects on specific species, for the development of pest
CC   monitoring systems or non-toxic, species-specific pesticide alternatives,
CC   for controlling insect feeding and breeding behaviour, detecting the
CC   presence of small air-borne molecules, etc
XX
SQ   Sequence 23 BP; 16 A; 3 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match              0.6%;  Score 17.2;  DB 1;  Length 23;
  Best Local Similarity   86.4%;  Pred. No. 1.8e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTAACTTTG 2193
              |||||||||||||||| || | |
Db         23 TTTTTTTTTTTTTTTGACATGG 2


RESULT 1974
ABV74139
ID   ABV74139 standard; DNA; 23 BP.
XX
AC   ABV74139;
XX
DT   23-JAN-2003  (first entry)
XX
DE   Oligonucleotide used in cDNA library array.
XX
KW   G-protein coupled receptor; odourant; receptor; olfaction; array;
KW   microarray; anosmia; attractant; arometic; pesticide; PCR; primer; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "5' polylinker"
XX
PN   WO200277200-A2.
XX
PD   03-OCT-2002.
XX
PF   26-MAR-2002; 2002WO-US009559.
XX
PR   27-MAR-2001; 2001US-0279168P.
PR   31-JAN-2002; 2002US-0353392P.
XX
PA   (INSC-) INSCENT INC.
XX
PI   Woods D,  Dimitratos S;
XX
DR   WPI; 2003-029930/02.
XX
PT   Identifying nucleic acid encoding novel sex-linked-tissue-linked
PT   receptors, useful for isolating odorant binding proteins or pesticide
PT   alternatives, by analyzing sequences from a male- and female-specific
PT   nucleic acid library.
XX
PS   Disclosure; Fig 5; 83pp; English.
XX
CC   The present sequence is that of an oligonucleotide used in a method
CC   designed to rapidly array and normalize a complex cDNA library obtained
CC   from a target species. Clones are arrayed into multi-well plates. Each
CC   well contains 16 oligonucleotides with a 5' polylinker, a poly-T run
CC   capable of binding cDNAs by their poly-A tail and a unique 3' sequence,
CC   which allows an anchored oligonucleotide in each well to selectively
CC   hybridise only to those cDNA clones with a complementary 5' end. The
CC   unique 3' key sequences are designed to give a comprehensive level of
CC   degeneracy since they are diverse and numerous enough to ensure that
CC   every possible cDNA sequence can be bound by an individual, specific
CC   oligonucleotide in a single well. The cDNA library is heated to denature
CC   the clones into single stranded DNA, and an aliquot is added to every
CC   well. The anchored oligonucleotide serves as the 3' primer in PCR, and
CC   the common 5' region present in every cDNA clone serves as the 5' priming
CC   site. Denaturing and washing leave anchored cDNA in each well. The
CC   library is now arrayed and normalised. The method was used to identify
CC   and isolate clones encoding G-protein coupled receptors, especially
CC   odourant receptors, and active effectors involved in the olfactory
CC   pathway of invertebrates and vertebrates, e.g. odourant binding proteins,
CC   or other olfactory or neuronal proteins. The identified receptors and
CC   proteins are useful for identifying compounds that reduce a target
```

```
CC   animal's sensitivity to odours, for manufacturing compounds or devices
CC   that mask odours, or trapping invertebrates with odourants.
CC   Semiochemicals (e.g. arometics or pheromone mimetics) can be developed
CC   with desirable effects on specific species, for the development of pest
CC   monitoring systems or non-toxic, species-specific pesticide alternatives,
CC   for controlling insect feeding and breeding behaviour, detecting the
CC   presence of small air-borne molecules, etc
XX
SQ   Sequence 23 BP; 2 A; 2 C; 3 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 23;
  Best Local Similarity   86.4%;  Pred. No. 1.8e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTAACTTTG 2193
              ||||||||||||||| || | |
Db          1 TTTTTTTTTTTTTTTGACATGG 22


RESULT 1975
AAH75510/c
ID   AAH75510 standard; DNA; 24 BP.
XX
AC   AAH75510;
XX
DT   18-OCT-2001  (first entry)
XX
DE   Human CCR4 related protein 31 PCR primer 2.
XX
KW   Human; CCR4; cancer; HIV; Human immunodeficiency virus; infection;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1296960-A.
XX
PD   30-MAY-2001.
XX
PF   22-NOV-1999;   99CN-00124049.
XX
PR   22-NOV-1999;   99CN-00124049.
XX
PA   (SHAN-) SHANGHAI BORONG GENE DEV CO LTD.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2001-489558/54.
XX
PT   Polypeptide-human CCR4 related protein 31 and polynucleotide for coding
PT   polypeptide, useful for treating e.g. cancer and HIV infection, is
PT   prepared by DNA recombination.
XX
PS   Example 3; Page 17 (Disclosure); 34pp; Chinese.
XX
CC   The invention relates to human CCR4 related protein 31, the
CC   polynucleotide encoding it and the use of the protein in treating e.g.
CC   cancer and HIV infection. The present sequence is that of a human CCR4
CC   PCR primer of the invention
XX
SQ   Sequence 24 BP; 3 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 24;
  Best Local Similarity   86.4%;  Pred. No. 2e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAAAA 2804
              || | ||||| ||||||||||||
Db         23 TTAATAAAAAGAAAAAAAAAAA 2


RESULT 1976
AAV82670
ID   AAV82670 standard; DNA; 24 BP.
XX
AC   AAV82670;
XX
DT   16-FEB-1999  (first entry)
XX
DE   Primer used to identify cDNA encoding ST38.2.
XX
KW   Rat; chemokine; ST38.2; chemotaxis; leucocyte-activating; inflammation;
KW   immune response; brain injury; trauma; ischaemia;
KW   autoimmune inflammation; multiple sclerosis; stroke;
KW   rheumatoid arthritis; meningitis; encephalitis; PCR primer; ss.
XX
OS   Synthetic.
OS   Rattus sp.
XX
PN   WO9849309-A1.
XX
PD   05-NOV-1998.
XX
PF   23-APR-1998;   98WO-EP002405.
XX
PR   30-APR-1997;   97EP-00107135.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Lesslauer W,  Utansschneitz U;
XX
DR   WPI; 1999-009430/01.
XX
PT   New chemokine ST38.2 with chemotactic and leucocyte-activating properties
PT   - used to treat inflammation and immune responses and to identify
PT   specific modulators.
XX
PS   Example 3; Page 28; 64pp; English.
XX
CC   PCR primers AAV82670-71 were used to amplify cDNA encoding a novel rat
CC   chemokine designated ST38.2. In addition, primer AAV82670 was used to
CC   reverse transcribe rat RNA. The protein has chemotactic and leucocyte-
CC   activating properties. ST38.2 is involved in inflammation and immune
CC   responses, particularly inflammatory response to brain injury (trauma,
CC   ischaemia or autoimmune inflammation) but also in multiple sclerosis,
CC   stroke, rheumatoid arthritis and infections (particularly meningitis and
CC   encephalitis)
XX
SQ   Sequence 24 BP; 2 A; 2 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 24;
  Best Local Similarity   86.4%;  Pred. No. 2e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTTTT 2182
              |||   |||||||||||||||||
Db          3 TCTAGATTTTTTTTTTTTTTT 24


RESULT 1977
AAI69702/c
ID   AAI69702 standard; DNA; 24 BP.
XX
AC   AAI69702;
XX
DT   12-DEC-2001  (first entry)
XX
DE   Human neuropeptide 11 PCR primer #2.
XX
KW   Human; neuropeptide 11; cytostatic; virucidal; immunomodulatory;
KW   antiinflammatory; haemostatic; anti-HIV; gene therapy; malignant tumour;
KW   haemopathy; HIV infection; immunological disease; inflammation;
KW   vegetative nervous function disturbance; vascular function disturbance;
KW   endocrinosis; developmental disturbance; PCR primer; ss.
XX
OS   Homo sapiens.
XX
```

```
PN   WO200172807-A1.
XX
PD   04-OCT-2001.
XX
PF   26-MAR-2001; 2001WO-CN000466.
XX
PR   28-MAR-2000; 2000CN-00115223.
XX
PA   (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2001-602848/68.
XX
PT   New human neuropeptide 11 for diagnosing and treating endocrinosis,
PT   malignant tumor, hemopathy, human immunodeficiency virus infection,
PT   immunological diseases and various inflammations.
XX
PS   Example 2; Page 17; 35pp; Chinese.
XX
CC   The present invention relates to human neuropeptide 11 (see AAI65200 and
CC   AAG78860). The neuropeptide and its coding sequence are useful in the
CC   diagnosis and treatment of malignant tumours, haemopathy, HIV infection,
CC   immunological diseases, various inflammations, vegetative nervous
CC   function disturbance, vascular function disturbance, endocrinosis and
CC   developmental disturbance. The present sequence is a PCR primer which was
CC   used in an example from the present invention
XX
SQ   Sequence 24 BP; 4 A; 7 C; 2 G; 11 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 24;
  Best Local Similarity   86.4%;  Pred. No. 2e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1504 GAAACACAGGAAATAAAATTGG 1525
              ||||||||| ||| ||| ||||
Db         23 GAAACACAGTAAAGAAAGTTGG 2

RESULT 1978
ABV77761/c
ID   ABV77761 standard; DNA; 24 BP.
XX
AC   ABV77761;
XX
DT   03-FEB-2003  (first entry)
XX
DE   Human DNA-PK interaction protein 9.9 PCR primer #2.
XX
KW   Human; DNA-PK interaction protein 9.9; cancer; HIV infection; cytostatic;
KW   anti-HIV; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1351066-A.
XX
PD   29-MAY-2002.
XX
PF   26-OCT-2000; 2000CN-00125835.
XX
PR   26-OCT-2000; 2000CN-00125835.
XX
PA   (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-609430/66.
XX
PT   New polypeptide-human DNA-PK interaction protein 9.9 for treating
PT   diseases, such as, cancer, and human immunodeficiency virus infection.
XX
PS   Example 2; Page 16 (Disclosure); 31pp; Chinese.
XX
CC   The present invention relates to human DNA-PK interaction protein 9.9.
CC   The protein can be used for treating diseases such as cancer and HIV
CC   infection. The present sequence is a PCR primer, which was used in an
CC   example from the invention
XX
SQ   Sequence 24 BP; 4 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 24;
  Best Local Similarity   86.4%;  Pred. No. 2e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAA 2801
              || || |||||||||||||| |
Db         22 GATTTCAAAAAAAAAAAAAACA 1

RESULT 1979
ABQ78896
ID   ABQ78896 standard; DNA; 24 BP.
XX
AC   ABQ78896;
XX
DT   17-OCT-2002  (first entry)
XX
DE   Human zinc finger protein 27.50 PCR primer 2.
XX
KW   Human; zinc finger protein 27.50; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1341649-A.
XX
PD   27-MAR-2002.
XX
PF   07-SEP-2000; 2000CN-00125059.
XX
PR   07-SEP-2000; 2000CN-00125059.
XX
PA   (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-520724/56.
XX
PT   Novel human zinc finger protein 27.50.
XX
PS   Example 3; Page 17 (Disclosure); 31pp; Chinese.
XX
CC   The invention relates to a novel human zinc finger protein 27.50, and the
CC   polynucleotide encoding it. The polypeptide is useful for treating
CC   several diseases, such as solid tumour, nervous system disease, malignant
CC   disease of blood, development disturbance and HIV infection. The sequence
CC   represents a PCR primer used in example 3 of the invention
XX
SQ   Sequence 24 BP; 5 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 24;
  Best Local Similarity   86.4%;  Pred. No. 2e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTA 2187
              |||| |||| |||| |||||||
Db          3 TTTTATTTTATTTTATTTTTA 24

RESULT 1980
AAC96060/c
ID   AAC96060 standard; DNA; 25 BP.
XX
AC   AAC96060;
XX
DT   26-FEB-2001  (first entry)
XX
```

```
DE   16s rRNA gene PCR primer #27.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 44; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 3 A; 3 C; 3 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 25;
  Best Local Similarity   86.4%;  Pred. No. 2.1e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAA 2800
                ||  || ||||||||||||||||
Db         22 AGCGTTTAAAAAAAAAAAAAAA 1


RESULT 1981
AAC96204
ID   AAC96204 standard; DNA; 25 BP.
XX
AC   AAC96204;
XX
DT   26-FEB-2001  (first entry)
XX
DE   16s rRNA gene PCR primer #171.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 47; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 1 A; 5 C; 3 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 25;
  Best Local Similarity   86.4%;  Pred. No. 2.1e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTAACTTTG 2193
                ||||||||||||||| | | |||
Db          1 TTTTTTTTTTTTTTCACCCTTG 22


RESULT 1982
AAC96129
ID   AAC96129 standard; DNA; 25 BP.
XX
AC   AAC96129;
XX
DT   26-FEB-2001  (first entry)
XX
DE   16s rRNA gene PCR primer #96.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 46; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
```

```
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 2 A; 5 C; 2 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 25;
  Best Local Similarity   86.4%;  Pred. No. 2.1e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTAACTTTG 2193
              ||||||||||||||  ||||| |
Db          1 TTTTTTTTTTTTTCCAACTTCG 22


RESULT 1983
AAC95960/c
ID   AAC95960 standard; DNA; 25 BP.
XX
AC   AAC95960;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA HLA-B gene PCR primer #71.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 43; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 3 A; 7 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 25;
  Best Local Similarity   86.4%;  Pred. No. 2.1e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAA 2801
              | ||||  ||||||||||||||
Db         22 GGATTGGGAAAAAAAAAAAAAA 1


RESULT 1984
AAC96115/c
ID   AAC96115 standard; DNA; 25 BP.
XX
AC   AAC96115;
XX
DT   26-FEB-2001  (first entry)
XX
DE   16s rRNA gene PCR primer #82.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 45; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 2 A; 4 C; 3 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 25;
  Best Local Similarity   86.4%;  Pred. No. 2.1e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2777 TTAGAATTGAAAAAAAAAAAAA 2798
              | || | ||||||||||||||||
Db         22 TGAGGACTGAAAAAAAAAAAAA 1


RESULT 1985
AAC96175
ID   AAC96175 standard; DNA; 25 BP.
XX
AC   AAC96175;
XX
DT   26-FEB-2001  (first entry)
XX
DE   16s rRNA gene PCR primer #142.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
```

```
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 46; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 2 A; 5 C; 3 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 25;
  Best Local Similarity   86.4%;  Pred. No. 2.1e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTAACTTTG 2193
              |||||||||||||  ||| |||
Db          1 TTTTTTTTTTTTTCCAACCTTG 22


RESULT 1986
ACI84885/c
ID   ACI84885 standard; DNA; 25 BP.
XX
AC   ACI84885;
XX
DT   14-OCT-2003  (first entry)
XX
DE   Human microarray DNA oligonucleotide SEQ ID NO 84876.
XX
KW   EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW   genetic variation; biallelic marker; polymorphism; human;
KW   cross-species comparison.
XX
OS   Homo sapiens.
XX
PN   US2003104410-A1.
XX
PD   05-JUN-2003.
XX
PF   15-MAR-2002; 2002US-00098263.
XX
PR   16-MAR-2001; 2001US-0276759P.
XX
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Mittmann MP;
XX
DR   WPI; 2003-567953/53.
XX
PT   New array of nucleic acid probes, useful for in situ hybridization, in
PT   Southern, Northern or dot-blot hybridization to identify or detect the
PT   sequence or specific mutations of any gene.
XX
PS   Claim 1; SEQ ID NO 84876; 9pp; English.
XX
CC   The invention discloses a microarray comprising a plurality of nucleic
CC   acid probes including one of 2,018,500 fully defined sequences, or its
CC   perfect match, perfect mismatch, antisense match or antisense mismatch.
CC   Also disclosed is a method of gene expression analysis. The array is used
CC   in monitoring gene expression levels by hybridisation to a DNA library,
CC   in analysis of genetic variation or in hybridisation of tag-labelled
CC   compounds. The nucleic acid probes are specifically designed for analysis
CC   of at least one target sequence. The method of analysis comprises
CC   hybridising at least one or more nucleic acids to at least two or more
CC   nucleic acid probes and detecting the hybridisation. The nucleic acid
CC   probes are attached to a solid support. The analysis comprises monitoring
CC   gene expression levels, identifying biallelic markers or polymorphisms,
CC   or family members of a gene and a cross-species comparison. Each of the
CC   nucleic acids further comprises a tag sequence. The array of nucleic acid
CC   probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC   blot hybridisation to identify or detect the sequence or specific
CC   mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC   primer extensions or in screening cDNA or genomic libraries or subclones
CC   for additional subclones containing segments of DNA that have been
CC   isolated and previously sequenced. The sequence presented is one of the
CC   nucleic acid probes incorporated in the microarray. Note: The sequence
CC   data for this patent can also be obtained in electronic format directly
CC   from USPTO at seqdata.uspto.goc/sequence.html
XX
SQ   Sequence 25 BP; 8 A; 7 C; 1 G; 9 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 25;
  Best Local Similarity   86.4%;  Pred. No. 2.1e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2348 GGAGGTTCTGTATTTTAAGAAA 2369
              ||||||||  ||| ||||||||
Db         25 GGAGGTTCGATATGTTAAGAAA 4


RESULT 1987
ACI81786/c
ID   ACI81786 standard; DNA; 25 BP.
XX
AC   ACI81786;
XX
DT   14-OCT-2003  (first entry)
XX
DE   Human microarray DNA oligonucleotide SEQ ID NO 81777.
XX
KW   EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW   genetic variation; biallelic marker; polymorphism; human;
KW   cross-species comparison.
XX
OS   Homo sapiens.
XX
PN   US2003104410-A1.
XX
PD   05-JUN-2003.
XX
PF   15-MAR-2002; 2002US-00098263.
XX
PR   16-MAR-2001; 2001US-0276759P.
XX
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Mittmann MP;
XX
DR   WPI; 2003-567953/53.
XX
PT   New array of nucleic acid probes, useful for in situ hybridization, in
PT   Southern, Northern or dot-blot hybridization to identify or detect the
PT   sequence or specific mutations of any gene.
XX
PS   Claim 1; SEQ ID NO 81777; 9pp; English.
XX
CC   The invention discloses a microarray comprising a plurality of nucleic
CC   acid probes including one of 2,018,500 fully defined sequences, or its
CC   perfect match, perfect mismatch, antisense match or antisense mismatch.
```

CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.goc/sequence.html
XX
SQ Sequence 25 BP; 8 A; 4 C; 4 G; 9 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.2; DB 1; Length 25;
Best Local Similarity 86.4%; Pred. No. 2.1e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2277 ATGTTTCGAGTAAACTTGAAAA 2298
||||||||| ||||| | |||
Db 25 ATGTTTCGAGAAAACTCGTAAA 4

RESULT 1988
AAT61049/c
ID AAT61049 standard; DNA; 26 BP.
XX
AC AAT61049;
XX
DT 06-OCT-1997 (first entry)
XX
DE Primer Mt-2.
XX
KW primer; PCR; polymerase chain reaction; origin; test; cytochrombe b;
KW food control; processed meat; ss.
XX
OS Synthetic.
XX
PN DE19629166-A1.
XX
PD 27-FEB-1997.
XX
PF 19-JUL-1996; 96DE-01029166.
XX
PR 22-AUG-1995; 95DE-01031377.
PR 07-NOV-1995; 95DE-01041368.
XX
PA (ZTBT-) ZTB ZENT TECHNOLOGIETRANSFER BIOMEDIZIN.
XX
PI Puehler A, Arnold W, Kriete G, Weidner S;
XX
DR WPI; 1997-146900/14.
XX
PT Amplification primer for animal cytochrome b gene - and determining
PT origin of biological material, esp. of meat prods. used in foods.
XX
PS Claim 7; Col 5; 6pp; German.
XX
CC This oligonucleotide is primer Mt-2. It is used in a claimed method, with
CC primer Mt-11 (AAT61048) to determine the origin of a biological material.
CC The primers amplify the cytochrombe b gene. The method is especially
CC applied to material derived from chicken, poultry, pigs, cattle, sheep,
CC game, fish and seafoods, particularly for control of foods. The origin of
CC the material can be determined reliably and relatively quickly, in an
CC automated procedure capable of examining 100 samples per day. It uses
CC standard methods of genetic engineering, is highly sensitive and
CC universally applicable. Since the primers generate a relatively small
CC amplicon, the method can be used on processed meats where the DNA is
CC likely to be highly fragmented
XX
SQ Sequence 26 BP; 9 A; 9 C; 1 G; 7 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.2; DB 1; Length 26;
Best Local Similarity 86.4%; Pred. No. 2.3e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2678 GTGTGGGTGAAATGGAGATTTG 2699
|| |||||| |||||| |||||
Db 24 GTATGGGTGGAATGGAAATTTG 3

RESULT 1989
AAV07974
ID AAV07974 standard; DNA; 26 BP.
XX
AC AAV07974;
XX
DT 25-MAR-2003 (revised)
DT 02-FEB-1999 (first entry)
XX
DE Helicobacter pylori polypeptide GHPO 711 5' DNA primer.
XX
KW GHPO 711; infection; gastritis; ulcer; vaccine; diagnosis; therapy; PCR;
KW primer; ss.
XX
OS Synthetic.
OS Helicobacter pylori.
XX
PN WO9843479-A1.
XX
PD 08-OCT-1998.
XX
PF 31-MAR-1998; 98WO-US006421.
XX
PR 01-APR-1997; 97US-00831310.
PR 01-APR-1997; 97US-00834666.
XX
PA (INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Kleanthous H, Lissolo L, Tomb J, Miller C, Algarawi A;
XX
DR WPI; 1998-568251/48.
XX
PT New isolated Helicobacter polynucleotides - used to develop products for
PT the diagnosis, prevention and treatment of Helicobacter infections and
PT gastroduodenal diseases.
XX
PS Example 3.B; Page 64; 184pp; English.
XX
CC This 5' primer was used with a 3' primer (see AAV07975) in the PCR
CC amplification of Helicobacter pylori strain ORV2001 genomic DNA in order
CC to obtain DNA (see AAV07917) encoding a 76 kDa polypeptide (see AAW73028)
CC designated GHPO 711. The primer pair includes a 5' clamp and BamHI and
CC XhoI restriction enzyme reocgnition sequences for cloning purposes. The
CC PCR product was ligated into vector pET28a, and recombinant polypeptide
CC was expressed as a histidine-tagged fusion protein in E. coli host cells.
CC The polypeptide can be used to develop vaccines for the treatment and
CC prevention of Helicobacter infections. (Updated on 25-MAR-2003 to correct
CC PI field.)
XX
SQ Sequence 26 BP; 16 A; 3 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.2; DB 1; Length 26;
Best Local Similarity 86.4%; Pred. No. 2.3e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       2780 GAATTGAAAAAAAAAAAAAAAA 2801
              ||||| |||||||  |||||||
Db          3 GAATTCAAAAAAACGAAAAAAA 24
```

RESULT 1990
AAC92118/c
ID AAC92118 standard; DNA; 26 BP.
XX
AC AAC92118;
XX
DT 19-MAR-2001 (first entry)
XX
DE Human MLT gene intron-exon boundary #2.
XX
KW Human; API2-MLT chimera; chimeric; apoptosis inhibitor 2; MLT; API2;
KW mucosa-associated lymphoid tissue lymphoma associated translocation;
KW chromosome 11 region q21-22.3; chromosome 18 region q21.1-22;
KW molecular characterisation; chromosome translocation; carcinogenesis;
KW fusion protein; malignancy; ss.
XX
OS Homo sapiens.
XX
PN WO200073500-A1.
XX
PD 07-DEC-2000.
XX
PF 26-MAY-2000; 2000WO-EP004796.
XX
PR 27-MAY-1999; 99EP-00201683.
XX
PA (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
XX
PI Baens M, Marynen P, Dierlamm J;
XX
DR WPI; 2001-061556/07.
XX
PT Determining if a tissue sample has a chromosome (11:18) translocation
PT associated with malignancies by amplifying a nucleic acid sample using
PT primers complementary to chromosome 11 region q21-22.3 and chromosome 18
PT region q21.1-22.
XX
PS Example 3; Page 22; 47pp; English.
XX
CC The present invention describes a method for determining if a tissue
CC sample comprises a cell with a chromosome (11:18) translocation
CC associated with malignancies such as mucosa-associated lymphoid tissue
CC (MALT) lymphomas. The method comprises subjecting a sample nucleic acid
CC to amplification using primers complementary to sequences which are on
CC chromosome 11 region q21-22.3 and on chromosome 18 region q21.1-22. The
CC method can be used for determining if a tissue sample or analogue
CC comprises a chromosome (11:18) translocation associated with malignancies
CC such as mucosa-associated lymphoid tissue lymphomas. The nucleic acid or
CC the antibody may be used as a probe for detection, for hybridisation to
CC southern blot cell DNAs or for in situ hybridisation of cells, or for
CC determining the presence of complementary DNA. The present sequence
CC represents an intron-exon boundary oligonucleotide from the human MALT-
CC lymphoma associated translocation (MLT) gene, which is used in an example
CC from the present invention
XX
SQ Sequence 26 BP; 6 A; 0 C; 3 G; 17 T; 0 U; 0 Other;

```
  Query Match              0.6%;  Score 17.2;  DB 1;  Length 26;
  Best Local Similarity   86.4%;  Pred. No. 2.3e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAAAA 2803
              |||   |||||||||||||||
Db         22 ATTCCTAAAAAAAAAAAAAAAA 1
```

RESULT 1991
AAT13977/c
ID AAT13977 standard; DNA; 28 BP.
XX
AC AAT13977;
XX
DT 03-OCT-1996 (first entry)
XX
DE E. spinifera fumonisin esterase end-blocked polyT primer BamT17V.
XX
KW Fumonisin; esterase; transgenic plant; recombinant microorganism;
KW expression; probiotic; feed inoculant; degradation; detoxification;
KW maize seed; grain; animal feed; end blocked; polyT primer; nested;
KW polymerase chain reaction; Exophiala spinifera; ss.
XX
OS Synthetic.
XX
PN WO9606175-A2.
XX
PD 29-FEB-1996.
XX
PF 11-AUG-1995; 95WO-US010284.
XX
PR 12-AUG-1994; 94US-00289595.
PR 07-JUN-1995; 95US-00484815.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Duvick J, Rood TA;
XX
DR WPI; 1996-151378/15.
XX
PT Detoxification of fumonisin and related mycotoxin cpds. in grains - using
PT an enzyme esp. an esterase, from Exophiala spinifera, Rhinocladiella
PT atrovirens or a bacterium.
XX
PS Example 8; Page 33; 54pp; English.
XX
CC The present sequence is a primer for the nested PCR amplification of the
CC Exophiala spinifera (ATCC 74269), fumonisin esterase, cDNA, which was
CC isolated from a maize seed. The esterase cDNA can be used to produce
CC transgenic plants and genetically engineered microorganisms, capable of
CC expressing the esterase. The microorganisms can be used as a probiotic or
CC feed inoculant, along with the esterase to degrade fumonisins and related
CC cpds., partic. for the detoxification of maize seed pre- or post-harvest
CC (i.e. during the storage or processing of the harvested grain, or in the
CC processed grain) prior to its use as an animal feed
XX
SQ Sequence 28 BP; 1 A; 4 C; 4 G; 18 T; 0 U; 1 Other;

```
  Query Match              0.6%;  Score 17.2;  DB 1;  Length 28;
  Best Local Similarity   94.4%;  Pred. No. 2.6e+03;
  Matches   17;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              :|||||||||||||||||
Db         28 BAAAAAAAAAAAAAAAAA 11
```

RESULT 1992
AAV65735/c
ID AAV65735 standard; DNA; 28 BP.
XX
AC AAV65735;
XX
DT 17-DEC-1998 (first entry)
XX
DE A. phoenices APOXD DNA amplifying 5' RACE primer Bam T17V.
XX
KW APOXD; oxalate decarboxylase; oxalic acid; degradation; plant pathogen;
KW oxalic acid toxicity; oxalate; plant tissue; diagnosis; treatment;
KW enzyme; urinary tract disorder; hyperoxaluric syndrome; PCR primer; ss.
XX
OS Synthetic.
OS Aspergillus phoenicis.

```
XX
PN   WO9842827-A2.
XX
PD   01-OCT-1998.
XX
PF   19-MAR-1998;   98WO-US005432.
XX
PR   21-MAR-1997;   97US-00821827.
XX
PA   (PION-) PIONEER HI-BRED INT INC.
XX
PI   Scelonge CJ,  Bidney DL;
XX
DR   WPI; 1998-557032/47.
XX
PT   New isolated oxalate decarboxyalse gene - obtained from Aspergillus
PT   phoenices, used for e.g. degrading oxalic acid, protecting against oxalic
PT   toxicity or as a selectable marker in plants.
XX
PS   Example 1; Page 24; 58pp; English.
XX
CC   Sequences AAV65729 to AAV65740 represent primers used for the PCR
CC   amplification of the genomic DNA encoding an Aspergillus phoenices
CC   oxalate decarboxylase (APOXD) enzyme. A vector containing the APOXD
CC   nucleic acid can be used to transform host cells for the recombinant
CC   production of the enzyme. The APOXD can be used for the degradation of
CC   oxalic acid in providing protection against oxalic acid toxicity. It is
CC   useful in combating and providing protection against plant pathogens that
CC   utilise oxalate to gain access to plant tissue or otherwise in the course
CC   of the pathogenesis of the disease. The APOXD gene is also useful as a
CC   selectable marker of transformed cells, for diagnostic assay of oxalate,
CC   and for production of the enzyme in plants. The product can also be used
CC   in diagnostic assays to quantify oxalate, e.g. in the diagnosis and
CC   treatment of patients with urinary tract disorders or hyperoxaluric
CC   syndromes
XX
SQ   Sequence 28 BP; 1 A; 4 C; 4 G; 18 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 28;
  Best Local Similarity   94.4%;  Pred. No. 2.6e+03;
  Matches   17;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2802
              :|||||||||||||||||
Db         28 BAAAAAAAAAAAAAAAA 11


RESULT 1993
AAX05727/c
ID   AAX05727 standard; DNA; 28 BP.
XX
AC   AAX05727;
XX
DT   07-MAY-1999  (first entry)
XX
DE   E. spinifera fumonisin esterase (ESP26-1) cDNA amplifying polyT primer.
XX
KW   Fumonisin esterase; enzyme; fumonisin; degrade; harvesting; grain; ss;
KW   animal feed; plant tissue; silage; fruit; vegetable; detoxification;
KW   mycotoxin; phytohormone; tricarballylic acid; TCA; bacterium; PCR primer.
XX
OS   Synthetic.
OS   Exophiala spinifera.
XX
PN   WO9902703-A1.
XX
PD   21-JAN-1999.
XX
PF   07-JUL-1998;   98WO-US013987.
XX
PR   07-JUL-1997;   97US-00888949.
PR   07-JUL-1997;   97US-00888950.
XX
PA   (PION-) PIONEER HI-BRED INT INC.
XX
PI   Duvick J,  Maddox JR,  Rood TA,  Wang X,  Bowen BA,  Gilliam JT;
XX
DR   WPI; 1999-120904/10.
XX
PT   Newly isolated polynucleotides useful for degrading and detoxifying
PT   fumonisins - and methods for identifying transformed plant cells.
XX
PS   Example 8; Page 37; 88pp; English.
XX
CC   The invention relates to fumonisin esterases from E. spinifera and Gram-
CC   negative bacteria. This enzyme can degrade fumonisin. The polynucleotides
CC   encoding fumonisin degrading enzymes are useful for degrading fumonisins
CC   during the process of harvesting grain for animal feed, or in plant
CC   tissues, which are used for silage or as a spray on grain, fruit or
CC   vegetables. They are also useful for detoxifying fumonisins, structurally
CC   related mycotoxins, and fumonisin hydrolysis products of both. The
CC   fumonisin esterase genes (contained within an expression cassette,
CC   encoding a fumonisin degradative enzyme) is introduced into plant cells
CC   that are cultured on a medium containing a phytohormone linked to a
CC   tricarballylic acid (TCA), which inactivates the phytohormone unless it
CC   is cleaved by an esterase. The polynucleotides are also used in a method
CC   for measuring gene expression, comprising transforming cells with the
CC   esterase genes operably linked to a promoter, adding substrate, and
CC   measuring the level of hydrolysed product. The isolation of the
CC   polynucleotides encoding the fumonisin degrading enzymes permits the
CC   degradation and detoxification of fumonisins, which are toxic and
CC   potentially widespread in food and feed. The present sequence represents
CC   a E. spinifera fumonisin esterase gene specific primer used for the
CC   isolation of a full-length cDNA of ESP26-1
XX
SQ   Sequence 28 BP; 1 A; 4 C; 4 G; 18 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 28;
  Best Local Similarity   94.4%;  Pred. No. 2.6e+03;
  Matches   17;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2802
              :|||||||||||||||||
Db         28 BAAAAAAAAAAAAAAAA 11


RESULT 1994
ABZ70568/c
ID   ABZ70568 standard; DNA; 28 BP.
XX
AC   ABZ70568;
XX
DT   23-MAY-2003  (first entry)
XX
DE   5' RACE primer Bam T17V.
XX
KW   Oxalate decarboxylase; APOXD; enzyme; selectable marker;
KW   transgenic plant; crop protection; oxalic acid; degradation;
KW   Aspergillus phoenices; PCR; RACE; primer; ss.
XX
OS   Synthetic.
XX
PN   CA2350328-A1.
XX
PD   26-DEC-2002.
XX
PF   26-JUN-2001; 2001CA-02350328.
XX
PR   26-JUN-2001; 2001CA-02350328.
XX
PA   (PION-) PIONEER HI-BRED INT INC.
XX
PI   Scelonge C,  Bidney D;
XX
DR   WPI; 2003-248733/25.
XX
```

```
PT   New isolated nucleic acid encoding oxalate decarboxylase from Aspergillus
PT   phoenices, for degrading oxalic acid, identifying transformed plant
PT   cells, and preventing pathogenic disease in plants.
XX
PS   Example 1; Page 28; 60pp; English.
XX
CC   The present sequence is that of a dT-based primer, which was used in a 5'
CC   RACE to obtained a fragment of the Aspergillus phoenices oxalate-
CC   decarboxylase (APOXD) gene. Following 3' and 5' RACE, a full-length
CC   nucleic acid (see ABZ70560) encoding APOXD enzyme (see ABP72475) was
CC   obtained. The APOXD gene and its encoded protein are useful for degrading
CC   oxalate, protecting plants from pathogenic disease, in diagnostic assays
CC   of oxalate, and as a selectable marker
XX
SQ   Sequence 28 BP; 1 A; 4 C; 4 G; 18 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 28;
  Best Local Similarity   94.4%;  Pred. No. 2.6e+03;
  Matches   17;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              :||||||||||||||||||
Db         28 BAAAAAAAAAAAAAAAAA 11


RESULT 1995
AAQ52157/c
ID   AAQ52157 standard; RNA; 35 BP.
XX
AC   AAQ52157;
XX
DT   25-MAR-2003  (revised)
DT   26-MAY-1994  (first entry)
XX
DE   Breast cancer specific mRNA ribozyme cleavable nucleotide (4416).
XX
KW   Multiple drug resistance; mdr-1; ribozyme; membrane protein; liver;
KW   resistance; chemotherapeutic agent; colchicine; doxorubicin; colon;
KW   actinomycin D; vinblastine; small intestine; kidney; adrenal gland;
KW   adenocarcinoma; bowel; transformed phenotype; promyelocytic leukemia;
KW   human; chronic myelogenous leukemia; CML; follicular lymphoma;
KW   B-cell acute lymphocytic leukemia; breast cancer; colon carcinoma;
KW   neuroblastoma; lung cancer; genetic drift; mutation; hammerhead motif;
KW   hairpin; hepatitis delta virus; group I intron; RNaseP; leukaemia; ss.
XX
OS   Homo sapiens.
XX
PN   WO9323057-A1.
XX
PD   25-NOV-1993.
XX
PF   13-MAY-1993;   93WO-US004573.
XX
PR   14-MAY-1992;   92US-00882822.
PR   14-MAY-1992;   92US-00882885.
PR   26-AUG-1992;   92US-00936110.
PR   26-AUG-1992;   92US-00936421.
PR   26-AUG-1992;   92US-00936422.
PR   26-AUG-1992;   92US-00936531.
PR   26-AUG-1992;   92US-00936532.
PR   07-DEC-1992;   92US-00987131.
PR   19-JAN-1993;   93US-00006122.
PR   19-JAN-1993;   93US-00008910.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Thompson JD,  Draper KG;
XX
DR   WPI; 1993-386203/48.
XX
PT   New enzymatic RNA molecules (ribozymes) - which cleave mRNA associated
PT   with tumours or mRNA expressed from gene encoding multiple drug
PT   resistance.
XX
PS   Claim 3; Fig 8; 69pp; English.
XX
CC   The sequences given in AAQ51825-2266 represent areas of mRNAs which are
CC   associated with development or maintenance of chronic myelogenous
CC   leukemia (CML), promyelocytic leukemia, Burkitt's lymphoma, or acute
CC   lymphocytic leukemia, follicular lymphoma, B-cell acute lymphocytic
CC   leukemia, breast cancer, colon carcinoma, neuroblastoma and lung cancer.
CC   The full length mRNAs containing these target sequences, encode aberant
CC   cellular proteins which are able to control cellular proliferation and
CC   are directly linked to a leukemic phenotype. These target sequences are
CC   identified by the ribozyme of the invention. The ribozymes is formed in a
CC   hammerhead motif, but may also be formed in the motif of a hairpin,
CC   hepatitis delta virus, group I intron or RNaseP-like RNA. These ribozymes
CC   may be used to inhibit the development or expression of a transformed
CC   phenotype in man and other animals by modulating expression of the
CC   corresponding gene. Cleavage of target mRNAs expressed in pre-neoplastic
CC   and transformed cells elicits inhibition of the transformed state.
CC   Multiple drug resistance (mdr-1) mRNA specific ribozymes remove the
CC   mechanism of drug resistance used by transformed cells and thus enhances
CC   drug therapies for tumours. The ribozymes may also be used to study
CC   genetic drift and mutations within cells. (Updated on 25-MAR-2003 to
CC   correct PN field.)
XX
SQ   Sequence 35 BP; 5 A; 1 C; 4 G; 0 T; 25 U; 0 Other;

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 35;
  Best Local Similarity   86.4%;  Pred. No. 3.4e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAAA 2804
              || |||||| |||| |||||||
Db         33 TTAAAAAAACAAAACAAAAAAA 12


RESULT 1996
AAX69800
ID   AAX69800 standard; RNA; 17 BP.
XX
AC   AAX69800;
XX
DT   28-JUL-1999  (first entry)
XX
DE   Human flt1 VEGF receptor hammerhead ribozyme substrate #1095.
XX
KW   Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW   KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW   tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW   fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW   foetal liver kinase 1; ss.
XX
OS   Homo sapiens.
XX
PN   WO9715662-A2.
XX
PD   01-MAY-1997.
XX
PF   25-OCT-1996;   96WO-US017480.
XX
PR   26-OCT-1995;   95US-0005974P.
PR   11-JAN-1996;   96US-00584040.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (CHIR ) CHIRON CORP.
XX
PI   Pavco P,  Mcswiggen J,  Stinchcomb D,  Escobedo J;
XX
DR   WPI; 1997-259017/23.
XX
PT   Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT   stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT   rheumatoid arthritis, etc., in a human patient.
XX
```

```
PS   Claim 4; Page 79; 218pp; English.
XX
CC   The present invention describes nucleic acid molecules which modulate the
CC   synthesis, expression and/or stability of a mRNA encoding 1 or more
CC   receptors of vascular endothelial growth factor (VEGF). A patient
CC   (preferably human) having a condition associated with the level of the
CC   fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC   receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC   angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC   treated by administering the nucleic acid molecule or the expression
CC   vector to the patient. AAX67275 to AAX75752 represent specific examples
CC   of nucleic acid molecules from the present invention
XX
SQ   Sequence 17 BP; 0 A; 1 C; 0 G; 0 T; 16 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   5.9%;  Pred. No. 9.5e+02;
  Matches    1;  Conservative   16;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTT 2181
              |:::::::::::::::
Db          1 CUUUUUUUUUUUUUUU 17


RESULT 1997
AAX69801/c
ID   AAX69801 standard; RNA; 17 BP.
XX
AC   AAX69801;
XX
DT   28-JUL-1999  (first entry)
XX
DE   Human flt1 VEGF receptor hammerhead ribozyme substrate #1096.
XX
KW   Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW   KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW   tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW   fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW   foetal liver kinase 1; ss.
XX
OS   Homo sapiens.
XX
PN   WO9715662-A2.
XX
PD   01-MAY-1997.
XX
PF   25-OCT-1996;   96WO-US017480.
XX
PR   26-OCT-1995;   95US-0005974P.
PR   11-JAN-1996;   96US-00584040.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (CHIR ) CHIRON CORP.
XX
PI   Pavco P,  Mcswiggen J,  Stinchcomb D,  Escobedo J;
XX
DR   WPI; 1997-259017/23.
XX
PT   Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT   stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT   rheumatoid arthritis, etc., in a human patient.
XX
PS   Claim 4; Page 79; 218pp; English.
XX
CC   The present invention describes nucleic acid molecules which modulate the
CC   synthesis, expression and/or stability of a mRNA encoding 1 or more
CC   receptors of vascular endothelial growth factor (VEGF). A patient
CC   (preferably human) having a condition associated with the level of the
CC   fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC   receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC   angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC   treated by administering the nucleic acid molecule or the expression
CC   vector to the patient. AAX67275 to AAX75752 represent specific examples
CC   of nucleic acid molecules from the present invention
XX
SQ   Sequence 17 BP; 0 A; 1 C; 0 G; 0 T; 16 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2801
              |||||||||||||||||
Db         17 GAAAAAAAAAAAAAAAA 1


RESULT 1998
AAX18370
ID   AAX18370 standard; DNA; 17 BP.
XX
AC   AAX18370;
XX
DT   11-MAY-1999  (first entry)
XX
DE   RT-PCR primer of the invention SEQ ID 11.
XX
KW   RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS   Synthetic.
XX
PN   JP11032765-A.
XX
PD   09-FEB-1999.
XX
PF   18-JUL-1997;   97JP-00208312.
XX
PR   18-JUL-1997;   97JP-00208312.
XX
PA   (TAKI ) TAKARA SHUZO CO LTD.
XX
DR   WPI; 1999-183822/16.
XX
PT   Peptides having at least two new nucleotides - useful as primers in RT-
PT   PCR.
XX
PS   Disclosure; Page 11; 19pp; Japanese.
XX
CC   This sequence represents a primer of the invention. The invention relates
CC   to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC   -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC   a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC   natural number indicating the repetition of alpha; beta, delta = V or N;
CC   V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC   thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC   repetition of gamma, in which thymine expressed by gamma is composed of
CC   1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC   useful as primers for RT-PCR and determination of base sequences. The new
CC   sequences allow for reproductive and highly efficient analysis of gene
CC   sequences
XX
SQ   Sequence 17 BP; 2 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTAA 2188
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTAA 17


RESULT 1999
AAA25450
ID   AAA25450 standard; DNA; 17 BP.
XX
AC   AAA25450;
```

```
XX
DT   19-JUL-2000  (first entry)
XX
DE   Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1948.
XX
KW   Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW   hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW   gene expression modification; cancer; phosphorothioate; endonuclease;
KW   anticancer; breast cancer; endometrium cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9954459-A2.
XX
PD   28-OCT-1999.
XX
PF   19-APR-1999;   99WO-US008547.
XX
PR   20-APR-1998;   98US-0082404P.
PR   23-JUN-1998;   98US-00103636.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Thompson JD,  Beigelman L,  Mcswiggen JA,  Karpeisky A,  Bellon L;
PI   Reynolds M,  Zwick M,  Jarvis T,  Woolf T,  Haeberli P;
PI   Matulic-Adamic J;
XX
DR   WPI; 2000-013248/01.
XX
PT   New nucleic acids that interact, and optionally cleave, target sequences,
PT   used to treat cancer.
XX
PS   Claim 77; Page 79; 148pp; English.
XX
CC   The present invention describes nucleic acids (A) that interact stably
CC   with a target sequence and contain at least one phosphoro(di)thioate
CC   link, having endonuclease activity. (A), and more generally any catalytic
CC   nucleic acid (A') that modulates expression of the oestrogen receptor
CC   gene, are used to treat cancer (particularly of breast or endometrium),
CC   in vivo or by transforming cells ex vivo and implanting treated cells, or
CC   for other conditions associated with levels of oestrogen receptor.
CC   Because of the high selectivity for targeted RNA, (A) can also be used to
CC   correlate inhibition of gene expression with alterations in phenotype,
CC   particularly for identification of therapeutic targets, and as research
CC   reagents (for RNA, in the same way that restriction endonucleases are
CC   used with DNA). The combination of modifications in (A) improves
CC   resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC   AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
CC   AAA24748 to AAA25992 represent their corresponding target sequences.
CC   AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC   sequences, and AAA26107 to AAA26218 represent their corresponding target
CC   sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC   antisense oligonucleotides used in the exemplification of the present
CC   invention
XX
SQ   Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 17


RESULT 2000
AAA25450/c
ID   AAA25450 standard; DNA; 17 BP.
XX
AC   AAA25450;
XX
DT   19-JUL-2000  (first entry)
XX
DE   Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1948.
XX
KW   Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW   hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW   gene expression modification; cancer; phosphorothioate; endonuclease;
KW   anticancer; breast cancer; endometrium cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9954459-A2.
XX
PD   28-OCT-1999.
XX
PF   19-APR-1999;   99WO-US008547.
XX
PR   20-APR-1998;   98US-0082404P.
PR   23-JUN-1998;   98US-00103636.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Thompson JD,  Beigelman L,  Mcswiggen JA,  Karpeisky A,  Bellon L;
PI   Reynolds M,  Zwick M,  Jarvis T,  Woolf T,  Haeberli P;
PI   Matulic-Adamic J;
XX
DR   WPI; 2000-013248/01.
XX
PT   New nucleic acids that interact, and optionally cleave, target sequences,
PT   used to treat cancer.
XX
PS   Claim 77; Page 79; 148pp; English.
XX
CC   The present invention describes nucleic acids (A) that interact stably
CC   with a target sequence and contain at least one phosphoro(di)thioate
CC   link, having endonuclease activity. (A), and more generally any catalytic
CC   nucleic acid (A') that modulates expression of the oestrogen receptor
CC   gene, are used to treat cancer (particularly of breast or endometrium),
CC   in vivo or by transforming cells ex vivo and implanting treated cells, or
CC   for other conditions associated with levels of oestrogen receptor.
CC   Because of the high selectivity for targeted RNA, (A) can also be used to
CC   correlate inhibition of gene expression with alterations in phenotype,
CC   particularly for identification of therapeutic targets, and as research
CC   reagents (for RNA, in the same way that restriction endonucleases are
CC   used with DNA). The combination of modifications in (A) improves
CC   resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC   AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
CC   AAA24748 to AAA25992 represent their corresponding target sequences.
CC   AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC   sequences, and AAA26107 to AAA26218 represent their corresponding target
CC   sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC   antisense oligonucleotides used in the exemplification of the present
CC   invention
XX
SQ   Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2802
              ||||||||||||||||
Db         17 AAAAAAAAAAAAAAAA 1


RESULT 2001
AAA98232
ID   AAA98232 standard; DNA; 17 BP.
XX
AC   AAA98232;
XX
DT   30-JAN-2001  (first entry)
XX
DE   Human retrovirus HERV LTR PCR primer #31.
```

```
XX
KW   Cell-specific expression; tissue-specific expression; gene therapy; LTR;
KW   U3-R segment; long terminal repeat; retroviral expression vector;
KW   PCR primer; ss.
XX
OS   Human endogenous retrovirus.
XX
PN   WO200053789-A2.
XX
PD   14-SEP-2000.
XX
PF   09-MAR-2000; 2000WO-EP002064.
XX
PR   10-MAR-1999;   99DE-01010650.
XX
PA   (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEI.
XX
PI   Leib-Moesch C,  Schoen U,  Baust C;
XX
DR   WPI; 2000-587442/55.
XX
PT   Retroviral expression vector, useful in gene therapy, contains a promoter
PT   from a human endogenous retrovirus to provide cell-specific expression.
XX
PS   Disclosure; Page 27; 67pp; German.
XX
CC   This invention describes a novel retroviral expression vector (A)
CC   containing DNA sequences (I) for packaging vector RNA and for cell-
CC   specific expression of proteins or peptides encoding by heterologous DNA
CC   (II). The sequences controlling cell-specific expression contain a cell-
CC   specifically regulatable promoter region (P) from a human endogenous
CC   retrovirus (HERV) DNA sequence. The invention also describes (a) mRNA and
CC   RNA of (A); (b) prokaryotic and eukaryotic cells containing (A); (c)
CC   eukaryotic cells containing (A) in integrated form; (d) virions
CC   containing a retroviral expression vector RNA derived from (A); (e) a
CC   method for producing the virions of (d); (f) a method for incorporating
CC   protein-encoding nucleic acid sequences into a eukaryotic cell by
CC   infection with the virions of (d); and (g) a retroviral vector system
CC   containing (A) and a packaging cell line, that contains at least one
CC   (recombinant) retrovirus construct that encodes for the packaging
CC   proteins of (A). (A) are used for cell- or tissue-specific expression of
CC   foreign genes for gene therapy and to produce virions for introducing
CC   (II) into the chromosomal DNA of eukaryotic cells, preferably mammalian
CC   and specifically human. (A) retain the advantages of usual retroviral
CC   promoters with all the signal structures required for transcription in a
CC   small region within the U3-R segment, but without their disadvantages
CC   (excessive strength and limited cell specificity). Since (A) are derived
CC   from endogenous (harmless) viral sequences, they do not introduce any new
CC   viral sequences into the genome and recombination will not create new
CC   types of retrovirus. The promoters provide cell or tissue specific
CC   expression, according to which HERV they are derived from
XX
SQ   Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2002
AAA98232/c
ID   AAA98232 standard; DNA; 17 BP.
XX
AC   AAA98232;
XX
DT   30-JAN-2001  (first entry)
XX
DE   Human retrovirus HERV LTR PCR primer #31.
XX
KW   Cell-specific expression; tissue-specific expression; gene therapy; LTR;
KW   U3-R segment; long terminal repeat; retroviral expression vector;
KW   PCR primer; ss.
XX
OS   Human endogenous retrovirus.
XX
PN   WO200053789-A2.
XX
PD   14-SEP-2000.
XX
PF   09-MAR-2000; 2000WO-EP002064.
XX
PR   10-MAR-1999;   99DE-01010650.
XX
PA   (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEI.
XX
PI   Leib-Moesch C,  Schoen U,  Baust C;
XX
DR   WPI; 2000-587442/55.
XX
PT   Retroviral expression vector, useful in gene therapy, contains a promoter
PT   from a human endogenous retrovirus to provide cell-specific expression.
XX
PS   Disclosure; Page 27; 67pp; German.
XX
CC   This invention describes a novel retroviral expression vector (A)
CC   containing DNA sequences (I) for packaging vector RNA and for cell-
CC   specific expression of proteins or peptides encoding by heterologous DNA
CC   (II). The sequences controlling cell-specific expression contain a cell-
CC   specifically regulatable promoter region (P) from a human endogenous
CC   retrovirus (HERV) DNA sequence. The invention also describes (a) mRNA and
CC   RNA of (A); (b) prokaryotic and eukaryotic cells containing (A); (c)
CC   eukaryotic cells containing (A) in integrated form; (d) virions
CC   containing a retroviral expression vector RNA derived from (A); (e) a
CC   method for producing the virions of (d); (f) a method for incorporating
CC   protein-encoding nucleic acid sequences into a eukaryotic cell by
CC   infection with the virions of (d); and (g) a retroviral vector system
CC   containing (A) and a packaging cell line, that contains at least one
CC   (recombinant) retrovirus construct that encodes for the packaging
CC   proteins of (A). (A) are used for cell- or tissue-specific expression of
CC   foreign genes for gene therapy and to produce virions for introducing
CC   (II) into the chromosomal DNA of eukaryotic cells, preferably mammalian
CC   and specifically human. (A) retain the advantages of usual retroviral
CC   promoters with all the signal structures required for transcription in a
CC   small region within the U3-R segment, but without their disadvantages
CC   (excessive strength and limited cell specificity). Since (A) are derived
CC   from endogenous (harmless) viral sequences, they do not introduce any new
CC   viral sequences into the genome and recombination will not create new
CC   types of retrovirus. The promoters provide cell or tissue specific
CC   expression, according to which HERV they are derived from
XX
SQ   Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 2003
AAA50197
ID   AAA50197 standard; DNA; 17 BP.
XX
AC   AAA50197;
XX
DT   07-NOV-2000  (first entry)
XX
DE   2'-Methoxyethoxy-modified phosphorothioate oligonucleotide.
XX
KW   Phosphorothioate oligonucleotide; H-phosphonate chemistry; ss.
```

```
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .19
FT                   /*tag=  a
FT                   /note= "2'-methoxyethoxy modified thymidine"
FT   modified_base   1. .17
FT                   /*tag=  b
FT                   /note= "phosphorothioate internucleoside linkages"
XX
PN   WO200047593-A1.
XX
PD   17-AUG-2000.
XX
PF   11-FEB-2000; 2000WO-US003543.
XX
PR   12-FEB-1999;   99US-00250075.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Manoharan M,  Maier MA;
XX
DR   WPI; 2000-558188/51.
XX
PT   Preparation of mixed backbone oligomeric compounds useful as e.g. primers
PT   for diagnostic tests, involves oxidation of H-phosphonate internucleoside
PT   linkages to phosphodiester internucleoside linkages.
XX
PS   Example 12; Page 34; 49pp; English.
XX
CC   The present sequence is that of a phosphorothioate oligonucleotide
CC   containing 20 T nucleobases, each having a 2'-methoxyethoxy group on its
CC   5' ribosyl sugar moiety. It is an example of an oligomeric compound
CC   produced according to the methods of the invention. The invention
CC   provides compounds and methods for the preparation of mixed backbone
CC   oligomeric, or chimeric, compounds having phosphodiester internucleoside
CC   linkages in addition to phosphorothioate and/or phosphoramidate
CC   internucleoside linkages. The methods also include incorporation of
CC   boranophosphate internucleoside linkages. The methods utilise H-
CC   phosphonate intermediates that are coupled together forming contiguous
CC   regions of 1 or more H-phosphonate internucleoside linkages. Each
CC   contiguous region is subsequently oxidized to phosphodiester,
CC   phosphorothioate, phosphoramidate or boranophosphate internucleoside
CC   linkages prior to further elongation. Mixed backbone oligomeric compounds
CC   are prepared in this manner by oxidizing adjacent regions with different
CC   reagents. Oligomeric compounds of the invention are prepared using novel
CC   oxidation steps that oxidize a region of 1 or more H-phosphonate
CC   internucleoside linkages without degrading existing linkages that have
CC   been previously oxidized. The oligonucleotides obtained are useful as
CC   primers in PCR, probes, linkers, gene fragments and for other diagnostic
CC   tests on e.g. biological tissue, fluid, cells etc., as research reagents,
CC   and as antiviral agents
XX
SQ   Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2004
AAA50197/c
ID   AAA50197 standard; DNA; 17 BP.
XX
AC   AAA50197;
XX
DT   07-NOV-2000  (first entry)
XX
DE   2'-Methoxyethoxy-modified phosphorothioate oligonucleotide.
XX
KW   Phosphorothioate oligonucleotide; H-phosphonate chemistry; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .19
FT                   /*tag=  a
FT                   /note= "2'-methoxyethoxy modified thymidine"
FT   modified_base   1. .17
FT                   /*tag=  b
FT                   /note= "phosphorothioate internucleoside linkages"
XX
PN   WO200047593-A1.
XX
PD   17-AUG-2000.
XX
PF   11-FEB-2000; 2000WO-US003543.
XX
PR   12-FEB-1999;   99US-00250075.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Manoharan M,  Maier MA;
XX
DR   WPI; 2000-558188/51.
XX
PT   Preparation of mixed backbone oligomeric compounds useful as e.g. primers
PT   for diagnostic tests, involves oxidation of H-phosphonate internucleoside
PT   linkages to phosphodiester internucleoside linkages.
XX
PS   Example 12; Page 34; 49pp; English.
XX
CC   The present sequence is that of a phosphorothioate oligonucleotide
CC   containing 20 T nucleobases, each having a 2'-methoxyethoxy group on its
CC   5' ribosyl sugar moiety. It is an example of an oligomeric compound
CC   produced according to the methods of the invention. The invention
CC   provides compounds and methods for the preparation of mixed backbone
CC   oligomeric, or chimeric, compounds having phosphodiester internucleoside
CC   linkages in addition to phosphorothioate and/or phosphoramidate
CC   internucleoside linkages. The methods also include incorporation of
CC   boranophosphate internucleoside linkages. The methods utilise H-
CC   phosphonate intermediates that are coupled together forming contiguous
CC   regions of 1 or more H-phosphonate internucleoside linkages. Each
CC   contiguous region is subsequently oxidized to phosphodiester,
CC   phosphorothioate, phosphoramidate or boranophosphate internucleoside
CC   linkages prior to further elongation. Mixed backbone oligomeric compounds
CC   are prepared in this manner by oxidizing adjacent regions with different
CC   reagents. Oligomeric compounds of the invention are prepared using novel
CC   oxidation steps that oxidize a region of 1 or more H-phosphonate
CC   internucleoside linkages without degrading existing linkages that have
CC   been previously oxidized. The oligonucleotides obtained are useful as
CC   primers in PCR, probes, linkers, gene fragments and for other diagnostic
CC   tests on e.g. biological tissue, fluid, cells etc., as research reagents,
CC   and as antiviral agents
XX
SQ   Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 2005
AAS06654
ID   AAS06654 standard; DNA; 17 BP.
XX
AC   AAS06654;
```

```
XX
DT   12-SEP-2001  (first entry)
XX
DE   Human cDNA synthesis and differential display primer, HT11GA.
XX
KW   Human; Estrogen response element; ERE; DDRT-PCR; ss; PCR primer;
KW   differential display of reverse transcribed mRNAs by PCR;
KW   testicular cancer; breast cancer; prostate cancer; endometrial cancer;
KW   asthma; hypospadia; cryptorchism; allergy; hormone replacement therapy;
KW   HRT; endocrine system; HT11GA.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200134834-A2.
XX
PD   17-MAY-2001.
XX
PF   10-NOV-2000; 2000WO-DK000628.
XX
PR   11-NOV-1999;   99DK-00001626.
XX
PA   (RIGS-) RIGSHOSPITALET.
XX
PI   Leffers H,  Jorgensen M,  Skakkebaek NE;
XX
DR   WPI; 2001-335941/35.
XX
PT   Evaluating a cellular response to an environmental compound, for use in
PT   toxicological analysis, involves determining or comparing the expression
PT   levels of at least one endogenous gene.
XX
PS   Example 3; Page 27; 77pp; English.
XX
CC   The sequence represents a downstream PCR primer used in a DDRT-PCR
CC   experiment (and in cDNA synthesis), demonstrating the method of the
CC   invention. The method relates to evaluating a cellular response to an
CC   environmental compound, comprising determining or comparing the
CC   expression levels of at least one endogenous gene e.g by differential
CC   display of reverse transcribed mRNAs by PCR (DDRT-PCR). The method can be
CC   adapted to identify compounds that act on the level of endogenous gene
CC   expression through activating nuclear receptors. The method is useful in
CC   toxicological analysis, diagnostics, for diagnosing cancer (e.g.
CC   testicular, breast, prostate and endometrium), asthma, hypospadia,
CC   cryptorchism and/or allergy, and for evaluating the efficiency of a
CC   treatment for hormonal deficiency or hormonal replacement therapy, in a
CC   human such as a post-menopausal female. The method is also useful for
CC   identifying environmental chemicals or pharmaceutical compositions that
CC   interact with endocrine systems, and for detecting chemicals that pose a
CC   health threat. Expression levels of endogenous genes are determined
CC   rapidly using a sensitive technique, and the expression of any gene can
CC   be monitored. The assays are far more informative than the currently used
CC   assays, and significantly reduces the number of animals required for the
CC   testing, as it is expected that essentially all the animals in a test
CC   group will respond to the compound
XX
SQ   Sequence 17 BP; 3 A; 1 C; 2 G; 11 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTGA 1783
              |||||||||||||||||
Db          1 AAGCTTTTTTTTTTTGA 17


RESULT 2006
ABK13941/c
ID   ABK13941 standard; DNA; 17 BP.
XX
AC   ABK13941;
XX
DT   21-MAY-2002  (first entry)
XX
DE   5'-PCR primer used to produce single pattern characteristic by FokI.
XX
KW   Identification of transcribed gene; mRNA profile; gene expression;
KW   cellular process; fingerprinting; susceptibility to external factor;
KW   development; disease; PCR; primer; ss.
XX
OS   Synthetic.
XX
PN   WO200208461-A2.
XX
PD   31-JAN-2002.
XX
PF   23-JUL-2001; 2001WO-IB001539.
XX
PR   21-JUL-2000; 2000GB-00018016.
PR   21-JUL-2000; 2000US-0219925P.
XX
PA   (GLOB-) GLOBAL GENOMICS AB.
XX
PI   Linnarsson S,  Ernfors P,  Bauren G;
XX
DR   WPI; 2002-217065/27.
XX
PT   Providing mRNA profile, by generating two independent patterns
PT   characteristic of sample mRNA population, analyzing patterns, comparing
PT   gene expression by cell types under varied conditions, and identifying
PT   genes.
XX
PS   Disclosure; Fig 2; 67pp; English.
XX
CC   The present invention relates to a method for providing a profile of mRNA
CC   molecules present in a sample. The method comprises generating two
CC   independent patterns characteristic of the population of mRNA molecules
CC   expressed in the sample and analysing the patterns using a combinatorial
CC   algorithm, comparing gene expression by different or same cell types
CC   under different conditions, and identifying genes having a role in
CC   various cellular processes. The method is useful for the analysis and
CC   identification of transcribed genes, and fingerprinting. The method can
CC   be used to identify genes which play a role in determining various
CC   cellular processes, including susceptibility to external factors,
CC   development, and disease. The present sequence for a PCR primer is used
CC   in the production of a single pattern characteristic of a sample,
CC   employing a Type IIS restriction enzyme (i.e. FokI) in the methods of the
CC   present invention
XX
SQ   Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2801
              |||||||||||||||||
Db         17 GAAAAAAAAAAAAAAAA 1


RESULT 2007
ADB04271
ID   ADB04271 standard; DNA; 17 BP.
XX
AC   ADB04271;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ7 scanning oligonucleotide SEQ ID 5257.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
```

OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
DR WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS Example 8; SEQ ID NO 5257; 103pp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 0.6%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       2165 CTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          1 CTTTTTTTTTTTTTTT 17
```

RESULT 2008
AAD56441
ID AAD56441 standard; DNA; 17 BP.
XX
AC AAD56441;
XX
DT 07-AUG-2003 (first entry)
XX
DE Antisense oligo #2, to elicit RNase H degradation of target RNA.
XX
KW Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
KW antisense; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT misc_feature 9. .10
FT /*tag= a
FT /note= "Bases 9 and 10 are linked by a butanediol linker
FT which is represented as B in page 49 and X in page 59,
FT Fig 9 and 10 of the specification"
XX
PN WO2003037909-A1.
XX
PD 08-MAY-2003.
XX
PF 29-OCT-2002; 2002WO-CA001628.
XX
PR 29-OCT-2001; 2001US-0330719P.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;
XX
DR WPI; 2003-421516/39.
XX
PT Novel acyclic linker-containing oligonucleotide useful for preventing or
PT decreasing translation, reverse transcription and/or replication of a
PT target RNA in a system, comprises a modified deoxyribonucleotide.
XX
PS Example 2; Page 90; 104pp; English.
XX
CC The invention relates to an acyclic linker-containing oligonucleotide
CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC the invention are useful for preventing or decreasing translation,
CC reverse transcription and/or replication of a target RNA in a system.
CC They are useful for selectively preventing gene expression in a sequence-
CC specific manner, for hybridising to complementary RNA such as cellular
CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC RNA. They are also useful therapeutically in formulations or medicaments
CC to prevent or treat a disease characterised by the expression of a
CC particular target RNA. The invention is used in gene therapy. The present
CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC H degradation of target RNA. This sequence is used in the exemplification
CC of the invention
XX
SQ Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       2166 TTTTTTTTTTTTTTTT 2182
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 17
```

RESULT 2009
AAD56441/c
ID AAD56441 standard; DNA; 17 BP.
XX
AC AAD56441;
XX
DT 07-AUG-2003 (first entry)
XX
DE Antisense oligo #2, to elicit RNase H degradation of target RNA.
XX
KW Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
KW antisense; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT misc_feature 9. .10
FT /*tag= a
FT /note= "Bases 9 and 10 are linked by a butanediol linker
FT which is represented as B in page 49 and X in page 59,
FT Fig 9 and 10 of the specification"
XX
PN WO2003037909-A1.
XX
PD 08-MAY-2003.
XX
PF 29-OCT-2002; 2002WO-CA001628.
XX
PR 29-OCT-2001; 2001US-0330719P.

```
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Viazovkina E,  Mangos MM,  Parniak MA,  Min K;
XX
DR   WPI; 2003-421516/39.
XX
PT   Novel acyclic linker-containing oligonucleotide useful for preventing or
PT   decreasing translation, reverse transcription and/or replication of a
PT   target RNA in a system, comprises a modified deoxyribonucleotide.
XX
PS   Example 2; Page 90; 104pp; English.
XX
CC   The invention relates to an acyclic linker-containing oligonucleotide
CC   comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC   the invention are useful for preventing or decreasing translation,
CC   reverse transcription and/or replication of a target RNA in a system.
CC   They are useful for selectively preventing gene expression in a sequence-
CC   specific manner, for hybridising to complementary RNA such as cellular
CC   mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC   RNA. They are also useful therapeutically in formulations or medicaments
CC   to prevent or treat a disease characterised by the expression of a
CC   particular target RNA. The invention is used in gene therapy. The present
CC   sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC   H degradation of target RNA. This sequence is used in the exemplification
CC   of the invention
XX
SQ   Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 2010
AAD56448
ID   AAD56448 standard; DNA; 17 BP.
XX
AC   AAD56448;
XX
DT   07-AUG-2003  (first entry)
XX
DE   2'F-ANA antisense oligo #3, to elicit RNase H degradation of target RNA.
XX
KW   Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
KW   antisense; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .17
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "2'-deoxy-2'-fluoroarabinothymidine"
FT   misc_feature     9. .10
FT                    /*tag=  b
FT                    /note= "Bases 9 and 10 are linked by a butanediol linker
FT                    which is represented as B in page 49 and Fig 5 and as X
FT                    in page 52, 55 and Fig 6 of the specification"
XX
PN   WO2003037909-A1.
XX
PD   08-MAY-2003.
XX
PF   29-OCT-2002; 2002WO-CA001628.
XX
PR   29-OCT-2001; 2001US-0330719P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Viazovkina E,  Mangos MM,  Parniak MA,  Min K;
XX
DR   WPI; 2003-421516/39.
XX
PT   Novel acyclic linker-containing oligonucleotide useful for preventing or
PT   decreasing translation, reverse transcription and/or replication of a
PT   target RNA in a system, comprises a modified deoxyribonucleotide.
XX
PS   Example 2; Fig 5; 104pp; English.
XX
CC   The invention relates to an acyclic linker-containing oligonucleotide
CC   comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC   the invention are useful for preventing or decreasing translation,
CC   reverse transcription and/or replication of a target RNA in a system.
CC   They are useful for selectively preventing gene expression in a sequence-
CC   specific manner, for hybridising to complementary RNA such as cellular
CC   mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC   RNA. They are also useful therapeutically in formulations or medicaments
CC   to prevent or treat a disease characterised by the expression of a
CC   particular target RNA. The invention is used in gene therapy. The present
CC   sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC   H degradation of target RNA. This sequence is used in the exemplification
CC   of the invention
XX
SQ   Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2011
AAD56448/c
ID   AAD56448 standard; DNA; 17 BP.
XX
AC   AAD56448;
XX
DT   07-AUG-2003  (first entry)
XX
DE   2'F-ANA antisense oligo #3, to elicit RNase H degradation of target RNA.
XX
KW   Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
KW   antisense; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .17
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "2'-deoxy-2'-fluoroarabinothymidine"
FT   misc_feature     9. .10
FT                    /*tag=  b
FT                    /note= "Bases 9 and 10 are linked by a butanediol linker
FT                    which is represented as B in page 49 and Fig 5 and as X
FT                    in page 52, 55 and Fig 6 of the specification"
XX
PN   WO2003037909-A1.
XX
PD   08-MAY-2003.
XX
PF   29-OCT-2002; 2002WO-CA001628.
XX
PR   29-OCT-2001; 2001US-0330719P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Viazovkina E,  Mangos MM,  Parniak MA,  Min K;
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```
XX
DR   WPI; 2003-421516/39.
XX
PT   Novel acyclic linker-containing oligonucleotide useful for preventing or
PT   decreasing translation, reverse transcription and/or replication of a
PT   target RNA in a system, comprises a modified deoxyribonucleotide.
XX
PS   Example 2; Fig 5; 104pp; English.
XX
CC   The invention relates to an acyclic linker-containing oligonucleotide
CC   comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC   the invention are useful for preventing or decreasing translation,
CC   reverse transcription and/or replication of a target RNA in a system.
CC   They are useful for selectively preventing gene expression in a sequence-
CC   specific manner, for hybridising to complementary RNA such as cellular
CC   mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC   RNA. They are also useful therapeutically in formulations or medicaments
CC   to prevent or treat a disease characterised by the expression of a
CC   particular target RNA. The invention is used in gene therapy. The present
CC   sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC   H degradation of target RNA. This sequence is used in the exemplification
CC   of the invention
XX
SQ   Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 2012
AAD56449
ID   AAD56449 standard; DNA; 17 BP.
XX
AC   AAD56449;
XX
DT   07-AUG-2003  (first entry)
XX
DE   2'F-ANA antisense oligo #4, to elicit RNase H degradation of target RNA.
XX
KW   Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
KW   antisense; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .17
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "2'-deoxy-2'-fluoroarabinothymidine"
FT   misc_feature     12. .13
FT                    /*tag=  b
FT                    /note= "Bases 12 and 13 are linked by a butanediol linker
FT                    which is represented as B in page 49 and Fig 5 and as X
FT                    in page 55 and Fig 6 of the specification"
XX
PN   WO2003037909-A1.
XX
PD   08-MAY-2003.
XX
PF   29-OCT-2002; 2002WO-CA001628.
XX
PR   29-OCT-2001; 2001US-0330719P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Viazovkina E,  Mangos MM,  Parniak MA,  Min K;
XX
DR   WPI; 2003-421516/39.
XX
PT   Novel acyclic linker-containing oligonucleotide useful for preventing or
PT   decreasing translation, reverse transcription and/or replication of a
PT   target RNA in a system, comprises a modified deoxyribonucleotide.
XX
PS   Example 2; Fig 5; 104pp; English.
XX
CC   The invention relates to an acyclic linker-containing oligonucleotide
CC   comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC   the invention are useful for preventing or decreasing translation,
CC   reverse transcription and/or replication of a target RNA in a system.
CC   They are useful for selectively preventing gene expression in a sequence-
CC   specific manner, for hybridising to complementary RNA such as cellular
CC   mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC   RNA. They are also useful therapeutically in formulations or medicaments
CC   to prevent or treat a disease characterised by the expression of a
CC   particular target RNA. The invention is used in gene therapy. The present
CC   sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC   H degradation of target RNA. This sequence is used in the exemplification
CC   of the invention
XX
SQ   Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2013
AAD56449/c
ID   AAD56449 standard; DNA; 17 BP.
XX
AC   AAD56449;
XX
DT   07-AUG-2003  (first entry)
XX
DE   2'F-ANA antisense oligo #4, to elicit RNase H degradation of target RNA.
XX
KW   Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
KW   antisense; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .17
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "2'-deoxy-2'-fluoroarabinothymidine"
FT   misc_feature     12. .13
FT                    /*tag=  b
FT                    /note= "Bases 12 and 13 are linked by a butanediol linker
FT                    which is represented as B in page 49 and Fig 5 and as X
FT                    in page 55 and Fig 6 of the specification"
XX
PN   WO2003037909-A1.
XX
PD   08-MAY-2003.
XX
PF   29-OCT-2002; 2002WO-CA001628.
XX
PR   29-OCT-2001; 2001US-0330719P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Viazovkina E,  Mangos MM,  Parniak MA,  Min K;
XX
DR   WPI; 2003-421516/39.
XX
PT   Novel acyclic linker-containing oligonucleotide useful for preventing or
```

```
PT   decreasing translation, reverse transcription and/or replication of a
PT   target RNA in a system, comprises a modified deoxyribonucleotide.
XX
PS   Example 2; Fig 5; 104pp; English.
XX
CC   The invention relates to an acyclic linker-containing oligonucleotide
CC   comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC   the invention are useful for preventing or decreasing translation,
CC   reverse transcription and/or replication of a target RNA in a system.
CC   They are useful for selectively preventing gene expression in a sequence-
CC   specific manner, for hybridising to complementary RNA such as cellular
CC   mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC   RNA. They are also useful therapeutically in formulations or medicaments
CC   to prevent or treat a disease characterised by the expression of a
CC   particular target RNA. The invention is used in gene therapy. The present
CC   sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC   H degradation of target RNA. This sequence is used in the exemplification
CC   of the invention
XX
SQ   Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 2014
AAD56447
ID   AAD56447 standard; DNA; 17 BP.
XX
AC   AAD56447;
XX
DT   07-AUG-2003  (first entry)
XX
DE   2'F-ANA antisense oligo #2, to elicit RNase H degradation of target RNA.
XX
KW   Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
KW   antisense; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .17
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "2'-deoxy-2'-fluoroarabinothymidine"
FT   misc_feature     4. .5
FT                    /*tag=  b
FT                    /note= "Bases 4 and 5 are linked by a butanediol linker
FT                    which is represented as B in page 49 and Fig 5 and as X
FT                    in page 55 and Fig 6 of the specification"
XX
PN   WO2003037909-A1.
XX
PD   08-MAY-2003.
XX
PF   29-OCT-2002; 2002WO-CA001628.
XX
PR   29-OCT-2001; 2001US-0330719P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Viazovkina E,  Mangos MM,  Parniak MA,  Min K;
XX
DR   WPI; 2003-421516/39.
XX
PT   Novel acyclic linker-containing oligonucleotide useful for preventing or
PT   decreasing translation, reverse transcription and/or replication of a
PT   target RNA in a system, comprises a modified deoxyribonucleotide.
XX
PS   Example 2; Fig 5; 104pp; English.
XX
CC   The invention relates to an acyclic linker-containing oligonucleotide
CC   comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC   the invention are useful for preventing or decreasing translation,
CC   reverse transcription and/or replication of a target RNA in a system.
CC   They are useful for selectively preventing gene expression in a sequence-
CC   specific manner, for hybridising to complementary RNA such as cellular
CC   mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC   RNA. They are also useful therapeutically in formulations or medicaments
CC   to prevent or treat a disease characterised by the expression of a
CC   particular target RNA. The invention is used in gene therapy. The present
CC   sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC   H degradation of target RNA. This sequence is used in the exemplification
CC   of the invention
XX
SQ   Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2015
AAD56447/c
ID   AAD56447 standard; DNA; 17 BP.
XX
AC   AAD56447;
XX
DT   07-AUG-2003  (first entry)
XX
DE   2'F-ANA antisense oligo #2, to elicit RNase H degradation of target RNA.
XX
KW   Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
KW   antisense; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .17
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "2'-deoxy-2'-fluoroarabinothymidine"
FT   misc_feature     4. .5
FT                    /*tag=  b
FT                    /note= "Bases 4 and 5 are linked by a butanediol linker
FT                    which is represented as B in page 49 and Fig 5 and as X
FT                    in page 55 and Fig 6 of the specification"
XX
PN   WO2003037909-A1.
XX
PD   08-MAY-2003.
XX
PF   29-OCT-2002; 2002WO-CA001628.
XX
PR   29-OCT-2001; 2001US-0330719P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Viazovkina E,  Mangos MM,  Parniak MA,  Min K;
XX
DR   WPI; 2003-421516/39.
XX
PT   Novel acyclic linker-containing oligonucleotide useful for preventing or
PT   decreasing translation, reverse transcription and/or replication of a
PT   target RNA in a system, comprises a modified deoxyribonucleotide.
XX
PS   Example 2; Fig 5; 104pp; English.
```

```
XX
CC   The invention relates to an acyclic linker-containing oligonucleotide
CC   comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC   the invention are useful for preventing or decreasing translation,
CC   reverse transcription and/or replication of a target RNA in a system.
CC   They are useful for selectively preventing gene expression in a sequence-
CC   specific manner, for hybridising to complementary RNA such as cellular
CC   mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC   RNA. They are also useful therapeutically in formulations or medicaments
CC   to prevent or treat a disease characterised by the expression of a
CC   particular target RNA. The invention is used in gene therapy. The present
CC   sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC   H degradation of target RNA. This sequence is used in the exemplification
CC   of the invention
XX
SQ   Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 2016
AAD56450
ID   AAD56450 standard; DNA; 17 BP.
XX
AC   AAD56450;
XX
DT   07-AUG-2003  (first entry)
XX
DE   2'F-ANA antisense oligo #5, to elicit RNase H degradation of target RNA.
XX
KW   Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
KW   antisense; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .17
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "2'-deoxy-2'-fluoroarabinothymidine"
FT   misc_feature     9. .10
FT                    /*tag=  b
FT                    /note= "Bases 9 and 10 are linked by a secouridine linker
FT                    which is represented as S in page 49 and X in page 57 and
FT                    Fig 1, 2, 7 and 8 of the specification"
XX
PN   WO2003037909-A1.
XX
PD   08-MAY-2003.
XX
PF   29-OCT-2002; 2002WO-CA001628.
XX
PR   29-OCT-2001; 2001US-0330719P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Viazovkina E,  Mangos MM,  Parniak MA,  Min K;
XX
DR   WPI; 2003-421516/39.
XX
PT   Novel acyclic linker-containing oligonucleotide useful for preventing or
PT   decreasing translation, reverse transcription and/or replication of a
PT   target RNA in a system, comprises a modified deoxyribonucleotide.
XX
PS   Example 2; Fig 7; 104pp; English.
XX
CC   The invention relates to an acyclic linker-containing oligonucleotide
CC   comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC   the invention are useful for preventing or decreasing translation,
CC   reverse transcription and/or replication of a target RNA in a system.
CC   They are useful for selectively preventing gene expression in a sequence-
CC   specific manner, for hybridising to complementary RNA such as cellular
CC   mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC   RNA. They are also useful therapeutically in formulations or medicaments
CC   to prevent or treat a disease characterised by the expression of a
CC   particular target RNA. The invention is used in gene therapy. The present
CC   sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC   H degradation of target RNA. This sequence is used in the exemplification
CC   of the invention
XX
SQ   Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2017
AAD56450/c
ID   AAD56450 standard; DNA; 17 BP.
XX
AC   AAD56450;
XX
DT   07-AUG-2003  (first entry)
XX
DE   2'F-ANA antisense oligo #5, to elicit RNase H degradation of target RNA.
XX
KW   Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
KW   antisense; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .17
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "2'-deoxy-2'-fluoroarabinothymidine"
FT   misc_feature     9. .10
FT                    /*tag=  b
FT                    /note= "Bases 9 and 10 are linked by a secouridine linker
FT                    which is represented as S in page 49 and X in page 57 and
FT                    Fig 1, 2, 7 and 8 of the specification"
XX
PN   WO2003037909-A1.
XX
PD   08-MAY-2003.
XX
PF   29-OCT-2002; 2002WO-CA001628.
XX
PR   29-OCT-2001; 2001US-0330719P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Viazovkina E,  Mangos MM,  Parniak MA,  Min K;
XX
DR   WPI; 2003-421516/39.
XX
PT   Novel acyclic linker-containing oligonucleotide useful for preventing or
PT   decreasing translation, reverse transcription and/or replication of a
PT   target RNA in a system, comprises a modified deoxyribonucleotide.
XX
PS   Example 2; Fig 7; 104pp; English.
XX
CC   The invention relates to an acyclic linker-containing oligonucleotide
CC   comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC   the invention are useful for preventing or decreasing translation,
```

```
CC   reverse transcription and/or replication of a target RNA in a system.
CC   They are useful for selectively preventing gene expression in a sequence-
CC   specific manner, for hybridising to complementary RNA such as cellular
CC   mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC   RNA. They are also useful therapeutically in formulations or medicaments
CC   to prevent or treat a disease characterised by the expression of a
CC   particular target RNA. The invention is used in gene therapy. The present
CC   sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC   H degradation of target RNA. This sequence is used in the exemplification
CC   of the invention
XX
SQ   Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 2018
ACF36345/c
ID   ACF36345 standard; DNA; 17 BP.
XX
AC   ACF36345;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Nucleotide sequence of a double stranded product DNA fragment.
XX
KW   Gene variant identification; restriction enzyme; FokI; ds.
XX
OS   Synthetic.
XX
PN   WO2003064689-A2.
XX
PD   07-AUG-2003.
XX
PF   28-JAN-2003; 2003WO-IB000255.
XX
PR   29-JAN-2002; 2002US-0352245P.
XX
PA   (GLOB-) GLOBAL GENOMICS AB.
XX
PI   Lonnerberg P,  Oldin M,  Linnarsson S,  Ernfors P;
XX
DR   WPI; 2003-627619/59.
XX
PT   Determining polyadenylation sites within transcribed gene sequences
PT   present in a sample comprises assigning to gene fragments gene candidates
PT   within a database by comparing signals in the dataset with the database.
XX
PS   Example; Fig 3; 81pp; English.
XX
CC   The invention relates to determining the presence of and/or identifying a
CC   polyadenylation site within a sequence of a transcribed gene or variants
CC   present in a sample. The method involves assigning to gene fragments gene
CC   candidates within a database by comparing signals in the dataset with the
CC   database, the database comprising data representing mRNAs with known
CC   polyA sites and/or 'virtual genes' representing a possible
CC   polyadenylation site within an actual gene. The method is useful for
CC   determining the presence of and/or identifying a polyadenylation site or
CC   alternative polyadenylation sites within a sequence of a transcribed gene
CC   or sequences of transcribed gene variants present or potentially present
CC   in a sample, in identifying gene features, particularly in identifying
CC   differences between sequence variants that occur in a population of
CC   nucleic acid molecules, especially in identifying or discovering polyA
CC   site usage or determining polyA site usage in a nucleic acid sample, and
CC   gene variants arising from alternative polyA sites. The present sequence
CC   represents a double stranded product DNA fragment
XX
SQ   Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2801
              |||||||||||||||||
Db         17 GAAAAAAAAAAAAAAAA 1


RESULT 2019
ACF36370/c
ID   ACF36370 standard; DNA; 17 BP.
XX
AC   ACF36370;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Nucleotide sequence of a double stranded product DNA.
XX
KW   Nucleic acid manipulation; mRNA profiling; polymerase chain reaction;
KW   electrophoresis; type II restriction enzyme; FokI; ds.
XX
OS   Synthetic.
XX
PN   WO2003064691-A2.
XX
PD   07-AUG-2003.
XX
PF   28-JAN-2003; 2003WO-IB000843.
XX
PR   29-JAN-2002; 2002US-0352215P.
XX
PA   (GLOB-) GLOBAL GENOMICS AB.
XX
PI   Linnarsson S,  Ernfors P,  Bauren G,  Metsis A,  Pihlak A;
PI   Montelius A;
XX
DR   WPI; 2003-618365/58.
XX
PT   Producing a population of double-stranded product DNA molecules, useful
PT   for mRNA profiling, comprises amplification by nested polymerase chain
PT   reaction.
XX
PS   Example; Fig 2; 105pp; English.
XX
CC   The invention relates to producing a population of double-stranded
CC   product DNA molecules comprising amplification by a nested PCR method.
CC   The method is useful in profiling mRNA transcribed in a system under
CC   investigation. The oligonucleotides are used as size standards in
CC   electrophoresis, and as internal controls allowing for calculation of
CC   relative amounts of material present. The present sequence represents a
CC   double stranded product DNA, which aids in outlining an approach to
CC   production of a single pattern characteristic of a sample, employing a
CC   type II restriction enzyme (FokI)
XX
SQ   Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2801
              |||||||||||||||||
Db         17 GAAAAAAAAAAAAAAAA 1


RESULT 2020
ADB45110
ID   ADB45110 standard; DNA; 17 BP.
XX
AC   ADB45110;
```

```
XX
DT   18-DEC-2003  (first entry)
XX
DE   Tumour suppression/reversion associated nucleotide #5433.
XX
KW   cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW   primer; probe; tumour suppression; tumour reversion; apoptosis;
KW   virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW   diagnosis.
XX
OS   Homo sapiens.
XX
PN   WO2003040369-A2.
XX
PD   15-MAY-2003.
XX
PF   17-SEP-2002; 2002WO-IB004219.
XX
PR   17-SEP-2001; 2001FR-00011981.
XX
PA   (MOLE-) MOLECULAR ENGINES LAB.
XX
PI   Telerman A,  Amson R,  Tuijnder M;
XX
DR   WPI; 2003-441574/41.
XX
PT   New nucleic acid encoding human prostate membrane-specific antigen,
PT   useful e.g. for treatment of tumors and viral infection, also related
PT   polypeptide and antibodies.
XX
PS   Disclosure; Page 667; 771pp; French.
XX
CC   The invention relates to the isolation of 6327 nucleotide sequences,
CC   fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC   sequence having at least 80% identity, after optimal alignment, with the
CC   nucleotides, a sequence that hybridizes under stringent conditions with
CC   the nucleotides, or the complement, or corresponding RNA, of the
CC   nucleotides. The nucleotides are used as probes or primers for detecting,
CC   identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC   sense and antisense sequences, of nucleotides involved in tumour
CC   suppression or reversion, apoptosis and or viral resistance, to produce
CC   recombinant polypeptides, and to prepare transgenic animals, as
CC   experimental models. The nucleotides (also vectors containing them and
CC   cells containing the vectors), the encoded polypeptides and antibodies
CC   (Ab) against the polypeptide are useful for prevention and/or treatment
CC   of viral infections or diseases characterized by development of tumours
CC   or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC   Analysis of the expression of the nucleotides can be used for diagnosis
CC   and/or prognosis of these diseases. The nucleotides and polypeptides can
CC   also be used to screen for their specific interactive molecules,
CC   potentially useful for treating diseases associated with abnormal
CC   expression of the nucleotides.
XX
SQ   Sequence 17 BP; 6 A; 2 C; 1 G; 8 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2460 GATCCAATTTTAATATT 2476
              |||||||||||||||||
Db          1 GATCCAATTTTAATATT 17


RESULT 2021
AAT94667/c
ID   AAT94667 standard; DNA; 18 BP.
XX
AC   AAT94667;
XX
DT   27-MAR-1998  (first entry)
XX
DE   Anchored poly(T) oligonucleotide polyT-AnchA.
XX
KW   Flavonoid 3' hydroxylase; pigmentation; flower colour; transgenic plant;
KW   snapdragon; primer; ss.
XX
OS   Synthetic.
XX
PN   WO9732023-A1.
XX
PD   04-SEP-1997.
XX
PF   28-FEB-1997;   97WO-AU000124.
XX
PR   01-MAR-1996;   96AU-00008386.
XX
PA   (FLOR-) FLORIGENE LTD.
XX
PI   Brugliera F,  Holton TA,  Michael MZ;
XX
DR   WPI; 1997-448691/41.
XX
PT   Novel flavonoid 3'-hydroxylase(s) from flowering plants - and
PT   corresponding DNA, used in the manipulation of pigmentation in plants.
XX
PS   Example 15; Page 59; 234pp; English.
XX
CC   Anchored poly(T) oligonucleotides polyT-anchA (AAT94667), polyT-anchC
CC   (AAT94668) and polyT-anchG (AAT94669) are complementary to the upstream
CC   region of a polyadenylation sequence. They were used to prime cDNA
CC   synthesis from snapdragon (Antirrhinum majus) petal and leaf RNA, and
CC   were also utilised in the PCR amplification of plant cytochrome P450
CC   sequences (see also AAT94670-73). A cDNA clone (see AAT94657) encoding
CC   flavonoid 3' hydroxylase (see AAW35704) was isolated using a differential
CC   display approach. This can be used to manipulate the pigmentation of
CC   transgenic plants
XX
SQ   Sequence 18 BP; 1 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 2022
AAT94668
ID   AAT94668 standard; DNA; 18 BP.
XX
AC   AAT94668;
XX
DT   27-MAR-1998  (first entry)
XX
DE   Anchored poly(T) oligonucleotide polyT-AnchC.
XX
KW   Flavonoid 3' hydroxylase; pigmentation; flower colour; transgenic plant;
KW   snapdragon; primer; ss.
XX
OS   Synthetic.
XX
PN   WO9732023-A1.
XX
PD   04-SEP-1997.
XX
PF   28-FEB-1997;   97WO-AU000124.
XX
PR   01-MAR-1996;   96AU-00008386.
XX
PA   (FLOR-) FLORIGENE LTD.
XX
PI   Brugliera F,  Holton TA,  Michael MZ;
XX
```

```
DR   WPI; 1997-448691/41.
XX
PT   Novel flavonoid 3'-hydroxylase(s) from flowering plants - and
PT   corresponding DNA, used in the manipulation of pigmentation in plants.
XX
PS   Example 15; Page 59; 234pp; English.
XX
CC   Anchored poly(T) oligonucleotides polyT-anchA (AAT94667), polyT-anchC
CC   (AAT94668) and polyT-anchG (AAT94669) are complementary to the upstream
CC   region of a polyadenylation sequence. They were used to prime cDNA
CC   synthesis from snapdragon (Antirrhinum majus) petal and leaf RNA, and
CC   were also utilised in the PCR amplification of plant cytochrome P450
CC   sequences (see also AAT94670-73). A cDNA clone (see AAT94657) encoding
CC   flavonoid 3' hydroxylase (see AAW35704) was isolated using a differential
CC   display approach. This can be used to manipulate the pigmentation of
CC   transgenic plants
XX
SQ   Sequence 18 BP; 0 A; 1 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2023
AAV37712/c
ID   AAV37712 standard; cDNA; 18 BP.
XX
AC   AAV37712;
XX
DT   25-MAR-2003  (revised)
DT   07-SEP-1998  (first entry)
XX
DE   Human protein AQ2_1i 3'-portion and polyA tail.
XX
KW   Human; secreted protein; murine adult spleen; human foetal kidney; ovary;
KW   bone marrow; thymus; AE648_1i; AE693_1i; AK438_1i; AK609_1i; AM1060_1i;
KW   AQ2_1i; K433_1i; L256_1i; prevent; treat; ameliorate; medical; ds.
XX
OS   Homo sapiens.
XX
PN   WO9820130-A2.
XX
PD   14-MAY-1998.
XX
PF   31-OCT-1997;   97WO-US019857.
XX
PR   01-NOV-1996;   96US-00742973.
PR   29-OCT-1997;   97US-00960024.
XX
PA   (GEMY ) GENETICS INST INC.
XX
PI   Jacobs K,  Mccoy JM,  Lavallie ER,  Racie LA,  Merberg D,  Treacy M;
PI   Spaulding V,  Agostino MJ;
XX
DR   WPI; 1998-286946/25.
XX
PT   New secreted proteins and associated polynucleotides - obtained from
PT   murine adult spleen, human foetal kidney, human ovary, murine bone marrow
PT   and murine adult thymus.
XX
PS   Disclosure; Page 58; 75pp; English.
XX
CC   The present invention describes novel proteins isolated from cDNA clones:
CC   AE648_1i; AE693_1i; AK438_1i; AK609_1i; AM1060_1i; AQ2_1i; K433_1i; or
CC   L256_1i, deposited as ATCC 98237. The present sequence represents the 3'-
CC   portion of AQ2_1i isolated from a human ovary cDNA library. The proteins
CC   from the present invention may be administered in a composition to
CC   prevent, treat or ameliorate a medical condition. The proteins may
CC   exhibit biological activities such as nutritional activity, cytokine and
CC   cell proliferation/differentiation activity, immune stimulating or
CC   suppressing activity, haematopoiesis regulating activity, tissue growth
CC   activity, activin/inhibin activity, chemotactic/chemokinetic activity,
CC   haemostatic and thrombotic activity, receptor/ligand activity, anti-
CC   inflammatory activity, cadherin/tumour invasion suppressor activity,
CC   tumour inhibition activity and other activities. (Updated on 25-MAR-2003
CC   to correct PR field.)
XX
SQ   Sequence 18 BP; 17 A; 0 C; 1 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          18 TTTTTTTTTTTTTTTTT 2


RESULT 2024
AAA40563/c
ID   AAA40563 standard; cDNA; 18 BP.
XX
AC   AAA40563;
XX
DT   16-NOV-2000  (first entry)
XX
DE   Human adult ovary cDNA fragment AQ2_1i #2.
XX
KW   Secreted protein; cytostatic; immunostimulatory; antimicrobial;
KW   antiviral; immunosuppressive; antiinflammatory; vulnerary; cytokine;
KW   cell proliferation; differentiation; regulator; treatment; tumor;
KW   autoimmune disease; inflammatory disorder; wound; microbial infection;
KW   viral disease; graft versus host reaction suppression; ss.
XX
OS   Homo sapiens.
XX
PN   WO200037630-A1.
XX
PD   29-JUN-2000.
XX
PF   22-DEC-1999;   99WO-US031005.
XX
PR   23-DEC-1998;   98US-00220876.
XX
PA   (GEMY ) GENETICS INST INC.
XX
PI   Jacobs K,  Mccoy JM,  Lavallie ER,  Collins-Racie LA,  Evans C;
PI   Merberg D,  Treacy M,  Bowman MR;
XX
DR   WPI; 2000-442661/38.
DR   P-PSDB; AAB10274.
XX
PT   Secreted human proteins AS296-1i and AS34-1i, useful for treating tumors,
PT   autoimmune diseases, inflammatory disorders, wounds, microbial infections
PT   and viral diseases.
XX
PS   Disclosure; Page 269; 293pp; English.
XX
CC   This invention describes novel secreted human proteins (I) which have
CC   cytostatic, immunostimulatory, antimicrobial, antiviral,
CC   immunosuppressive, antiinflammatory and vulnerary activity and which act
CC   as cytokine, cell proliferation or differentiation regulators. (I) is
CC   useful for treating tumors, autoimmune diseases, inflammatory disorders,
CC   wounds, microbial infections and viral diseases. (I) is also useful for
CC   suppressing graft versus host reaction. AAA40490-A40580 represent cDNA
CC   fragments that encode the secreted proteins AAB10226-B10288 described in
CC   the method of the invention
XX
SQ   Sequence 18 BP; 17 A; 0 C; 1 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 18;
```

```
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db         18 TTTTTTTTTTTTTTTTT 2


RESULT 2025
AAT94669
ID   AAT94669 standard; DNA; 18 BP.
XX
AC   AAT94669;
XX
DT   27-MAR-1998  (first entry)
XX
DE   Anchored poly(T) oligonucleotide polyT-AnchG.
XX
KW   Flavonoid 3' hydroxylase; pigmentation; flower colour; transgenic plant;
KW   snapdragon; primer; ss.
XX
OS   Synthetic.
XX
PN   WO9732023-A1.
XX
PD   04-SEP-1997.
XX
PF   28-FEB-1997;   97WO-AU000124.
XX
PR   01-MAR-1996;   96AU-00008386.
XX
PA   (FLOR-) FLORIGENE LTD.
XX
PI   Brugliera F,  Holton TA,  Michael MZ;
XX
DR   WPI; 1997-448691/41.
XX
PT   Novel flavonoid 3'-hydroxylase(s) from flowering plants - and
PT   corresponding DNA, used in the manipulation of pigmentation in plants.
XX
PS   Example 15; Page 59; 234pp; English.
XX
CC   Anchored poly(T) oligonucleotides polyT-anchA (AAT94667), polyT-anchC
CC   (AAT94668) and polyT-anchG (AAT94669) are complementary to the upstream
CC   region of a polyadenylation sequence. They were used to prime cDNA
CC   synthesis from snapdragon (Antirrhinum majus) petal and leaf RNA, and
CC   were also utilised in the PCR amplification of plant cytochrome P450
CC   sequences (see also AAT94670-73). A cDNA clone (see AAT94657) encoding
CC   flavonoid 3' hydroxylase (see AAW35704) was isolated using a differential
CC   display approach. This can be used to manipulate the pigmentation of
CC   transgenic plants
XX
SQ   Sequence 18 BP; 0 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2026
AAT94669/c
ID   AAT94669 standard; DNA; 18 BP.
XX
AC   AAT94669;
XX
DT   27-MAR-1998  (first entry)
XX
DE   Anchored poly(T) oligonucleotide polyT-AnchG.
XX
KW   Flavonoid 3' hydroxylase; pigmentation; flower colour; transgenic plant;
KW   snapdragon; primer; ss.
XX
OS   Synthetic.
XX
PN   WO9732023-A1.
XX
PD   04-SEP-1997.
XX
PF   28-FEB-1997;   97WO-AU000124.
XX
PR   01-MAR-1996;   96AU-00008386.
XX
PA   (FLOR-) FLORIGENE LTD.
XX
PI   Brugliera F,  Holton TA,  Michael MZ;
XX
DR   WPI; 1997-448691/41.
XX
PT   Novel flavonoid 3'-hydroxylase(s) from flowering plants - and
PT   corresponding DNA, used in the manipulation of pigmentation in plants.
XX
PS   Example 15; Page 59; 234pp; English.
XX
CC   Anchored poly(T) oligonucleotides polyT-anchA (AAT94667), polyT-anchC
CC   (AAT94668) and polyT-anchG (AAT94669) are complementary to the upstream
CC   region of a polyadenylation sequence. They were used to prime cDNA
CC   synthesis from snapdragon (Antirrhinum majus) petal and leaf RNA, and
CC   were also utilised in the PCR amplification of plant cytochrome P450
CC   sequences (see also AAT94670-73). A cDNA clone (see AAT94657) encoding
CC   flavonoid 3' hydroxylase (see AAW35704) was isolated using a differential
CC   display approach. This can be used to manipulate the pigmentation of
CC   transgenic plants
XX
SQ   Sequence 18 BP; 0 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 2027
AAV54164
ID   AAV54164 standard; cDNA; 18 BP.
XX
AC   AAV54164;
XX
DT   21-DEC-1998  (first entry)
XX
DE   Nucleotide sequence PCR primer 1.
XX
KW   PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW   immunohistological staining.
XX
OS   Synthetic.
XX
PN   WO9839437-A1.
XX
PD   11-SEP-1998.
XX
PF   05-MAR-1998;   98WO-JP000905.
XX
PR   05-MAR-1997;   97JP-00050302.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Sakaki Y;
XX
DR   WPI; 1998-495844/42.
```

```
XX
PT   Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT   treating diseases associated with apoptosis.
XX
PS   Example 1; Page 47; 70pp; Japanese.
XX
CC   This is the nucleotide sequence of a PCR primer used in the method of the
CC   invention, involving the use of novel apoptosis-related DNAs and
CC   proteins. The inventions can be used as diagnostic reagents for apoptosis
CC   e.g. (monoclonal) antibodies for the protein, as a reagent in
CC   immunohistological staining, as apoptosis inhibitors. It can also be used
CC   for treatment of apoptosis-related diseases
XX
SQ   Sequence 18 BP; 2 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTAA 2188
              |||||||||||||||||
Db          2 TTTTTTTTTTTTTTTAA 18


RESULT 2028
AAV54166/c
ID   AAV54166 standard; cDNA; 18 BP.
XX
AC   AAV54166;
XX
DT   21-DEC-1998  (first entry)
XX
DE   Nucleotide sequence PCR primer 3.
XX
KW   PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW   immunohistological staining.
XX
OS   Synthetic.
XX
PN   WO9839437-A1.
XX
PD   11-SEP-1998.
XX
PF   05-MAR-1998;   98WO-JP000905.
XX
PR   05-MAR-1997;   97JP-00050302.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Sakaki Y;
XX
DR   WPI; 1998-495844/42.
XX
PT   Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT   treating diseases associated with apoptosis.
XX
PS   Example 1; Page 48; 70pp; Japanese.
XX
CC   This is the nucleotide sequence of a PCR primer used in the method of the
CC   invention, involving the use of novel apoptosis-related DNAs and
CC   proteins. The inventions can be used as diagnostic reagents for apoptosis
CC   e.g. (monoclonal) antibodies for the protein, as a reagent in
CC   immunohistological staining, as apoptosis inhibitors. It can also be used
CC   for treatment of apoptosis-related diseases
XX
SQ   Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAA 2800
              |||||||||||||||||
Db         18 TGAAAAAAAAAAAAAAA 2


RESULT 2029
AAV07750
ID   AAV07750 standard; DNA; 18 BP.
XX
AC   AAV07750;
XX
DT   02-DEC-1998  (first entry)
XX
DE   Phosphorothioate oligodeoxynucleotide.
XX
KW   phosphorothioate; electrospray ionisation-Fourier transform;
KW   mass spectrometry; off-resonance excitation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1. .18
FT                   /*tag=  a
FT                   /note= "phosphorothioate internucleotide linkages"
XX
PN   WO9840520-A1.
XX
PD   17-SEP-1998.
XX
PF   12-MAR-1998;   98WO-US004919.
XX
PR   14-MAR-1997;   97US-0040717P.
XX
PA   (HYBR-) HYBRIDON INC.
XX
PI   Wang BH;
XX
DR   WPI; 1998-520830/44.
XX
PT   Determining the nucleotide sequence of a nucleic acid analyte - using
PT   electro-spray ionisation.
XX
PS   Example 1; Fig 3A; 25pp; English.
XX
CC   The invention relates to an analytical method for determining the
CC   nucleotide sequence of nucleic acid analytes, including chemically
CC   modified oligonucleotides. This new method utilises electrospray
CC   ionisation-Fourier transform mass spectrometry. The ions are excited by
CC   sustained off-resonance excitation with single shot excitation, and the
CC   target fragmented by collisionally activated dissociation by a neutral
CC   gas, e.g. carbon dioxide. Alternatively, the excitation and dissociation
CC   can be nozzle skimmer dissociation. The method is used in molecular
CC   biology and biomedical applications. The method, utilising electrospray
CC   ionisation-Fourier transform ion cyclotron resonance mass spectrometry,
CC   is extremely rapid and acts directly on the oligonucleotide. The method
CC   is effective for a variety of nucleic acid analytes, particularly
CC   chemically modified oligonucleotides which have not previously been
CC   successfully sequenced. The present sequence represents a
CC   phosphorothioate oligodeoxynucleotide
XX
SQ   Sequence 18 BP; 17 A; 0 C; 0 G; 1 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAA 17


RESULT 2030
AAV07750/c
ID   AAV07750 standard; DNA; 18 BP.
XX
```

```
AC   AAV07750;
XX
DT   02-DEC-1998  (first entry)
XX
DE   Phosphorothioate oligodeoxynucleotide.
XX
KW   phosphorothioate; electrospray ionisation-Fourier transform;
KW   mass spectrometry; off-resonance excitation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1. .18
FT                   /*tag= a
FT                   /note= "phosphorothioate internucleotide linkages"
XX
PN   WO9840520-A1.
XX
PD   17-SEP-1998.
XX
PF   12-MAR-1998;   98WO-US004919.
XX
PR   14-MAR-1997;   97US-0040717P.
XX
PA   (HYBR-) HYBRIDON INC.
XX
PI   Wang BH;
XX
DR   WPI; 1998-520830/44.
XX
PT   Determining the nucleotide sequence of a nucleic acid analyte - using
PT   electro-spray ionisation.
XX
PS   Example 1; Fig 3A; 25pp; English.
XX
CC   The invention relates to an analytical method for determining the
CC   nucleotide sequence of nucleic acid analytes, including chemically
CC   modified oligonucleotides. This new method utilises electrospray
CC   ionisation-Fourier transform mass spectrometry. The ions are excited by
CC   sustained off-resonance excitation with single shot excitation, and the
CC   target fragmented by collisionally activated dissociation by a neutral
CC   gas, e.g. carbon dioxide. Alternatively, the excitation and dissociation
CC   can be nozzle skimmer dissociation. The method is used in molecular
CC   biology and biomedical applications. The method, utilising electrospray
CC   ionisation-Fourier transform ion cyclotron resonance mass spectrometry,
CC   is extremely rapid and acts directly on the oligonucleotide. The method
CC   is effective for a variety of nucleic acid analytes, particularly
CC   chemically modified oligonucleotides which have not previously been
CC   successfully sequenced. The present sequence represents a
CC   phosphorothioate oligodeoxynucleotide
XX
SQ   Sequence 18 BP; 17 A; 0 C; 0 G; 1 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db         17 TTTTTTTTTTTTTTTTT 1


RESULT 2031
AAX18373
ID   AAX18373 standard; DNA; 18 BP.
XX
AC   AAX18373;
XX
DT   11-MAY-1999  (first entry)
XX
DE   RT-PCR primer of the invention SEQ ID 14.
XX
KW   RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS   Synthetic.
XX
PN   JP11032765-A.
XX
PD   09-FEB-1999.
XX
PF   18-JUL-1997;   97JP-00208312.
XX
PR   18-JUL-1997;   97JP-00208312.
XX
PA   (TAKI ) TAKARA SHUZO CO LTD.
XX
DR   WPI; 1999-183822/16.
XX
PT   Peptides having at least two new nucleotides - useful as primers in RT-
PT   PCR.
XX
PS   Disclosure; Page 11; 19pp; Japanese.
XX
CC   This sequence represents a primer of the invention. The invention relates
CC   to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC   -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC   a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC   natural number indicating the repetition of alpha; beta, delta = V or N;
CC   V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC   thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC   repetition of gamma, in which thymine expressed by gamma is composed of
CC   1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC   useful as primers for RT-PCR and determination of base sequences. The new
CC   sequences allow for reproductive and highly efficient analysis of gene
CC   sequences
XX
SQ   Sequence 18 BP; 1 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTA 17


RESULT 2032
AAZ90648/c
ID   AAZ90648 standard; DNA; 18 BP.
XX
AC   AAZ90648;
XX
DT   13-JUN-2000  (first entry)
XX
DE   Human adipose tissue gene amplifying primer #9.
XX
KW   Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW   arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2000037190-A.
XX
PD   08-FEB-2000.
XX
PF   23-JUL-1998;   98JP-00225228.
XX
PR   23-JUL-1998;   98JP-00225228.
XX
PA   (NISB ) JAPAN TOBACCO INC.
XX
DR   WPI; 2000-306578/27.
XX
PT   A physiologically active protein specifically derived from mammal tissue.
XX
```

```
PS   Example 2; Page 18; 50pp; Japanese.
XX
CC   The invention relates to identification of genes and proteins of adipose
CC   tissue relating to obesity, particularly complications of visceral
CC   obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC   hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC   proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention
CC   and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC   represent PCR primers amplifying the human adipose tissue genes
XX
SQ   Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAA 2800
              |||||||||||||||||
Db         18 TGAAAAAAAAAAAAAAA 2


RESULT 2033
AAZ90646
ID   AAZ90646 standard; DNA; 18 BP.
XX
AC   AAZ90646;
XX
DT   13-JUN-2000  (first entry)
XX
DE   Human adipose tissue gene amplifying primer #7.
XX
KW   Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW   arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2000037190-A.
XX
PD   08-FEB-2000.
XX
PF   23-JUL-1998;   98JP-00225228.
XX
PR   23-JUL-1998;   98JP-00225228.
XX
PA   (NISB ) JAPAN TOBACCO INC.
XX
DR   WPI; 2000-306578/27.
XX
PT   A physiologically active protein specifically derived from mammal tissue.
XX
PS   Example 2; Page 18; 50pp; Japanese.
XX
CC   The invention relates to identification of genes and proteins of adipose
CC   tissue relating to obesity, particularly complications of visceral
CC   obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC   hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC   proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention
CC   and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC   represent PCR primers amplifying the human adipose tissue genes
XX
SQ   Sequence 18 BP; 2 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTAA 2188
              |||||||||||||||||
Db          2 TTTTTTTTTTTTTTTAA 18


RESULT 2034
AAD20091
ID   AAD20091 standard; mRNA; 18 BP.
XX
AC   AAD20091;
XX
DT   03-JAN-2002  (first entry)
XX
DE   mRNA fragment used in 3' end PCR/IVT method of the invention.
XX
KW   RNA polymerase; RNAP; RNA detection; IVT; in vitro transcription; ss.
XX
OS   Unidentified.
XX
PN   US6271002-B1.
XX
PD   07-AUG-2001.
XX
PF   04-OCT-1999;   99US-00411074.
XX
PR   04-OCT-1999;   99US-00411074.
XX
PA   (ROSE-) ROSETTA INPHARMATICS INC.
XX
PI   Linsley PS,  Schelter JM;
XX
DR   WPI; 2001-624273/72.
XX
PT   Amplifying and detecting RNA derived from a population of cells by
PT   employing a primer that contains an RNA polymerase promoter in a
PT   polymerase chain reaction.
XX
PS   Example 3; Fig 1; 29pp; English.
XX
CC   The invention relates to methods and kits for amplification of mRNA using
CC   a primer in PCR that contains an RNA polymerase (RNAP) promoter. The
CC   invention provides methods for amplification and detection of RNA derived
CC   from a population of cells, preferably eukaryotic cells and most
CC   preferably mammalian cells, which methods preserve fidelity with respect
CC   to sequence and transcript representation and additionally enable
CC   amplification of extremely small amounts of mRNA. The method and kit are
CC   useful for amplifying and detecting RNA derived from a population of
CC   cells, especially eukaryotic cells like mammals. The RNAs generated are
CC   useful for profiling gene expression in different populations of cells.
CC   The present sequence is a mRNA fragment used in 3' end PCR/IVT (in vitro
CC   transcription) method of the invention
XX
SQ   Sequence 18 BP; 17 A; 0 C; 0 G; 0 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db          2 AAAAAAAAAAAAAAAAA 18


RESULT 2035
AAD20091/c
ID   AAD20091 standard; mRNA; 18 BP.
XX
AC   AAD20091;
XX
DT   03-JAN-2002  (first entry)
XX
DE   mRNA fragment used in 3' end PCR/IVT method of the invention.
XX
KW   RNA polymerase; RNAP; RNA detection; IVT; in vitro transcription; ss.
XX
OS   Unidentified.
XX
PN   US6271002-B1.
XX
PD   07-AUG-2001.
```

```
XX
PF   04-OCT-1999;   99US-00411074.
XX
PR   04-OCT-1999;   99US-00411074.
XX
PA   (ROSE-) ROSETTA INPHARMATICS INC.
XX
PI   Linsley PS,  Schelter JM;
XX
DR   WPI; 2001-624273/72.
XX
PT   Amplifying and detecting RNA derived from a population of cells by
PT   employing a primer that contains an RNA polymerase promoter in a
PT   polymerase chain reaction.
XX
PS   Example 3; Fig 1; 29pp; English.
XX
CC   The invention relates to methods and kits for amplification of mRNA using
CC   a primer in PCR that contains an RNA polymerase (RNAP) promoter. The
CC   invention provides methods for amplification and detection of RNA derived
CC   from a population of cells, preferably eukaryotic cells and most
CC   preferably mammalian cells, which methods preserve fidelity with respect
CC   to sequence and transcript representation and additionally enable
CC   amplification of extremely small amounts of mRNA. The method and kit are
CC   useful for amplifying and detecting RNA derived from a population of
CC   cells, especially eukaryotic cells like mammals. The RNAs generated are
CC   useful for profiling gene expression in different populations of cells.
CC   The present sequence is a mRNA fragment used in 3' end PCR/IVT (in vitro
CC   transcription) method of the invention
XX
SQ   Sequence 18 BP; 17 A; 0 C; 0 G; 0 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db         18 TTTTTTTTTTTTTTTTT 2

RESULT 2036
ABK13935/c
ID   ABK13935 standard; DNA; 18 BP.
XX
AC   ABK13935;
XX
DT   21-MAY-2002  (first entry)
XX
DE   5'-PCR primer used to produce single pattern characteristic by HaeII.
XX
KW   Identification of transcribed gene; mRNA profile; gene expression;
KW   cellular process; fingerprinting; susceptibility to external factor;
KW   development; disease; PCR; primer; ss.
XX
OS   Synthetic.
XX
PN   WO200208461-A2.
XX
PD   31-JAN-2002.
XX
PF   23-JUL-2001; 2001WO-IB001539.
XX
PR   21-JUL-2000; 2000GB-00018016.
PR   21-JUL-2000; 2000US-0219925P.
XX
PA   (GLOB-) GLOBAL GENOMICS AB.
XX
PI   Linnarsson S,  Ernfors P,  Bauren G;
XX
DR   WPI; 2002-217065/27.
XX
PT   Providing mRNA profile, by generating two independent patterns
PT   characteristic of sample mRNA population, analyzing patterns, comparing
PT   gene expression by cell types under varied conditions, and identifying
PT   genes.
XX
PS   Disclosure; Fig 1; 67pp; English.
XX
CC   The present invention relates to a method for providing a profile of mRNA
CC   molecules present in a sample. The method comprises generating two
CC   independent patterns characteristic of the population of mRNA molecules
CC   expressed in the sample and analysing the patterns using a combinatorial
CC   algorithm, comparing gene expression by different or same cell types
CC   under different conditions, and identifying genes having a role in
CC   various cellular processes. The method is useful for the analysis and
CC   identification of transcribed genes, and fingerprinting. The method can
CC   be used to identify genes which play a role in determining various
CC   cellular processes, including susceptibility to external factors,
CC   development, and disease. The present sequence for a PCR primer is used
CC   in the production of a single pattern characteristic of a sample,
CC   employing a Type II restriction enzyme (i.e. HaeII) in the methods of the
CC   present invention
XX
SQ   Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2801
              |||||||||||||||||
Db         17 GAAAAAAAAAAAAAAAA 1

RESULT 2037
ACF36339/c
ID   ACF36339 standard; DNA; 18 BP.
XX
AC   ACF36339;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Nucleotide sequence of a double stranded product DNA fragment.
XX
KW   Gene variant identification; restriction enzyme; HaeII; ds.
XX
OS   Synthetic.
XX
PN   WO2003064689-A2.
XX
PD   07-AUG-2003.
XX
PF   28-JAN-2003; 2003WO-IB000255.
XX
PR   29-JAN-2002; 2002US-0352245P.
XX
PA   (GLOB-) GLOBAL GENOMICS AB.
XX
PI   Lonnerberg P,  Oldin M,  Linnarsson S,  Ernfors P;
XX
DR   WPI; 2003-627619/59.
XX
PT   Determining polyadenylation sites within transcribed gene sequences
PT   present in a sample comprises assigning to gene fragments gene candidates
PT   within a database by comparing signals in the dataset with the database.
XX
PS   Example; Fig 2; 81pp; English.
XX
CC   The invention relates to determining the presence of and/or identifying a
CC   polyadenylation site within a sequence of a transcribed gene or variants
CC   present in a sample. The method involves assigning to gene fragments gene
CC   candidates within a database by comparing signals in the dataset with the
CC   database, the database comprising data representing mRNAs with known
CC   polyA sites and/or 'virtual genes' representing a possible
CC   polyadenylation site within an actual gene. The method is useful for
```

```
CC   determining the presence of and/or identifying a polyadenylation site or
CC   alternative polyadenylation sites within a sequence of a transcribed gene
CC   or sequences of transcribed gene variants present or potentially present
CC   in a sample, in identifying gene features, particularly in identifying
CC   differences between sequence variants that occur in a population of
CC   nucleic acid molecules, especially in identifying or discovering polyA
CC   site usage or determining polyA site usage in a nucleic acid sample, and
CC   gene variants arising from alternative polyA sites. The present sequence
CC   represents a double stranded product DNA fragment
XX
SQ   Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2801
              |||||||||||||||||
Db         17 GAAAAAAAAAAAAAAAA 1


RESULT 2038
ACF36364/c
ID   ACF36364 standard; DNA; 18 BP.
XX
AC   ACF36364;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Nucleotide sequence of a double stranded product DNA.
XX
KW   Nucleic acid manipulation; mRNA profiling; polymerase chain reaction;
KW   electrophoresis; type II restriction enzyme; HaeII; ds.
XX
OS   Synthetic.
XX
PN   WO2003064691-A2.
XX
PD   07-AUG-2003.
XX
PF   28-JAN-2003; 2003WO-IB000843.
XX
PR   29-JAN-2002; 2002US-0352215P.
XX
PA   (GLOB-) GLOBAL GENOMICS AB.
XX
PI   Linnarsson S,  Ernfors P,  Bauren G,  Metsis A,  Pihlak A;
PI   Montelius A;
XX
DR   WPI; 2003-618365/58.
XX
PT   Producing a population of double-stranded product DNA molecules, useful
PT   for mRNA profiling, comprises amplification by nested polymerase chain
PT   reaction.
XX
PS   Example; Fig 1; 105pp; English.
XX
CC   The invention relates to producing a population of double-stranded
CC   product DNA molecules comprising amplification by a nested PCR method.
CC   The method is useful in profiling mRNA transcribed in a system under
CC   investigation. The oligonucleotides are used as size standards in
CC   electrophoresis, and as internal controls allowing for calculation of
CC   relative amounts of material present. The present sequence represents a
CC   double stranded product DNA, which aids in outlining an approach to
CC   production of a single pattern characteristic of a sample, employing a
CC   type II restriction enzyme (HaeII)
XX
SQ   Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2801
              |||||||||||||||||
Db         17 GAAAAAAAAAAAAAAAA 1


RESULT 2039
AAQ75558
ID   AAQ75558 standard; DNA; 19 BP.
XX
AC   AAQ75558;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 19 BP; 0 A; 2 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2040
AAQ75551/c
ID   AAQ75551 standard; DNA; 19 BP.
XX
AC   AAQ75551;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
```

```
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 19 BP; 1 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 2041
AAQ75555
ID   AAQ75555 standard; DNA; 19 BP.
XX
AC   AAQ75555;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 19 BP; 0 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2042
AAQ75550
ID   AAQ75550 standard; DNA; 19 BP.
XX
AC   AAQ75550;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 19 BP; 0 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2043
AAQ75547
ID   AAQ75547 standard; DNA; 19 BP.
XX
AC   AAQ75547;
XX
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```
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 19 BP; 0 A; 0 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 17


RESULT 2044
AAQ75547/c
ID   AAQ75547 standard; DNA; 19 BP.
XX
AC   AAQ75547;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 19 BP; 0 A; 0 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2802
              ||||||||||||||||
Db         17 AAAAAAAAAAAAAAAA 1


RESULT 2045
AAQ49436/c
ID   AAQ49436 standard; cDNA; 20 BP.
XX
AC   AAQ49436;
XX
DT   25-MAR-2003  (revised)
DT   27-APR-1994  (first entry)
XX
DE   Cytochrome P450 sequence amplification PCR primer polyT.
XX
KW   Transgenic plants; altered petal colour; polymerase chain reaction; ss.
XX
OS   Synthetic.
XX
PN   WO9320206-A1.
XX
PD   14-OCT-1993.
XX
PF   25-MAR-1993;   93WO-AU000127.
XX
PR   27-MAR-1992;   92AU-00001538.
PR   07-JAN-1993;   93AU-00006698.
XX
PA   (ITFL-) INT FLOWER DEV PTY LTD.
XX
PI   Holton TA,  Cornish EC,  Tanaka Y;
XX
DR   WPI; 1993-336914/42.
XX
PT   Nucleic acid isolate encoding flavonoid-3'-hydroxylase - is used to
PT   create transgenic plants with altered petal colour.
XX
PS   Disclosure; Page 25; 86pp; English.
XX
CC   The sequence is that of a PCR primer which was used in polymerase chain
CC   reactions for the amplification of cloned cytochrome P450 sequences.
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2802
              ||||||||||||||||
Db         17 AAAAAAAAAAAAAAAA 1
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RESULT 2046
AAQ75572
ID   AAQ75572 standard; DNA; 20 BP.
XX
AC   AAQ75572;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 17


RESULT 2047
AAQ75604
ID   AAQ75604 standard; DNA; 20 BP.
XX
AC   AAQ75604;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 1 A; 2 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 17


RESULT 2048
AAQ75578/c
ID   AAQ75578 standard; DNA; 20 BP.
XX
AC   AAQ75578;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
```

```
XX
SQ   Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 2049
AAQ75592
ID   AAQ75592 standard; DNA; 20 BP.
XX
AC   AAQ75592;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2050
ABZ88266
ID   ABZ88266 standard; DNA; 20 BP.
XX
AC   ABZ88266;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 3508; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 17 A; 1 C; 1 G; 1 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db          4 AAAAAAAAAAAAAAAAA 20


RESULT 2051
AAQ75591
ID   AAQ75591 standard; DNA; 20 BP.
XX
AC   AAQ75591;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
```

```
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 0 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2052
AAQ75605
ID   AAQ75605 standard; DNA; 20 BP.
XX
AC   AAQ75605;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 0 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2053
AAQ75575/c
ID   AAQ75575 standard; DNA; 20 BP.
XX
AC   AAQ75575;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 1 A; 0 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1
```

```
RESULT 2054
AAQ75577/c
ID   AAQ75577 standard; DNA; 20 BP.
XX
AC   AAQ75577;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 2055
AAQ75593
ID   AAQ75593 standard; DNA; 20 BP.
XX
AC   AAQ75593;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2056
AAQ75594
ID   AAQ75594 standard; DNA; 20 BP.
XX
AC   AAQ75594;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
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```
SQ   Sequence 20 BP; 0 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2057
AAQ75606
ID   AAQ75606 standard; DNA; 20 BP.
XX
AC   AAQ75606;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 0 A; 3 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2058
AAQ75603
ID   AAQ75603 standard; DNA; 20 BP.
XX
AC   AAQ75603;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 0 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2059
AAQ75576/c
ID   AAQ75576 standard; DNA; 20 BP.
XX
AC   AAQ75576;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
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XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 2 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 2060
ABZ89896/c
ID   ABZ89896 standard; DNA; 20 BP.
XX
AC   ABZ89896;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 5138; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 18 A; 0 C; 2 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTT 4


RESULT 2061
ABZ89719
ID   ABZ89719 standard; DNA; 20 BP.
XX
AC   ABZ89719;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 4961; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
```

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CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          3 TTTTTTTTTTTTTTTTT 19


RESULT 2062
AAQ75574
ID   AAQ75574 standard; DNA; 20 BP.
XX
AC   AAQ75574;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 0 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2063
AAQ75573
ID   AAQ75573 standard; DNA; 20 BP.
XX
AC   AAQ75573;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2064
AAQ75571
ID   AAQ75571 standard; DNA; 20 BP.
XX
AC   AAQ75571;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
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PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 0 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2065
AAQ75559
ID   AAQ75559 standard; DNA; 20 BP.
XX
AC   AAQ75559;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 0 A; 0 C; 3 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2066
AAQ75559/c
ID   AAQ75559 standard; DNA; 20 BP.
XX
AC   AAQ75559;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 0 A; 0 C; 3 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 2067
AAQ75560
ID   AAQ75560 standard; DNA; 20 BP.
XX
AC   AAQ75560;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
```

```
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 1 A; 0 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2068
AAQ75560/c
ID   AAQ75560 standard; DNA; 20 BP.
XX
AC   AAQ75560;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 1 A; 0 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 2069
AAQ75561
ID   AAQ75561 standard; DNA; 20 BP.
XX
AC   AAQ75561;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2070
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```
AAQ75561/c
ID   AAQ75561 standard; DNA; 20 BP.
XX
AC   AAQ75561;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 2071
AAQ75562
ID   AAQ75562 standard; DNA; 20 BP.
XX
AC   AAQ75562;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 0 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2072
AAQ75562/c
ID   AAQ75562 standard; DNA; 20 BP.
XX
AC   AAQ75562;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 0 A; 1 C; 2 G; 17 T; 0 U; 0 Other;
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```
  Query Match             0.6%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 2073
ABQ79871
ID   ABQ79871 standard; DNA; 20 BP.
XX
AC   ABQ79871;
XX
DT   23-DEC-2002  (first entry)
XX
DE   Nucleotide sequence of a PCR primer #1.
XX
KW   Polymerase chain reaction; thermal cycle; immobilisation;
KW   genetic engineering; PCR; primer; ss.
XX
OS   Synthetic.
XX
PN   JP2002191369-A.
XX
PD   09-JUL-2002.
XX
PF   27-DEC-2000; 2000JP-00399573.
XX
PR   27-DEC-2000; 2000JP-00399573.
XX
PA   (TOJO ) TOYO KOHAN CO LTD.
PA   (TAKA/) TAKAHASHI K.
XX
DR   WPI; 2002-630904/68.
XX
PT   Carrying out a thermal cycle of polymerase chain reaction (PCR) by using
PT   a substrate on which a DNA is immobilized used in medical, biochemical,
PT   molecular biological and gene engineering fields.
XX
PS   Example; Page 9; 13pp; Japanese.
XX
CC   The invention relates to performing a thermal cycle of PCR by using a
CC   substrate on which a deoxyribonucleic acid (DNA) is immobilized. The
CC   method is useful in the medical, biochemical, molecular biological and
CC   genetic engineering fields. Sequences ABQ79871-881 represent PCR primers
CC   used in the method of the invention
XX
SQ   Sequence 20 BP; 3 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          4 TTTTTTTTTTTTTTTTT 20


RESULT 2074
ABQ79871/c
ID   ABQ79871 standard; DNA; 20 BP.
XX
AC   ABQ79871;
XX
DT   23-DEC-2002  (first entry)
XX
DE   Nucleotide sequence of a PCR primer #1.
XX
KW   Polymerase chain reaction; thermal cycle; immobilisation;
KW   genetic engineering; PCR; primer; ss.
XX
OS   Synthetic.
XX
PN   JP2002191369-A.
XX
PD   09-JUL-2002.
XX
PF   27-DEC-2000; 2000JP-00399573.
XX
PR   27-DEC-2000; 2000JP-00399573.
XX
PA   (TOJO ) TOYO KOHAN CO LTD.
PA   (TAKA/) TAKAHASHI K.
XX
DR   WPI; 2002-630904/68.
XX
PT   Carrying out a thermal cycle of polymerase chain reaction (PCR) by using
PT   a substrate on which a DNA is immobilized used in medical, biochemical,
PT   molecular biological and gene engineering fields.
XX
PS   Example; Page 9; 13pp; Japanese.
XX
CC   The invention relates to performing a thermal cycle of PCR by using a
CC   substrate on which a deoxyribonucleic acid (DNA) is immobilized. The
CC   method is useful in the medical, biochemical, molecular biological and
CC   genetic engineering fields. Sequences ABQ79871-881 represent PCR primers
CC   used in the method of the invention
XX
SQ   Sequence 20 BP; 3 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         20 AAAAAAAAAAAAAAAAA 4


RESULT 2075
ABZ91658/c
ID   ABZ91658 standard; DNA; 20 BP.
XX
AC   ABZ91658;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
```

PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 6900; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 15 A; 1 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 0.6%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2172 TTTTTTTTTTTTTTTAA 2188
||||||||||||||||
Db 20 TTTTTTTTTTTTTTTAA 4

RESULT 2076
ABZ89872/c
ID ABZ89872 standard; DNA; 20 BP.
XX
AC ABZ89872;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 5114; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 16 A; 2 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2165 CTTTTTTTTTTTTTTTT 2181
|||||||||||||||||
Db 20 CTTTTTTTTTTTTTTTT 4

RESULT 2077
AAQ75741
ID AAQ75741 standard; DNA; 21 BP.
XX
AC AAQ75741;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)

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CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 17


RESULT 2078
AAQ75717/c
ID   AAQ75717 standard; DNA; 21 BP.
XX
AC   AAQ75717;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2802
              ||||||||||||||||
Db         17 AAAAAAAAAAAAAAAA 1


RESULT 2079
AAQ75789
ID   AAQ75789 standard; DNA; 21 BP.
XX
AC   AAQ75789;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 17


RESULT 2080
AAQ75661
ID   AAQ75661 standard; DNA; 21 BP.
XX
AC   AAQ75661;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
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DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2081
AAQ75739
ID   AAQ75739 standard; DNA; 21 BP.
XX
AC   AAQ75739;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2082
AAQ75787
ID   AAQ75787 standard; DNA; 21 BP.
XX
AC   AAQ75787;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2083
AAQ75718/c
ID   AAQ75718 standard; DNA; 21 BP.
XX
AC   AAQ75718;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
```

```
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 2084
AAQ75659
ID   AAQ75659 standard; DNA; 21 BP.
XX
AC   AAQ75659;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2085
AAQ75715/c
ID   AAQ75715 standard; DNA; 21 BP.
XX
AC   AAQ75715;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 2086
AAQ75735
ID   AAQ75735 standard; DNA; 21 BP.
XX
AC   AAQ75735;
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XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 1 C; 3 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2087
AAQ75738
ID   AAQ75738 standard; DNA; 21 BP.
XX
AC   AAQ75738;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 2 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2088
AAQ75748
ID   AAQ75748 standard; DNA; 21 BP.
XX
AC   AAQ75748;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2089
AAQ75795
ID   AAQ75795 standard; DNA; 21 BP.
XX
AC   AAQ75795;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 3 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2090
AAQ75736
ID   AAQ75736 standard; DNA; 21 BP.
XX
AC   AAQ75736;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2091
AAQ75798
ID   AAQ75798 standard; DNA; 21 BP.
XX
AC   AAQ75798;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
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CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 4 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2092
AAQ75794
ID   AAQ75794 standard; DNA; 21 BP.
XX
AC   AAQ75794;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 3 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2093
AAQ75747
ID   AAQ75747 standard; DNA; 21 BP.
XX
AC   AAQ75747;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 2 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2094
AAQ75786
ID   AAQ75786 standard; DNA; 21 BP.
XX
AC   AAQ75786;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
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```
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 3 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 17


RESULT 2095
AAQ75791
ID   AAQ75791 standard; DNA; 21 BP.
XX
AC   AAQ75791;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 17


RESULT 2096
AAQ75743
ID   AAQ75743 standard; DNA; 21 BP.
XX
AC   AAQ75743;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 17


RESULT 2097
AAQ75796
ID   AAQ75796 standard; DNA; 21 BP.
XX
AC   AAQ75796;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
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PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 3 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2098
AAQ75703/c
ID   AAQ75703 standard; DNA; 21 BP.
XX
AC   AAQ75703;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 0 C; 3 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 2099
AAQ75714/c
ID   AAQ75714 standard; DNA; 21 BP.
XX
AC   AAQ75714;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 2100
AAQ75705/c
ID   AAQ75705 standard; DNA; 21 BP.
XX
AC   AAQ75705;
XX
DT   04-AUG-1995  (first entry)
```

```
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 2101
AAQ75712/c
ID   AAQ75712 standard; DNA; 21 BP.
XX
AC   AAQ75712;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 2102
AAQ75737
ID   AAQ75737 standard; DNA; 21 BP.
XX
AC   AAQ75737;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
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Db          1 TTTTTTTTTTTTTTTT 17


RESULT 2103
AAQ75706/c
ID   AAQ75706 standard; DNA; 21 BP.
XX
AC   AAQ75706;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match              0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 2104
AAQ75746
ID   AAQ75746 standard; DNA; 21 BP.
XX
AC   AAQ75746;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match              0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 17


RESULT 2105
AAQ75784
ID   AAQ75784 standard; DNA; 21 BP.
XX
AC   AAQ75784;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
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```
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 17


RESULT 2106
AAQ75785
ID   AAQ75785 standard; DNA; 21 BP.
XX
AC   AAQ75785;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 17


RESULT 2107
AAQ75704/c
ID   AAQ75704 standard; DNA; 21 BP.
XX
AC   AAQ75704;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2802
              ||||||||||||||||
Db         17 AAAAAAAAAAAAAAAA 1


RESULT 2108
AAQ75707/c
ID   AAQ75707 standard; DNA; 21 BP.
XX
AC   AAQ75707;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
```

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XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 2109
AAQ75750
ID   AAQ75750 standard; DNA; 21 BP.
XX
AC   AAQ75750;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 3 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2110
AAQ75710/c
ID   AAQ75710 standard; DNA; 21 BP.
XX
AC   AAQ75710;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 2111
AAQ75711/c
ID   AAQ75711 standard; DNA; 21 BP.
XX
AC   AAQ75711;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
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PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 2112
AAQ75783
ID   AAQ75783 standard; DNA; 21 BP.
XX
AC   AAQ75783;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 2 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2113
AAQ75620
ID   AAQ75620 standard; DNA; 21 BP.
XX
AC   AAQ75620;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2114
AAQ75668
ID   AAQ75668 standard; DNA; 21 BP.
XX
AC   AAQ75668;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
```

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XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2115
AAQ75614/c
ID   AAQ75614 standard; DNA; 21 BP.
XX
AC   AAQ75614;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 2116
AAQ75621/c
ID   AAQ75621 standard; DNA; 21 BP.
XX
AC   AAQ75621;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1
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RESULT 2117
AAQ75656
ID   AAQ75656 standard; DNA; 21 BP.
XX
AC   AAQ75656;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2118
AAQ75617/c
ID   AAQ75617 standard; DNA; 21 BP.
XX
AC   AAQ75617;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 0 C; 2 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 2119
AAQ75613
ID   AAQ75613 standard; DNA; 21 BP.
XX
AC   AAQ75613;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
```

```
SQ   Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2120
AAQ75616/c
ID   AAQ75616 standard; DNA; 21 BP.
XX
AC   AAQ75616;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 2121
AAQ75670
ID   AAQ75670 standard; DNA; 21 BP.
XX
AC   AAQ75670;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 3 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2122
AAQ75657
ID   AAQ75657 standard; DNA; 21 BP.
XX
AC   AAQ75657;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
```

```
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2123
AAQ75667
ID   AAQ75667 standard; DNA; 21 BP.
XX
AC   AAQ75667;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 2 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2124
AAQ75655
ID   AAQ75655 standard; DNA; 21 BP.
XX
AC   AAQ75655;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 1 C; 3 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2125
AAQ75663
ID   AAQ75663 standard; DNA; 21 BP.
XX
AC   AAQ75663;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
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PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2126
AAQ75666
ID   AAQ75666 standard; DNA; 21 BP.
XX
AC   AAQ75666;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2127
AAQ75658
ID   AAQ75658 standard; DNA; 21 BP.
XX
AC   AAQ75658;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 2 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2128
AAQ75611
ID   AAQ75611 standard; DNA; 21 BP.
XX
AC   AAQ75611;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
```

```
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 0 C; 3 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2129
AAQ75611/c
ID   AAQ75611 standard; DNA; 21 BP.
XX
AC   AAQ75611;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 0 C; 3 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 2130
AAQ75622
ID   AAQ75622 standard; DNA; 21 BP.
XX
AC   AAQ75622;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 2 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2131
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```
AAQ75622/c
ID   AAQ75622 standard; DNA; 21 BP.
XX
AC   AAQ75622;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 2 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 2132
AAQ75609
ID   AAQ75609 standard; DNA; 21 BP.
XX
AC   AAQ75609;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 0 C; 3 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2133
AAQ75609/c
ID   AAQ75609 standard; DNA; 21 BP.
XX
AC   AAQ75609;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 0 C; 3 G; 18 T; 0 U; 0 Other;
```

```
  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 2134
AAQ75607
ID   AAQ75607 standard; DNA; 21 BP.
XX
AC   AAQ75607;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 0 C; 4 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2135
AAQ75607/c
ID   AAQ75607 standard; DNA; 21 BP.
XX
AC   AAQ75607;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 0 C; 4 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 2136
AAQ75618
ID   AAQ75618 standard; DNA; 21 BP.
XX
AC   AAQ75618;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
```

```
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 17


RESULT 2137
AAQ75618/c
ID   AAQ75618 standard; DNA; 21 BP.
XX
AC   AAQ75618;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2802
              ||||||||||||||||
Db         17 AAAAAAAAAAAAAAAA 1


RESULT 2138
AAQ75608
ID   AAQ75608 standard; DNA; 21 BP.
XX
AC   AAQ75608;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 0 C; 3 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 17


RESULT 2139
AAQ75608/c
ID   AAQ75608 standard; DNA; 21 BP.
XX
AC   AAQ75608;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
```

```
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 0 C; 3 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 2140
AAQ75615
ID   AAQ75615 standard; DNA; 21 BP.
XX
AC   AAQ75615;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 0 C; 3 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2141
AAQ75615/c
ID   AAQ75615 standard; DNA; 21 BP.
XX
AC   AAQ75615;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 0 C; 3 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 2142
AAQ75610
ID   AAQ75610 standard; DNA; 21 BP.
XX
AC   AAQ75610;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
```

```
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 1 C; 3 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2143
AAQ75610/c
ID   AAQ75610 standard; DNA; 21 BP.
XX
AC   AAQ75610;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 1 C; 3 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 2144
AAQ75619
ID   AAQ75619 standard; DNA; 21 BP.
XX
AC   AAQ75619;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 1 C; 3 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2145
AAQ75619/c
ID   AAQ75619 standard; DNA; 21 BP.
```

```
XX
AC   AAQ75619;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 1 C; 3 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 2146
AAZ26584/c
ID   AAZ26584 standard; DNA; 21 BP.
XX
AC   AAZ26584;
XX
DT   30-NOV-1999  (first entry)
XX
DE   Human polymorphic region 773.
XX
KW   Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW   cell viability; loss of heterozygosity; precancerous condition; ASI;
KW   allele specific inhibitor; somatic cell; diagnosis; prevention;
KW   atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW   dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW   graft versus host disease; malignant cell removal; bone marrow; ss.
XX
OS   Homo sapiens.
XX
PN   WO9841648-A2.
XX
PD   24-SEP-1998.
XX
PF   19-MAR-1998;   98WO-US005419.
XX
PR   20-MAR-1997;   97US-0041057P.
XX
PA   (VARI-) VARIAGENICS INC.
XX
PI   Housman D,  Ledley FD,  Stanton VP;
XX
DR   WPI; 1998-521232/44.
XX
PT   Identifying target genes for allele-specific drugs - used for diagnosis,
PT   prevention and treatment of, e.g. cancers, atherosclerotic plaque,
PT   dysplastic lesions, endometriosis or graft versus host disease.
XX
PS   Disclosure; Fig 7; 605pp; English.
XX
CC   This invention describes a novel method for identifying an inhibitor
CC   potentially useful for treatment of cancer, where the inhibitor is active
CC   on a gene vital for cell growth or viability, and where the gene is
CC   subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC   used for preventing the development of cancer in a patient having a
CC   precancerous condition, by administering to the patient a first allele
CC   specific inhibitor (ASI) targeted to an allele of a first essential gene
CC   present in cells of the precancerous condition, where the normal somatic
CC   cells of the patient are heterozygous for the first gene, the inhibitor
CC   is active on at least one but less than all allelic forms of the gene
CC   present in a population and targets only one allelic form present in the
CC   normal somatic cells, and the first gene. The products and methods can be
CC   used in the diagnosis, prevention and treatment of LOH disorders, e.g.
CC   cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
CC   lesions, benign tumours, endometriosis, polycystic kidney disease, and
CC   graft versus host disease. The method can also be used to remove
CC   malignant cells from bone marrow transplants. AAZ25812-Z26825 represent
CC   human polymorphic sites described in the method of the invention
XX
SQ   Sequence 21 BP; 15 A; 0 C; 1 G; 5 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTAA 2188
              |||||||||||||||||
Db         21 TTTTTTTTTTTTTTTAA 5


RESULT 2147
AAT92356/c
ID   AAT92356 standard; DNA; 22 BP.
XX
AC   AAT92356;
XX
DT   26-JAN-1998  (first entry)
XX
DE   Amino modified oligodeoxyribonucleotide.
XX
KW   Amino modified oligodeoxyribonucleotide; oligonucleotide;
KW   achiral linker reagent; 5-(aminomethyl)-1,3-benzenedimethanol;
KW   N-flurescein-(5-aminomethyl)-1,3-benzenedimethanol;
KW   hybridisation probe; PCR primer; nucleic acid sequencing;
KW   affinity matrix; cloning recombinant DNA; in-vitro mutagenesis; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 11
FT                   /*tag=  a
FT                   /note= "n =  5-(aminomethyl)-1,3-benzenedimethanol"
FT   misc_difference 12
FT                   /*tag=  b
FT                   /note= "n =  5-(aminomethyl)-1,3-benzenedimethanol"
XX
PN   WO9705156-A1.
XX
```

```
PD   13-FEB-1997.
XX
PF   26-JUL-1996;   96WO-DK000330.
XX
PR   27-JUL-1995;   95DK-00000863.
XX
PA   (BEHR/) BEHRENS C.
PA   (PETE/) PETERSEN K H.
PA   (EGHO/) EGHOLM M.
PA   (NIEL/) NIELSEN J.
PA   (DAHL/) DAHL O.
XX
PI   Behrens C,  Petersen KH,  Egholm M,  Nielsen J,  Dahl O;
XX
DR   WPI; 1997-145615/13.
XX
PT   New achiral linker reagents - useful for incorporation of multiple amino
PT   gps. or reporter gps. into oligo:nucleotide(s).
XX
PS   Disclosure; Page 20; 42pp; English.
XX
CC   Achiral linker reagents have been developed for the incorporation of
CC   multiple amino groups into oligonucleotides. The present sequence
CC   represents a modified oligodeoxyribonucleotide. The achiral linker
CC   reagents can be used for incorporation of multiple primary amino groups
CC   or reporter groups into oligonucleotides. They are compatible with
CC   conventional DNA synthesis following the phosphoramidite methodology, and
CC   can be incorporated in good yields. The linker reagents may be used for
CC   labelling of oligonucleotides. They may also be used for preparation of
CC   oligonucleotides, e.g. for use as hybridisation probes, for use as
CC   primers in the polymerase chain reaction or in nucleic acid sequencing
CC   reactions, for production of affinity matrices for purification of DNA
CC   binding proteins or other biomolecules, for production of affinity
CC   matrices for detection of nucleic acid sequences, for cloning recombinant
CC   DNA or for in-vitro mutagenesis
XX
SQ   Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 2 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 22;
  Best Local Similarity   89.5%;  Pred. No. 1.8e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              ||||||||||  |||||||
Db         22 AAAAAAAAAANNAAAAAAA 4


RESULT 2148
AAA98276/c
ID   AAA98276 standard; DNA; 22 BP.
XX
AC   AAA98276;
XX
DT   02-FEB-2001  (first entry)
XX
DE   Human mismatch repair gene hMSH6 intron 9 DNA fragment.
XX
KW   Human mismatch repair gene; hMSH6; disease predisposition; genotype;
KW   mutation; carcinoma; colorectal; endometrial; ovarian; leukemia;
KW   neoplastic disease; drug development; ss.
XX
OS   Homo sapiens.
XX
PN   DE19909878-A1.
XX
PD   07-SEP-2000.
XX
PF   06-MAR-1999;   99DE-01009878.
XX
PR   06-MAR-1999;   99DE-01009878.
XX
PA   (UYDR ) UNIV DRESDEN TECH.
XX
PI   Plaschke J,  Kruppa C,  Schackert H;
XX
DR   WPI; 2000-588378/56.
XX
PT   Novel variants of the human mismatch repair gene, MSH6, useful e.g. for
PT   determining predisposition to cancer and for development of drugs.
XX
PS   Claim 1; Page 4; 14pp; German.
XX
CC   This invention describes a novel method of determining a predisposition
CC   to disease by genotyping a subject's DNA sequence (A) of the human
CC   mismatch repair gene, MSH6 at specified positions and comparing with
CC   reference DNA sequences, optionally taking into account all possible
CC   combinations of variations of the individual mutations, including any
CC   chosen absolute number of variations. (A), and analysis of their
CC   sequences, are useful for the following: (i) determining a predisposition
CC   to disease, especially colorectal, endometrial and ovarian carcinoma and
CC   leukemia; (ii) determining an increased mutation rate (frequency of base
CC   substitutions, insertions and/or deletions) in eukaryotic cells; (iii)
CC   predicting the progression, severity and survival time of patients with
CC   neoplastic disease; (iv) the development of therapeutic and 'life-style'
CC   drugs; (v) predicting individual differences in response to known
CC   chemotherapeutic agents (e.g. cis-platin) or drugs developed from (iv);
CC   (vi) optimizing individual treatments and interventions against neoplasia
CC   ; (vii) controlling the mutation rate in eukaryotic cells, in vitro or in
CC   vivo; (viii) constructing genes and vectors, particularly for development
CC   of pharmaceuticals; (ix) developing diagnostic kits and other systems for
CC   genotyping; and (x) developing in vivo and in vitro test systems for
CC   expressing individual forms of the MSH6 gene, e.g. for studying
CC   pathophysiology of disease or processes in which MSH6 is involved, and
CC   for drug development and testing
XX
SQ   Sequence 22 BP; 4 A; 1 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         22 AAAAAAAAAAAAAAAAA 6


RESULT 2149
AAA29753/c
ID   AAA29753 standard; DNA; 23 BP.
XX
AC   AAA29753;
XX
DT   15-AUG-2000  (first entry)
XX
DE   Synthetic oligonucleotide #1.
XX
KW   Primer; destabilise non-specific duplex formation; PCR; detection;
KW   purification; sequencing; genetic marker; RACE; DNA synthesis; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    8
FT                    /*tag=  a
FT                    /mod_base= i
FT                    /note= "inosine"
FT   modified_base    18
FT                    /*tag=  b
FT                    /mod_base= i
FT                    /note= "inosine"
XX
PN   WO200020630-A1.
XX
PD   13-APR-2000.
XX
PF   06-OCT-1999;   99WO-CA000933.
```

```
XX
PR   07-OCT-1998;   98CA-02246623.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Pelletier J,  Das M;
XX
DR   WPI; 2000-328943/28.
XX
PT   Novel method of stabilizing duplex formation, or destabilizing non-
PT   specific duplex formation using primer containing modified nucleotide
PT   analogs, useful for preventing mispriming during PCR, RACE, DNA synthesis
PT   or sequencing.
XX
PS   Example 1; Page 25; 46pp; English.
XX
CC   The present invention describes a method for destabilising non-specific
CC   duplex formation, between an oligonucleotide and a target nucleic acid
CC   (NA), comprising incubating the target NA with a modified oligonucleotide
CC   (I) comprising a homopolymeric sequence having a modification which
CC   decreases or abrogates H-bonding between the modified oligonucleotide and
CC   the non-specific target NA. The modified oligonucleotide is used to
CC   improve discrimination between the targeted homopolymeric sequence and a
CC   non-homopolymeric target sequence. It is used to increase the proportion
CC   of full length cDNA clones for a library, to reduce mispriming during
CC   sequencing, 5' or 3' RACE (rapid amplification of cDNA ends) or DNA
CC   synthesis or to generate bona fide genetic markers. The present sequence
CC   represents an oligonucleotide which is used in the exemplification of the
CC   present invention
XX
SQ   Sequence 23 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 2 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 23;
  Best Local Similarity   89.5%;  Pred. No. 1.9e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
                 ||||| ||||||||| |||
Db         23 AAAAANAAAAAAAAAANAAA 5


RESULT 2150
AAQ45360/c
ID   AAQ45360 standard; DNA; 23 BP.
XX
AC   AAQ45360;
XX
DT   25-MAR-2003  (revised)
DT   09-OCT-1994  (first entry)
XX
DE   Human protein-tyrosine-phosphatase-1D cDNA primer.
XX
KW   Protein-tyrosine-phosphatase; enzyme; disease diagnosis; DNA primer; ss.
XX
OS   Synthetic.
XX
PN   WO9408017-A1.
XX
PD   14-APR-1994.
XX
PF   06-OCT-1993;   93WO-EP002728.
XX
PR   06-OCT-1992;   92US-00956315.
PR   16-FEB-1993;   93US-00018129.
XX
PA   (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI   Ullrich A,  Vogel W;
XX
DR   WPI; 1994-135583/16.
XX
PT   New protein tyrosine phosphatase (PTP) protein, PTP-ID - are useful for
PT   diagnosis and treatment of diseases associated with abnormal PTP-ID
PT   levels.
XX
PS   Disclosure; Page 48; 99pp; English.
XX
CC   This DNA primer is used in the PCR-based amplification of protein-
CC   tyrosine-phosphatase-1B cDNA. (Updated on 25-MAR-2003 to correct PN
CC   field.)
XX
SQ   Sequence 23 BP; 1 A; 2 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
                 |||||||||||||||||
Db         23 AAAAAAAAAAAAAAAAA 7


RESULT 2151
AAT37316/c
ID   AAT37316 standard; DNA; 23 BP.
XX
AC   AAT37316;
XX
DT   06-FEB-1997  (first entry)
XX
DE   RT-PCR Primer for aromatic acyl transferase sequence.
XX
KW   Aromatic acyl transferase; transformation; anthocyanin pigment; plants;
KW   acylation; colour; tone; colouration; colour change; Gentiana triflora;
KW   Petunia hybrida; Perilla ocimoides; Scenecio cruentus;
KW   Lavandula angustifolia; ss.
XX
OS   Synthetic.
XX
PN   WO9625500-A1.
XX
PD   22-AUG-1996.
XX
PF   16-FEB-1996;   96WO-JP000348.
XX
PR   17-FEB-1995;   95JP-00067159.
PR   29-JUN-1995;   95JP-00196915.
PR   30-JAN-1996;   96JP-00046534.
XX
PA   (SUNR ) SUNTORY LTD.
XX
PI   Ashikari T,  Tanaka Y,  Fujiwara H,  Nakao M,  Fukui Y,  Yonekura K;
PI   Mizutani M,  Kusumi T;
XX
DR   WPI; 1996-393401/39.
XX
PT   DNA coding for aromatic acyl transferase - for transforming plants which
PT   produce anthocyanin pigments and thus altering colour tone, e.g. of
PT   flowers.
XX
PS   Example 2; Page 21; 94pp; Japanese.
XX
CC   Vectors containing DNA fragments encoding proteins of plant origin with
CC   aromatic acyl transferase activity may be used to transform plants which
CC   produce anthocyanin pigments. The aromatic acyl transferase acylates the
CC   pigments in the flower resulting in colour tone changes and allowing new
CC   colourations to be produced. Six specific DNA sequences encoding aromatic
CC   acyl transferase from different plants are described in AAT37308-T37313.
CC   This primer was used to reverse transcribe aromatic acyl transferase RNA
CC   to produce a cDNA ready for cloning into expression vectors
XX
SQ   Sequence 23 BP; 1 A; 2 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

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Qy       2786 AAAAAAAAAAAAAAAAA 2802
             |||||||||||||||||
Db         23 AAAAAAAAAAAAAAAAA 7


RESULT 2152
ABA97431/c
ID   ABA97431 standard; DNA; 23 BP.
XX
AC   ABA97431;
XX
DT   21-MAR-2002  (first entry)
XX
DE   Glycosyltransferase genes PCR primer #2.
XX
KW   Glycosyltransferase; anthocyanin; flower colour; enzyme; PCR primer; ss.
XX
OS   Unidentified.
XX
PN   WO200192509-A1.
XX
PD   06-DEC-2001.
XX
PF   01-JUN-2001; 2001WO-JP004675.
XX
PR   02-JUN-2000; 2000JP-00170436.
XX
PA   (ITFL-) INT FLOWER DEV PTY LTD.
XX
PI   Mizutani M,  Sakakibara K,  Tanaka Y,  Kusumi T,  Ono E;
XX
DR   WPI; 2002-114345/15.
XX
PT   New gene encoding protein that transfers a sugar to the 3' position of
PT   anthocyanin for changing flower color.
XX
PS   Example 3; Page 13; 50pp; Japanese.
XX
CC   The present invention provides the genes and proteins of
CC   glycosyltransferases from Gentiana triflora, Senesio cruentus and
CC   Clitoria ternatea. The protein transfers a sugar to the 3' position of
CC   anthocyanin, and can be used for changing the colour of flowers. The
CC   present sequence is a PCR primer used to isolate glycosyltransferase
CC   coding sequences of the invention
XX
SQ   Sequence 23 BP; 1 A; 2 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
             |||||||||||||||||
Db         23 AAAAAAAAAAAAAAAAA 7


RESULT 2153
AAF85497/c
ID   AAF85497 standard; DNA; 23 BP.
XX
AC   AAF85497;
XX
DT   23-JUL-2001  (first entry)
XX
DE   PCR primer for DNA encoding Kalata B1 polypeptide fragments.
XX
KW   Kalata B2; transgenic plant; cotton; calcium channel binding; pain;
KW   stroke; C5a binding; antiinflammatory; PCR primer; ss.
XX
OS   Oldenlandia affinis.
XX
PN   WO200134829-A2.
XX
PD   17-MAY-2001.
XX
PF   03-NOV-2000; 2000WO-AU001352.
XX
PR   05-NOV-1999;   99AU-00003884.
PR   25-NOV-1999;   99AU-00004235.
XX
PA   (UYQU ) UNIV QUEENSLAND.
PA   (UYLA-) UNIV LATROBE.
XX
PI   Craik DJ,  Anderson MA,  Jennings CV;
XX
DR   WPI; 2001-343607/36.
XX
PT   Novel nucleic acid molecule encoding amino acid sequence capable of
PT   forming cyclic structure, for generating transgenic plants capable of
PT   producing cyclic knotted protein and resistant to pathogens such as
PT   insects.
XX
PS   Example 10; Fig 1B; 112pp; English.
XX
CC   PCR primers AAF85495-97 were used to amplify a DNA fragment encoding
CC   Kalata B1. Kalata B1 is a macrocyclic peptide with diverse biological
CC   activities. The Kalata B1 polynucleotide represents a nucleic acid
CC   molecule of the invention. The specification describes nucleic acid
CC   molecules which encode an amino acid sequence which is capable of being
CC   cyclised within a cell or a membrane of a cell to form a cyclic backbone.
CC   The amino acid sequence comprises sufficient disulfide bonds to confer a
CC   stabilized folded structure on the three-dimensional structure of the
CC   backbone. The nucleic acid molecules of the invention are useful for
CC   producing transgenic genetically modified food or non-food crop plants,
CC   in particular cotton. The peptides or proteins can be manipulated to
CC   introduce modulating activity, for modulating activity of calcium channel
CC   binding is useful in treatment of pain or stroke and C5a binding activity
CC   useful as an antiinflammatory agent. The nucleic acid molecules are
CC   useful in the generation of molecules having animal or plant therapeutic
CC   properties as well as in a range of diagnostic, industrial and
CC   agricultural including horticultural applications and for protecting
CC   plants such as crop plants from pest and/or pathogen infestation
XX
SQ   Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
             |||||||||||||||||
Db         23 AAAAAAAAAAAAAAAAA 7


RESULT 2154
ABL95973
ID   ABL95973 standard; DNA; 23 BP.
XX
AC   ABL95973;
XX
DT   19-JUN-2002  (first entry)
XX
DE   Probe #48 for assaying nucleic acids.
XX
KW   Probe; polymorphism detection; mutation detection; disease diagnosis;
KW   microbial identification; ss.
XX
OS   Unidentified.
XX
PN   WO200208414-A1.
XX
PD   31-JAN-2002.
XX
PF   27-JUN-2001; 2001WO-IB001147.
XX
```

PR 27-JUN-2000; 2000JP-00193133.
PR 03-AUG-2000; 2000JP-00236115.
PR 26-SEP-2000; 2000JP-00292483.
XX
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (KANK-) KANKYO ENG CO LTD.
XX
PI Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;
PI Yokomaku T;
XX
DR WPI; 2002-195876/25.
XX
PT Fluorescently-labeled nucleic acid probes for assaying nucleic acids and
PT their polymorphism and mutation, particularly useful in science and
PT medicine for e.g. analytical applications, disease diagnosis and
PT microbial identification.
XX
PS Disclosure; Fig 3; 152pp; Japanese.
XX
CC The present invention relates to nucleic acid probes, which are useful
CC for assaying nucleic acids by hybridising with a target nucleic acid, in
CC which a single-stranded oligonucleotide is labelled with a fluorescent
CC substance and a quencher in a manner that the fluorescence intensity of
CC the hybridisation reaction system is increased after completion of the
CC hybridisation but no stem loop structure is formed. The probes are useful
CC for assaying nucleic acids and their polymorphism and mutation,
CC particularly useful for e.g. analytical applications, disease diagnosis
CC and microbial identification. The present sequence was used to illustrate
CC the invention
XX
SQ Sequence 23 BP; 0 A; 6 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 17; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTT 2182
||||||||||||||||| |
Db 1 TTTTTTTTTTTTTTTTT 17

RESULT 2155
ABQ96219
ID ABQ96219 standard; DNA; 23 BP.
XX
AC ABQ96219;
XX
DT 28-OCT-2002 (first entry)
XX
DE Tumour suppression-related oligonucleotide #1870.
XX
KW Tumour; cytostatic; antiviral; neuroprotective; nootropic; neuroleptic;
KW tumour suppression; tumour reversion; apoptosis; viral resistance; human;
KW viral infection; cell degeneration disease; neurodegeneration; ds;
KW Alzheimer's disease; schizophrenia; immune disease; inflammatory disease.
XX
OS Homo sapiens.
XX
PN FR2819824-A1.
XX
PD 26-JUL-2002.
XX
PF 23-JAN-2001; 2001FR-00000899.
XX
PR 23-JAN-2001; 2001FR-00000899.
XX
PA (MOLE-) MOLECULAR ENGINES LAB SA.
XX
PI Telerman A, Amson R, Tuijnder M, Susini L;
XX
DR WPI; 2002-610803/66.
XX
PT New nucleic acid implicated e.g. in tumor suppression, useful for
PT diagnosis of tumors, viral infection and cellular degeneration and for
PT drug screening.
XX
PS Claim 1; Page 512; 623pp; French.
XX
CC The present invention relates to novel human nucleic acid sequences (I).
CC The present sequence is one such nucleic acid sequence. Expression of (I)
CC are implicated in tumour suppression or reversion and apoptosis and viral
CC resistance. (I) are useful as probes or primers for detecting,
CC identifying, measuring and/or amplifying nucleic acid sequences, as
CC antisense reagents and for recombinant production of polypeptides. (I),
CC polypeptides (II) encoded by (I), vector containing (I), cells containing
CC these vectors and antibodies (Ab) against (II) are all useful for
CC treatment/prevention of viral, tumour and cell degeneration diseases
CC (especially neurodegeneration, such as Alzheimer's disease and
CC schizophrenia). Analysing the expression of (I) is also useful for
CC diagnosis and/or prognosis of such diseases. Transgenic animals carrying
CC (I) are used for studying the aetiology of these diseases (also immune
CC and inflammatory diseases). Note: In the present specification, SEQ ID 1
CC to 2280 are claimed in Claim 1, however only SEQ ID 1 to 2270 are shown
CC in the specification
XX
SQ Sequence 23 BP; 15 A; 0 C; 3 G; 3 T; 0 U; 2 Other;

Query Match 0.6%; Score 17; DB 1; Length 23;
Best Local Similarity 89.5%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2783 TTGAAAAAAAAAAAAAAAA 2801
| | ||||||||||||||||
Db 3 TNGNAAAAAAAAAAAAAAAA 21

RESULT 2156
ABQ96219/c
ID ABQ96219 standard; DNA; 23 BP.
XX
AC ABQ96219;
XX
DT 28-OCT-2002 (first entry)
XX
DE Tumour suppression-related oligonucleotide #1870.
XX
KW Tumour; cytostatic; antiviral; neuroprotective; nootropic; neuroleptic;
KW tumour suppression; tumour reversion; apoptosis; viral resistance; human;
KW viral infection; cell degeneration disease; neurodegeneration; ds;
KW Alzheimer's disease; schizophrenia; immune disease; inflammatory disease.
XX
OS Homo sapiens.
XX
PN FR2819824-A1.
XX
PD 26-JUL-2002.
XX
PF 23-JAN-2001; 2001FR-00000899.
XX
PR 23-JAN-2001; 2001FR-00000899.
XX
PA (MOLE-) MOLECULAR ENGINES LAB SA.
XX
PI Telerman A, Amson R, Tuijnder M, Susini L;
XX
DR WPI; 2002-610803/66.
XX
PT New nucleic acid implicated e.g. in tumor suppression, useful for
PT diagnosis of tumors, viral infection and cellular degeneration and for
PT drug screening.
XX
PS Claim 1; Page 512; 623pp; French.
XX
CC The present invention relates to novel human nucleic acid sequences (I).
CC The present sequence is one such nucleic acid sequence. Expression of (I)
CC are implicated in tumour suppression or reversion and apoptosis and viral

```
CC   resistance. (I) are useful as probes or primers for detecting,
CC   identifying, measuring and/or amplifying nucleic acid sequences, as
CC   antisense reagents and for recombinant production of polypeptides. (I),
CC   polypeptides (II) encoded by (I), vector containing (I), cells containing
CC   these vectors and antibodies (Ab) against (II) are all useful for
CC   treatment/prevention of viral, tumour and cell degeneration diseases
CC   (especially neurodegeneration, such as Alzheimer's disease and
CC   schizophrenia). Analysing the expression of (I) is also useful for
CC   diagnosis and/or prognosis of such diseases. Transgenic animals carrying
CC   (I) are used for studying the aetiology of these diseases (also immune
CC   and inflammatory diseases). Note: In the present specification, SEQ ID 1
CC   to 2280 are claimed in Claim 1, however only SEQ ID 1 to 2270 are shown
CC   in the specification
XX
SQ   Sequence 23 BP; 15 A; 0 C; 3 G; 3 T; 0 U; 2 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTTT 2180
              |||||||||||||||||
Db         23 CCTTTTTTTTTTTTTTT 7


RESULT 2157
AAV48089/c
ID   AAV48089 standard; DNA; 24 BP.
XX
AC   AAV48089;
XX
DT   27-OCT-1998  (first entry)
XX
DE   Oligonucleotide 25-P.
XX
KW   In situ translation; RNA-protein fusion; binding reagent; antibody;
KW   industrial catalyst; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   24
FT                   /*tag=  a
FT                   /note= "Puromycin"
XX
PN   WO9831700-A1.
XX
PD   23-JUL-1998.
XX
PF   14-JAN-1998;   98WO-US000807.
XX
PR   21-JAN-1997;   97US-0035963P.
PR   06-NOV-1997;   97US-0064491P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Szostak JW,  Roberts RW,  Liu R;
XX
DR   WPI; 1998-414032/35.
XX
PT   Selection of specific protein by screening protein-RNA fusions generated
PT   in vitro or in situ - useful for, e.g. identifying enzymes and antibodies
PT   with altered properties, potentially useful as catalysts or for therapy
PT   or diagnosis.
XX
PS   Disclosure; Page 39; 94pp; English.
XX
CC   The Oligonucleotides AAV48087, AAV48089-V48091 and AAV48096-V48098 and
CC   variations were used to generate RNA-protein fusions. These were used in
CC   the selection of a specific protein or RNA, by in vitro or in situ
CC   translation of candidate RNA molecules to produce RNA-protein fusions,
CC   then selecting specific RNA protein fusions. The method is used to select
CC   proteins (or DNA encoding them) having altered properties, e.g. for
CC   identification of new binding reagents, to identify improved human
CC   antibodies or new enzymes. These proteins are potentially useful in
CC   diagnosis and therapy, or as industrial catalysts. The methods allow many
CC   rounds of selection and amplification to be performed, resulting in
CC   enrichment of even very rare molecules and allowing isolation of proteins
CC   that bind specifically to almost any compound or catalyse almost any
CC   reaction
XX
SQ   Sequence 24 BP; 0 A; 4 C; 3 G; 16 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2801
              |||||||||||||||||
Db         22 GAAAAAAAAAAAAAAAA 6


RESULT 2158
AAT76905
ID   AAT76905 standard; DNA; 24 BP.
XX
AC   AAT76905;
XX
DT   02-JUL-1998  (first entry)
XX
DE   S. glaucescens dTDP-glucose-dehydratase PCR primer #2.
XX
KW   Acarbose biosynthesis; acbA gene; acbB gene; acbC gene; acbD gene;
KW   acbE gene; acbF gene; enzyme; alpha-amylase inhibitor; treatment;
KW   diabetes; PCR primer; ss.
XX
OS   Synthetic.
OS   Streptomyces glaucescens.
XX
PN   DE19622783-A1.
XX
PD   11-DEC-1997.
XX
PF   07-JUN-1996;   96DE-01022783.
XX
PR   07-JUN-1996;   96DE-01022783.
XX
PA   (FARH ) HOECHST AG.
XX
PI   Decker H;
XX
DR   WPI; 1998-033827/04.
XX
PT   Recombinant DNA molecule comprising genes for biosynthesis of acarbose -
PT   an alpha-amylase inhibitor useful in treatment of diabetes.
XX
PS   Example 1; Page 6; 35pp; German.
XX
CC   AAT76905 and AAT76904 are PCR primers used in a method to amplify a PstI
CC   fragment from Streptomyces glaucescens GLA.O which encodes the genes,
CC   acbA, acbB, acbC, acbD, acbE and acbF which are involved in the acarbose
CC   biosynthesis pathway. These genes and encoded enzymes are useful for
CC   producing acarbose, which is an alpha -amylase inhibitor useful in the
CC   treatment of diabetes
XX
SQ   Sequence 24 BP; 1 A; 3 C; 10 G; 4 T; 0 U; 6 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 24;
  Best Local Similarity   66.7%;  Pred. No. 2.1e+03;
  Matches   14;  Conservative    6;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        799 GGAGCTGGTGGGGGCCGTAAT 819
              ||::||||:::||:||||| |
Db          2 GGWRCTGGYRSGGSCCGTAGT 22
```

```
RESULT 2159
AAA63459
ID   AAA63459 standard; DNA; 24 BP.
XX
AC   AAA63459;
XX
DT   06-MAR-2001  (first entry)
XX
DE   dNDP-glucose 4,6-dehydratase degenerate PCR primer #2.
XX
KW   Enediyne C-1027 biosynthesis gene cluster; apoprotein; chromophore; NGDH;
KW   dNDP-glucose 4,6-dehydratase; PCR primer; ss.
XX
OS   Unidentified.
XX
PN   WO200040596-A1.
XX
PD   13-JUL-2000.
XX
PF   06-JAN-2000; 2000WO-US000446.
XX
PR   06-JAN-1999;   99US-0115434P.
PR   05-JAN-2000; 2000US-00477962.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Shen B,  Liu W,  Christenson SD,  Standage S;
XX
DR   WPI; 2000-465947/40.
XX
PT   Isolated nucleic acid comprising a nucleic acid encoding any of C-1027
PT   open reading frames (ORFs) -7 to 42, excluding ORF 9 (cagA), useful for
PT   the production of enediyne C-1027 antitumor antibiotics.
XX
PS   Example 1; Page 41; 160pp; English.
XX
CC   The present sequence is a PCR primer for the dNDP-glucose 4,6-dehydratase
CC   (NGDH) coding sequence, which was used in an assay to determine whether
CC   any of the Streptomyces globisporus enediyne C-1027 gene cluster encodes
CC   an NGDH protein. Enediyne C-1027 is an antibiotic, consisting of an
CC   apoprotein and a non-peptidic chromophore, which acts by damaging DNA.
CC   The sequences within the gene cluster can be used to produce the protein
CC   and to identify antagonists, both of which can be used in the treatment
CC   of cancer. It was shown that the cluster does include a NGDH gene,
CC   designated sgcA
XX
SQ   Sequence 24 BP; 1 A; 3 C; 10 G; 4 T; 0 U; 6 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 24;
  Best Local Similarity   66.7%;  Pred. No. 2.1e+03;
  Matches   14;  Conservative    6;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        799 GGAGCTGGTGGGGGCCGTAAT 819
              ||::||||:::||:||||| |
Db          2 GGWRCTGGYRSGGSCCGTAGT 22


RESULT 2160
AAH75424
ID   AAH75424 standard; DNA; 24 BP.
XX
AC   AAH75424;
XX
DT   18-OCT-2001  (first entry)
XX
DE   Human homo laminin protein 24 PCR primer 1.
XX
KW   Human; homo laminin protein 24; cytostatic; virucidal; immunomodulatory;
KW   antiinflammatory; haemostatic; cancer; haemopathy; HIV; phlogosis;
KW   Human Immunodeficiency Virus; immunological diseases; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200155183-A1.
XX
PD   02-AUG-2001.
XX
PF   21-JAN-2001; 2001WO-CN000093.
XX
PR   28-JAN-2000; 2000CN-00111622.
XX
PA   (BIOD-) BIODOOR GENE TECHNOLOGY LTD SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2001-483216/52.
XX
PT   Human laminin protein 24 and encoded polynucleotide, applicable in
PT   diagnosis and treatment of cancer, hemopathy, immunological diseases and
PT   phlogosis.
XX
PS   Example 3; Page 12; 38pp; Chinese.
XX
CC   The invention relates to the human homo laminin protein 24 with
CC   cytostatic, virucidal, immunomodulatory, antiinflammatory and haemostatic
CC   activity. The polypeptide and encoding polynucleotide are applicable in
CC   diagnosis and treatment of cancer, haemopathy, Human Immunodeficiency
CC   Virus (HIV) infection, immunological diseases and phlogosis. The present
CC   sequence is that of a homo laminin protein 24 PCR primer
XX
SQ   Sequence 24 BP; 1 A; 4 C; 3 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTT 2179
              |||||||||||||||||
Db          5 TCCTTTTTTTTTTTTTT 21


RESULT 2161
AAD03811
ID   AAD03811 standard; DNA; 24 BP.
XX
AC   AAD03811;
XX
DT   19-JUN-2001  (first entry)
XX
DE   S. galilaeus aclacinomycin biosynthetic gene amplifying reverse primer.
XX
KW   Aclacinomycin; sga; dehydratase; dTDP-glucose 4,6-dehydratase;
KW   oxidoreductase; glycosyl transferase; GTF; isomerase; KRII;
KW   aklaviketone reductase; polyketide assembler; cyclase; aminomethylase;
KW   glucose-1-phosphate thymidylyl transferase; aminotransferase; antibiotic;
KW   anticancer agent; PCR primer; ss.
XX
OS   Streptomyces galilaeus.
XX
PN   WO200123578-A1.
XX
PD   05-APR-2001.
XX
PF   25-SEP-2000; 2000WO-FI000819.
XX
PR   29-SEP-1999;   99FI-00002085.
XX
PA   (GALI-) GALILAEUS OY.
XX
PI   Ylihonko K,  Raety K,  Hakala J;
XX
DR   WPI; 2001-266165/27.
XX
PT   Novel gene cluster derived from Streptomyces galilaeus useful for
PT   obtaining hybrid antibiotics, or to increase yields of anthracycline
PT   metabolites, preferably aclacinomycin or related antibiotics.
```

```
XX
PS   Example 1; Page 10; 50pp; English.
XX
CC   The patent discloses a gene cluster for aclacinomycin biosynthesis being
CC   included in a 7 kilobases XhoI-NotI fragment and a flanked 8.5 kilobases
CC   BglII fragment derived from Streptomyces galilaeus (ATCC 31615). This
CC   gene cluster comprises thirteen genes namely sga1, sga2 (activator), sga3
CC   (dehydratase), sga4 (oxidoreductase), sga5 (dTDP-glucose 4,6-
CC   dehydratase), sga6 (glycosyl transferase; GTF), sga7 (putative
CC   isomerase), sga8 (aklaviketone reductase), sga9 (putative polyketide
CC   assembler), sga10 (putative cyclase), sga11 (aminomethylase), sga12
CC   (glucose-1-phosphate thymidylyl transferase) and sga13
CC   (aminotransferase). Aclacinomycin gene cluster is useful for producing
CC   metabolites, preferably anthracycline metabolites by transferring
CC   aclacinomycin gene cluster into Streptomyces peucetius host. It is useful
CC   for the production of hybrid antibiotics and for increasing the yield of
CC   aclacinomycin. It is also useful for genetic engineering and for
CC   producing anthracycline which is useful as an anticancer agent. The
CC   present sequence is a degenerate reverse PCR primer which is used to
CC   amplify 6345 to 6861 bases of the aclacinomycin biosynthetic gene cluster
CC   (AAD03809), which is internal to the 4, 6-dehydratase gene
XX
SQ   Sequence 24 BP; 1 A; 3 C; 10 G; 4 T; 0 U; 6 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 24;
  Best Local Similarity   66.7%;  Pred. No. 2.1e+03;
  Matches   14;  Conservative    6;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        799 GGAGCTGGTGGGGGCCGTAAT 819
              ||::||||:::||:||||| |
Db          2 GGWRCTGGYRSGGSCCGTAGT 22


RESULT 2162
ABQ73254
ID   ABQ73254 standard; DNA; 24 BP.
XX
AC   ABQ73254;
XX
DT   30-SEP-2002  (first entry)
XX
DE   Human macro protein 17.49 PCR primer 1 SEQ ID NO:3.
XX
KW   Human; macro protein 17.40; nerve system disorder disease;
KW   protein metabolic disorder relative disease; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1339462-A.
XX
PD   13-MAR-2002.
XX
PF   21-AUG-2000; 2000CN-00119647.
XX
PR   21-AUG-2000; 2000CN-00119647.
XX
PA   (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-455361/49.
XX
PT   New polypeptide-human macro protein 17.49 and polynucleotide for encoding
PT   such polypeptide.
XX
PS   Example 2; Page 18; 32pp; Chinese.
XX
CC   The present invention describes human macro protein 17.49 (I). Also
CC   described is a process for producing (I) using DNA recombination
CC   technology. (I) and the polynucleotide encoding it can be used for
CC   treating various diseases, such as nerve system disorder disease and
CC   protein metabolic disorder relative disease. The present sequence
CC   represents a PCR primer for (I), which is used in an example from the
CC   present invention
XX
SQ   Sequence 24 BP; 2 A; 0 C; 4 G; 17 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 24;
  Best Local Similarity   94.4%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2183
              ||||||||| |||||||
Db          2 TTTTTTTTTNTTTTTTT 19


RESULT 2163
ABQ73254/c
ID   ABQ73254 standard; DNA; 24 BP.
XX
AC   ABQ73254;
XX
DT   30-SEP-2002  (first entry)
XX
DE   Human macro protein 17.49 PCR primer 1 SEQ ID NO:3.
XX
KW   Human; macro protein 17.40; nerve system disorder disease;
KW   protein metabolic disorder relative disease; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1339462-A.
XX
PD   13-MAR-2002.
XX
PF   21-AUG-2000; 2000CN-00119647.
XX
PR   21-AUG-2000; 2000CN-00119647.
XX
PA   (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-455361/49.
XX
PT   New polypeptide-human macro protein 17.49 and polynucleotide for encoding
PT   such polypeptide.
XX
PS   Example 2; Page 18; 32pp; Chinese.
XX
CC   The present invention describes human macro protein 17.49 (I). Also
CC   described is a process for producing (I) using DNA recombination
CC   technology. (I) and the polynucleotide encoding it can be used for
CC   treating various diseases, such as nerve system disorder disease and
CC   protein metabolic disorder relative disease. The present sequence
CC   represents a PCR primer for (I), which is used in an example from the
CC   present invention
XX
SQ   Sequence 24 BP; 2 A; 0 C; 4 G; 17 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 24;
  Best Local Similarity   94.4%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2803
              ||||||| |||||||||
Db         19 AAAAAAANAAAAAAAAA 2


RESULT 2164
ABL40114
ID   ABL40114 standard; DNA; 24 BP.
XX
AC   ABL40114;
XX
DT   17-MAY-2002  (first entry)
```

XX
DE Human natriuretic peptide acceptor 10 PCR primer 2 SEQ ID NO:4.
XX
KW Human; natriuretic peptide acceptor 10; malignant tumour; blood disease;
KW HIV infection; immunity disease; inflammation; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN CN1323830-A.
XX
PD 28-NOV-2001.
XX
PF 16-MAY-2000; 2000CN-00115724.
XX
PR 16-MAY-2000; 2000CN-00115724.
XX
PA (SHAN-) SHANGHAI BODE GENE DEV CO LTD.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-148833/20.
XX
PT New polypeptide-human natriuretic peptide acceptor 10 and polynucleotides
PT for coding same.
XX
PS Example 2; Page 16 (Disclosure); 32pp; Chinese.
XX
CC The present invention describes human natriuretic peptide acceptor 10
CC (I). The present invention also describes a method for producing (I)
CC through DNA recombination techniques. (I) and the polynucleotide encoding
CC it can be used in the treatment of several diseases such as malignant
CC tumours, blood diseases, HIV infection and immunity diseases and various
CC inflammations. The present sequence represents a PCR primer for human
CC natriuretic peptide acceptor 10, which is used in an example from the
CC present invention
XX
SQ Sequence 24 BP; 2 A; 5 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.6%; Score 17; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2163 TCCTTTTTTTTTTTTTT 2179
||||||||||||||||||
Db 4 TCCTTTTTTTTTTTTTT 20

RESULT 2165
AAZ99741/c
ID AAZ99741 standard; DNA; 25 BP.
XX
AC AAZ99741;
XX
DT 12-JUL-2000 (first entry)
XX
DE Primer used to reverse transcribe barley 17 kDa foam protein mRNA.
XX
KW Barley; 17 kDa foam protein; foam; prolamin storage protein;
KW foaming beverage; beer; brewed product; foam head; primer; ss.
XX
OS Hordeum vulgare.
XX
PN WO200014237-A2.
XX
PD 16-MAR-2000.
XX
PF 02-SEP-1999; 99WO-IB001597.
XX
PR 03-SEP-1998; 98US-00146703.
PR 13-JAN-1999; 99US-0115756P.
XX
PA (VAAG/) VAAG P.
PA (BECH/) BECH L M.
PA (CAME/) CAMERON-MILLS V.
PA (SORE/) SORENSEN M B.
XX
PI Vaag P, Bech LM, Cameron-Mills V, Sorensen MB;
XX
DR WPI; 2000-317103/27.
XX
PT New foam protein from cereals useful for improving foam formation,
PT stability and half-life in foaming products such as beverages and
PT especially beer.
XX
PS Example 6; Page 22; 82pp; English.
XX
CC The present sequence represents a primer used to reverse transcribe mRNA
CC encoding the barley 17 kDa foam protein. The protein has foam enhancing
CC properties, and belongs to the prolamin storage protein family. It is
CC found in the endosperm tissue of mature cereal grain, and is synthesised
CC during grain development. The 17 kDa foam protein can be added to
CC products, e.g. foaming beverages such as beer, to enhance the foaming
CC quality of the product. The protein can be used to produce improved
CC brewed products. The proteins and polynucleotides are especially useful
CC for improving the formation, stability and half-life of the foam head on
CC beer. The antibodies are useful to detect, measure and purify the
CC proteins in samples such as transgenic cells/plants and foaming products
XX
SQ Sequence 25 BP; 2 A; 2 C; 2 G; 19 T; 0 U; 0 Other;

Query Match 0.6%; Score 17; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAA 2802
|||||||||||||||||
Db 25 AAAAAAAAAAAAAAAAA 9

RESULT 2166
AAC96419/c
ID AAC96419 standard; DNA; 25 BP.
XX
AC AAC96419;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA DQA1 gene PCR primer #21.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 51; 66pp; English.
XX

```
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 3 A; 2 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 2.3e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2776 GTTAGAATTGAAAAAAAAAAAAAAA 2800
                | |  |||  ||||||||||||||||
Db         25 GGTCAAATCTAAAAAAAAAAAAAAA 1


RESULT 2167
AAC96289
ID   AAC96289 standard; DNA; 25 BP.
XX
AC   AAC96289;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DPB1 gene PCR primer #21.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 48; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 4 A; 2 C; 3 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 2.3e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTAACTTTGAAAG 2197
                ||||||||||||||| | |   ||
Db          1 TTTTTTTTTTTTTTAAGTGTACCAG 25


RESULT 2168
AAT38116
ID   AAT38116 standard; cDNA; 25 BP.
XX
AC   AAT38116;
XX
DT   09-DEC-1996  (first entry)
XX
DE   NotI-oligo primer.
XX
KW   Tazarotene induced gene 1; TIG1; retinoid; psoriasis; antisporiatic;
KW   fibroblast; keratinocyte; skin raft culture; retinoic acid receptor;
KW   primer; vector; pSPORT; ss.
XX
OS   Synthetic.
XX
PN   WO9623080-A1.
XX
PD   01-AUG-1996.
XX
PF   26-JAN-1996;   96WO-US001339.
XX
PR   27-JAN-1995;   95US-00379280.
XX
PA   (ALLR ) ALLERGAN.
XX
PI   Nagpal S,  Chandraratna RA;
XX
DR   WPI; 1996-362702/36.
XX
PT   Retinoid-inducible polynucleotide, designated Tazarotene Induced Gene
PT   (TGI1) - having low basal expression, used in assay systems as an
PT   indicator of retinoid action in psoriatic skin cultures.
XX
PS   Example 4; Page 13; 50pp; English.
XX
CC   A NotI-oligo primer (AAT38116) was used to block the poly(A)+ region of
CC   vector pSPORT-1. cDNA derived from mock-treated and AGN-190168- treated
CC   skin raft cultures was ligated into pSPORT-1 and a cDNA library was
CC   created in bacterial host cells. A subtraction procedure and Southern
CC   hybridisation yielded a cDNA clone (AAT38115), designated TIG1
CC   (tazarotene induced gene 1), that corresponds to mRNA that is strongly
CC   induced upon treatment of skin raft cultures with the retinoic acid
CC   receptor beta/gamma selective antipsoriatic synthetic retinoid AGN-190168
XX
SQ   Sequence 25 BP; 0 A; 6 C; 4 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTTT 2180
                |||||||||||||||||
Db          9 CCTTTTTTTTTTTTTTT 25


RESULT 2169
AAV06660
ID   AAV06660 standard; DNA; 25 BP.
XX
AC   AAV06660;
XX
DT   19-MAY-1998  (first entry)
XX
DE   Unlabeled oligonucleotide (P0).
XX
KW   Nucleoside analogue; polycyclic aromatic group; anthracene;
KW   phenanthracene; pyrene; stilbene; tetracene; pentacene;
KW   fluorescent label; ss.
XX
OS   Synthetic.
```

XX
PN WO9743298-A1.
XX
PD 20-NOV-1997.
XX
PF 15-MAY-1997; 97WO-US008307.
XX
PR 15-MAY-1996; 96US-0017772P.
XX
PA (RESE) RESEARCH CORP TECHNOLOGIES INC.
XX
PI Kool ET;
XX
DR WPI; 1998-008790/01.
XX
PT Nucleoside derivatives comprising pyrene, anthracene or phenanthrene
PT joined to C-1 atom of ribose or de:oxy:ribose sugar moiety - useful in
PT preparation of fluorescently-labeled DNA.
XX
PS Example 5; Fig 13; 114pp; English.
XX
CC The present sequence represents an unlabeled oligonucleotide. The
CC invention relates to a new nucleoside derivative comprising a pyrene,
CC anthracene or phenanthrene joined to the C-1 atom of a sugar moiety
CC through a carbon-carbon bond in either an alpha or a beta configuration,
CC where the sugar moiety is ribose or deoxyribose. Also claimed is a
CC phosphoramidite derivative of the above nucleoside derivative. The above
CC nucleotide derivatives are useful in preparation of fluorescently-
CC labeled DNA or RNA. These may be used in detection of target nucleic
CC acids through hybridisation. The nucleoside analogues stack neatly into
CC an RNA or DNA helix and do not interfere with binding properties of
CC surrounding complementary bases
XX
SQ Sequence 25 BP; 0 A; 6 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 0.6%; Score 17; DB 1; Length 25;
Best Local Similarity 80.0%; Pred. No. 2.3e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2161 TCTCCTTTTTTTTTTTTTTTTTTT 2185
||| ||||| ||||| |||| || |
Db 1 TCTTCTTTTCTTTTTCTTTTCTTCT 25

RESULT 2170
AAX40404/c
ID AAX40404 standard; DNA; 25 BP.
XX
AC AAX40404;
XX
DT 18-JUN-1999 (first entry)
XX
DE Seq ID No:2 of WO9915702.
XX
KW Nucleic acid normalisation; haptenylated; subtractive hybridization;
KW normalised library; nucleic acid analysis; ss.
XX
OS Synthetic.
XX
PN WO9915702-A1.
XX
PD 01-APR-1999.
XX
PF 24-SEP-1998; 98WO-US019948.
XX
PR 24-SEP-1997; 97US-0059817P.
PR 23-SEP-1998; 98US-00159496.
XX
PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
PI Li W, Jessee J, Nisson PE;
XX
DR WPI; 1999-254725/21.
XX
PT Normalization of nucleic acid libraries.
XX
PS Example 2; Page 35; 59pp; English.
XX
CC The invention relates to a new method for normalisation of nucleic acid
CC molecules that comprises using haptenylated nucleic acid molecules in
CC subtractive hybridization to remove the more highly abundant molecules.
CC Normalised libraries produced by the method make all of the nucleic acid
CC molecules present in the library available for isolation and subsequent
CC analysis for the study of normal function of individual genes and the
CC genomes. Using the methods, normalised nucleic acid libraries having a
CC maximum variation in abundance of the member NAMs no greater than 2- to
CC 10-fold may be produced. The methods provide normalised libraries which
CC have significantly reduced background
XX
SQ Sequence 25 BP; 15 A; 4 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 17; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2164 CCTTTTTTTTTTTTTTT 2180
|||||||||||||||||
Db 17 CCTTTTTTTTTTTTTTT 1

RESULT 2171
AAC95828/c
ID AAC95828 standard; DNA; 25 BP.
XX
AC AAC95828;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA HLA-A gene PCR primer #8.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 40; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 3 A; 5 C; 0 G; 17 T; 0 U; 0 Other;

```
  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 2.3e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAA 2804
              ||  || | ||| ||||||||||||
Db         25 GATGTGGAGAAATAAAAAAAAAAAA 1


RESULT 2172
AAC96374/c
ID   AAC96374 standard; DNA; 25 BP.
XX
AC   AAC96374;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DPB1 gene PCR primer #106.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 50; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 4 A; 6 C; 2 G; 13 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 2.3e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2773 CTTGTTAGAATTGAAAAAAAAAAAA 2797
              ||| || ||   ||||||||||||
Db         25 CTTCTTGGAGGGGAAAAAAAAAAAA 1


RESULT 2173
AAC96624
ID   AAC96624 standard; DNA; 25 BP.
XX
AC   AAC96624;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA HLA-A gene PCR primer #1.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 54; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 2 A; 2 C; 4 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 2.3e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAACTTTGAAAGT 2198
              |||||||||||||| | | ||  |||
Db          1 TTTTTTTTTTTTTCAGTCTGTGAGT 25


RESULT 2174
AAC96817/c
ID   AAC96817 standard; DNA; 25 BP.
XX
AC   AAC96817;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA HLA-C gene PCR primer #22.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
```

```
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 57; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 4 A; 3 C; 4 G; 14 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 2.3e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2773 CTTGTTAGAATTGAAAAAAAAAAAA 2797
              |||  | | | ||||||||||||||
Db         25 CTTCATCGCAGTGAAAAAAAAAAAA 1


RESULT 2175
AAC96343
ID   AAC96343 standard; DNA; 25 BP.
XX
AC   AAC96343;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DPB1 gene PCR primer #75.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 49; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 4 A; 3 C; 2 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAACT 2190
              |||||||||||||||||
Db    .     1 TTTTTTTTTTTTTAACT 17


RESULT 2176
AAC95821
ID   AAC95821 standard; DNA; 25 BP.
XX
AC   AAC95821;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA HLA-A gene PCR primer #1.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 40; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 2 A; 2 C; 4 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 2.3e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAACTTTGAAAGT 2198
              |||||||||||||| | | ||  |||
Db         1 TTTTTTTTTTTTTCAGTCTGTGAGT 25


RESULT 2177
AAC96433/c
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```
ID   AAC96433 standard; DNA; 25 BP.
XX
AC   AAC96433;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DQA1 gene PCR primer #35.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 51; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 0 A; 7 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 2.3e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAA 2803
                ||||  ||  || ||||||||||||
Db         25 AGAAGGGAGGAAGAAAAAAAAAAAA 1


RESULT 2178
AAC96784
ID   AAC96784 standard; DNA; 25 BP.
XX
AC   AAC96784;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA HLA-A gene PCR primer #161.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 57; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 3 A; 2 C; 4 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 2.3e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2175 TTTTTTTTTTTTAACTTTGAAAGTT 2199
                ||||||||||||  | || ||| |
Db          1 TTTTTTTTTTTTACTTCTGGAAGGT 25


RESULT 2179
AAC96788
ID   AAC96788 standard; DNA; 25 BP.
XX
AC   AAC96788;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA HLA-A gene PCR primer #165.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 57; 66pp; English.
```

```
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 3 A; 2 C; 3 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 2.3e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAACTTTGAAAGT 2198
              ||||||||||||| | | ||  |||
Db          1 TTTTTTTTTTTTTCAATCTGTGAGT 25


RESULT 2180
AAC96788/c
ID   AAC96788 standard; DNA; 25 BP.
XX
AC   AAC96788;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA HLA-A gene PCR primer #165.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
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XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 57; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 3 A; 2 C; 3 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAA 2798
              |||||||||||||||||
Db         17 ATTGAAAAAAAAAAAAA 1


RESULT 2181
AAC95789
ID   AAC95789 standard; DNA; 25 BP.
XX
AC   AAC95789;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DRB1 gene PCR primer #33.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
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DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 40; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 2 A; 2 C; 4 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 2.3e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAACTTTGAAAGT 2198
              |||||||||||||  | |||  ||
Db          1 TTTTTTTTTTTTTACGTCTGAGTGT 25


RESULT 2182
AAC96182
ID   AAC96182 standard; DNA; 25 BP.
XX
AC   AAC96182;
XX
DT   26-FEB-2001  (first entry)
XX
DE   16s rRNA gene PCR primer #149.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
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```
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 46; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 4 A; 6 C; 1 G; 14 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTAAC 2189
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTAAC 17


RESULT 2183
AAC96830
ID   AAC96830 standard; DNA; 25 BP.
XX
AC   AAC96830;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA HLA-C gene PCR primer #35.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 58; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 2 A; 4 C; 3 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 2.3e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTAACTTTGAAAG 2197
              ||||||||||||||| |||   |  ||
Db          1 TTTTTTTTTTTTTTCACTCGGTCAG 25


RESULT 2184
AAC96172
ID   AAC96172 standard; DNA; 25 BP.
XX
AC   AAC96172;
XX
DT   26-FEB-2001  (first entry)
XX
DE   16s rRNA gene PCR primer #139.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 46; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 3 A; 0 C; 4 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
```

```
  Best Local Similarity   80.0%;  Pred. No. 2.3e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||||||||| || | || | |
Db          1 TTTTTTTTTTTTTGTTGTGAAATGT 25


RESULT 2185
AAC96172/c
ID   AAC96172 standard; DNA; 25 BP.
XX
AC   AAC96172;
XX
DT   26-FEB-2001  (first entry)
XX
DE   16s rRNA gene PCR primer #139.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 46; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 3 A; 0 C; 4 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 2.3e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAA 2803
              | | || | || ||||||||||||||
Db         25 ACATTTCACAACAAAAAAAAAAAAA 1


RESULT 2186
AAC96171
ID   AAC96171 standard; DNA; 25 BP.
XX
AC   AAC96171;
XX
DT   26-FEB-2001  (first entry)
XX
DE   16s rRNA gene PCR primer #138.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 46; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 7 A; 3 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTAAC 2189
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTAAC 17


RESULT 2187
AAC96171/c
ID   AAC96171 standard; DNA; 25 BP.
XX
AC   AAC96171;
XX
DT   26-FEB-2001  (first entry)
XX
DE   16s rRNA gene PCR primer #138.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
```

```
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 46; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 7 A; 3 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 2.3e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2774 TTGTTAGAATTGAAAAAAAAAAAAA 2798
              ||||  |  || ||||||||||||||
Db         25 TTGTATGTGTTAAAAAAAAAAAAA 1


RESULT 2188
AAC96219/c
ID   AAC96219 standard; DNA; 25 BP.
XX
AC   AAC96219;
XX
DT   26-FEB-2001  (first entry)
XX
DE   16s rRNA gene PCR primer #186.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 47; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 1 A; 5 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 2.3e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAA 2803
              | ||| |   ||||||||||||||||
Db         25 ACAATGGGGGAAAAAAAAAAAAAAA 1


RESULT 2189
AAC96598/c
ID   AAC96598 standard; DNA; 25 BP.
XX
AC   AAC96598;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DRB345 gene PCR primer #69.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 54; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 5 A; 3 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAA 2797
              |||||||||||||||||
Db         17 AATTGAAAAAAAAAAAA 1


RESULT 2190
AAC96121
ID   AAC96121 standard; DNA; 25 BP.
XX
```

```
AC   AAC96121;
XX
DT   26-FEB-2001  (first entry)
XX
DE   16s rRNA gene PCR primer #88.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 45; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 4 A; 1 C; 5 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 2.3e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTAACTTTGAAAG 2197
             ||||||||||||||| | |  | |||
Db          1 TTTTTTTTTTTTTTCAGTGAGGAAG 25


RESULT 2191
AAC96156
ID   AAC96156 standard; DNA; 25 BP.
XX
AC   AAC96156;
XX
DT   26-FEB-2001  (first entry)
XX
DE   16s rRNA gene PCR primer #123.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 46; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 3 A; 3 C; 3 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2175 TTTTTTTTTTTTAACTT 2191
             |||||||||||||||||
Db          1 TTTTTTTTTTTTAACTT 17


RESULT 2192
AAC95962/c
ID   AAC95962 standard; DNA; 25 BP.
XX
AC   AAC95962;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA HLA-B gene PCR primer #73.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 43; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
```

```
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 2 A; 7 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 2.3e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2776 GTTAGAATTGAAAAAAAAAAAAAA 2800
              | | || | | ||||||||||||||
Db         25 GGTGGACTGGGAAAAAAAAAAAAAA 1


RESULT 2193
AAC96197
ID   AAC96197 standard; DNA; 25 BP.
XX
AC   AAC96197;
XX
DT   26-FEB-2001  (first entry)
XX
DE   16s rRNA gene PCR primer #164.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 47; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 5 A; 1 C; 5 G; 14 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 2.3e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTAACTTTGAAAG 2197
              ||||||||||||  |  | ||||||
Db          1 TTTTTTTTTTTTCGAGATGTGAAAG 25


RESULT 2194
AAC95728/c
ID   AAC95728 standard; DNA; 25 BP.
XX
AC   AAC95728;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DQA1 gene PCR primer #25.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 39; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 5 A; 3 C; 1 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 2.3e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2773 CTTGTTAGAATTGAAAAAAAAAAAA 2797
              ||  | ||| || ||||||||||||
Db         25 CTGATGAGATTTAAAAAAAAAAAAA 1


RESULT 2195
AAC96429/c
ID   AAC96429 standard; DNA; 25 BP.
XX
AC   AAC96429;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DQA1 gene PCR primer #31.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
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```
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 51; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 5 A; 3 C; 1 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 2.3e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2773 CTTGTTAGAATTGAAAAAAAAAAAA 2797
              ||  | ||| || ||||||||||||
Db         25 CTGATGAGATTTAAAAAAAAAAAAA 1


RESULT 2196
AAC95855
ID   AAC95855 standard; DNA; 25 BP.
XX
AC   AAC95855;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA HLA-A gene PCR primer #35.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 41; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 3 A; 2 C; 3 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 2.3e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAACTTTGAAAGT 2198
              |||||||||||||  | | ||  |||
Db          1 TTTTTTTTTTTTTCAATCTGTGAGT 25


RESULT 2197
AAC95855/c
ID   AAC95855 standard; DNA; 25 BP.
XX
AC   AAC95855;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA HLA-A gene PCR primer #35.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 41; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 3 A; 2 C; 3 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy       2782 ATTGAAAAAAAAAAAAA 2798
              |||||||||||||||||
Db         17 ATTGAAAAAAAAAAAAA 1
```

RESULT 2198
AAC96075
ID AAC96075 standard; DNA; 25 BP.
XX
AC AAC96075;
XX
DT 26-FEB-2001 (first entry)
XX
DE 16s rRNA gene PCR primer #42.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 45; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 3 A; 2 C; 4 G; 16 T; 0 U; 0 Other;

Query Match 0.6%; Score 17; DB 1; Length 25;
Best Local Similarity 80.0%; Pred. No. 2.3e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy       2175 TTTTTTTTTTTTAACTTTGAAAGTT 2199
              ||||||||||||  |||| | || |
Db          1 TTTTTTTTTTTTGGCTTTCAGAGAT 25
```

RESULT 2199
AAS06803/c
ID AAS06803 standard; DNA; 25 BP.
XX
AC AAS06803;
XX
DT 12-SEP-2001 (first entry)
XX
DE Protein kinase cDNA PCR primer #26.
XX
KW Human; protein kinase; PTK; STK; cancer; cardiovascular disease;
KW metabolic disorder; immune related disease; neurological disorder;
KW neurodegenerative disorder; inflammatory disorder; infectious disease;
KW reproductive disorder; gene therapy; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200138503-A2.
XX
PD 31-MAY-2001.
XX
PF 22-NOV-2000; 2000WO-US032085.
XX
PR 24-NOV-1999; 99US-0167482P.
XX
PA (SUGE-) SUGEN INC.
XX
PI Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;
PI Flanagan P, Clary D;
XX
DR WPI; 2001-343950/36.
XX
PT Nucleic acids encoding human kinase polypeptides, useful for preventing
PT diagnosing and/or treating e.g. cancer, immune, cardiovascular and
PT neuronal-associated diseases, and microbial infections.
XX
PS Example 2C; Page 298; 433pp; English.
XX
CC AAS06778-AAS06827 represent PCR primers used to amplify human cDNA
CC sequences encoding for novel protein kinases (AAU03501-AAU03557). The
CC novel protein kinases have been identified as members of the tyrosine or
CC serine/threonine kinase (PTK and STK) families. The polynucleotides
CC encoding protein kinases and the polypeptides may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate kinase expression. For example, they may be used to treat
CC cancers (especially cancers of haematopoietic origin), cardiovascular
CC disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),
CC immune related diseases (e.g. rheumatoid arthritis), neurological
CC disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.
CC Parkinson's disease), inflammatory disorders (e.g. asthma), infectious
CC disease (e.g. HIV) and reproductive disorders (e.g. infertility).
CC Additionally, polynucleotides encoding protein kinases may be used for
CC gene therapy and as DNA probes in diagnostic assays. The protein kinase
CC polypeptides may be used as antigens in the production of antibodies
CC against the protein kinases and in assays to identify modulators of
CC protein kinase expression and activity
XX
SQ Sequence 25 BP; 12 A; 1 C; 10 G; 2 T; 0 U; 0 Other;

Query Match 0.6%; Score 17; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1786 CCCATTCTTTCCTTCTC 1802
              |||||||||||||||||
Db         19 CCCATTCTTTCCTTCTC 3
```

RESULT 2200
AAF99738
ID AAF99738 standard; DNA; 25 BP.
XX
AC AAF99738;
XX
DT 12-JUN-2001 (first entry)
XX
DE Immunostimulatory nucleic acid #854.
XX
KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS Synthetic.

XX
PN WO200122972-A2.
XX
PD 05-APR-2001.
XX
PF 25-SEP-2000; 2000WO-US026383.
XX
PR 25-SEP-1999; 99US-0156113P.
PR 27-SEP-1999; 99US-0156135P.
PR 23-AUG-2000; 2000US-0227436P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
XX
PI Krieg AM, Schetter C, Vollmer J;
XX
DR WPI; 2001-273485/28.
XX
PT Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids.
XX
PS Claim 101; Page 56; 338pp; English.
XX
CC The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells. Note: the
CC present sequence may have a phosphorothioate backbone
XX
SQ Sequence 25 BP; 0 A; 0 C; 6 G; 19 T; 0 U; 0 Other;

Query Match 0.6%; Score 17; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTT 2182
||||||||||||||||||
Db 9 TTTTTTTTTTTTTTTTT 25

RESULT 2201
AAF99738/c
ID AAF99738 standard; DNA; 25 BP.
XX
AC AAF99738;
XX
DT 12-JUN-2001 (first entry)
XX
DE Immunostimulatory nucleic acid #854.
XX
KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200122972-A2.
XX
PD 05-APR-2001.
XX
PF 25-SEP-2000; 2000WO-US026383.
XX
PR 25-SEP-1999; 99US-0156113P.
PR 27-SEP-1999; 99US-0156135P.
PR 23-AUG-2000; 2000US-0227436P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
XX
PI Krieg AM, Schetter C, Vollmer J;
XX
DR WPI; 2001-273485/28.
XX
PT Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids.
XX
PS Claim 101; Page 56; 338pp; English.
XX
CC The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells. Note: the
CC present sequence may have a phosphorothioate backbone
XX
SQ Sequence 25 BP; 0 A; 0 C; 6 G; 19 T; 0 U; 0 Other;

Query Match 0.6%; Score 17; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAA 2802
|||||||||||||||||
Db 25 AAAAAAAAAAAAAAAAA 9

RESULT 2202
AAH39959/c
ID AAH39959 standard; DNA; 25 BP.
XX
AC AAH39959;
XX
DT 14-AUG-2001 (first entry)
XX
DE SNP specific SNPE primer SEQ ID 2755.
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW inflammation; forensic investigation; paternity analysis; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200129262-A2.
XX
PD 26-APR-2001.
XX
PF 13-OCT-2000; 2000WO-US028436.
XX
PR 15-OCT-1999; 99US-0160096P.
XX
PA (ORCH-) ORCHID BIOSCIENCES INC.
XX
PI Picoult-Newburg L, Pohl M;
XX
DR WPI; 2001-290930/30.

XX
PT New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample.
XX
PS Claim 1; Page 64; 83pp; English.
XX
CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a single nucleotide
CC primer extension (SNPE) primer specific for a human SNP containing DNA
CC sequence
XX
SQ Sequence 25 BP; 16 A; 2 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 0.6%; Score 17; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2172 TTTTTTTTTTTTTTTAA 2188
||||||||||||||||||
Db 24 TTTTTTTTTTTTTTTAA 8

RESULT 2203
ABS78459
ID ABS78459 standard; DNA; 25 BP.
XX
AC ABS78459;
XX
DT 13-DEC-2002 (first entry)
XX
DE Angiogenesis inhibitory oligonucleotide #943.
XX
KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW plaque neovascularisation; telangiectasia; haemophiliac joint;
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW scleroderma; hypertrophic scar.
XX
OS Synthetic.
XX
PN WO200253141-A2.
XX
PD 11-JUL-2002.
XX
PF 14-DEC-2001; 2001WO-US048458.
XX
PR 14-DEC-2000; 2000US-0255534P.
XX
PA (COLE-) COLEY PHARM GROUP INC.
XX
PI Bratzler RL;
XX
DR WPI; 2002-566690/60.
XX
PT Inhibiting angiogenesis in a subject, involves administering at least one
PT antiangiogenic nucleic acid molecule to the subject.
XX
PS Claim 2; Page 36; 276pp; English.
XX
CC The invention relates to inhibiting angiogenesis in a subject, comprising
CC administering at least one antiangiogenic nucleic acid molecule. Also
CC included is a kit comprising a first container housing the antiangiogenic
CC nucleic acids, and instructions for administering them to a subject
CC having a condition characterised by unwanted angiogenesis. The method is
CC useful for inhibiting angiogenesis associated with solid tumour growth,
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC acid of the invention
XX
SQ Sequence 25 BP; 0 A; 0 C; 6 G; 19 T; 0 U; 0 Other;

Query Match 0.6%; Score 17; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTT 2182
|||||||||||||||||
Db 9 TTTTTTTTTTTTTTTTT 25

RESULT 2204
ABS78459/c
ID ABS78459 standard; DNA; 25 BP.
XX
AC ABS78459;
XX
DT 13-DEC-2002 (first entry)
XX
DE Angiogenesis inhibitory oligonucleotide #943.
XX
KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW plaque neovascularisation; telangiectasia; haemophiliac joint;
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW scleroderma; hypertrophic scar.
XX
OS Synthetic.
XX
PN WO200253141-A2.
XX
PD 11-JUL-2002.
XX
PF 14-DEC-2001; 2001WO-US048458.
XX
PR 14-DEC-2000; 2000US-0255534P.
XX
PA (COLE-) COLEY PHARM GROUP INC.
XX
PI Bratzler RL;
XX
DR WPI; 2002-566690/60.
XX
PT Inhibiting angiogenesis in a subject, involves administering at least one
PT antiangiogenic nucleic acid molecule to the subject.

```
XX
PS   Claim 2; Page 36; 276pp; English.
XX
CC   The invention relates to inhibiting angiogenesis in a subject, comprising
CC   administering at least one antiangiogenic nucleic acid molecule. Also
CC   included is a kit comprising a first container housing the antiangiogenic
CC   nucleic acids, and instructions for administering them to a subject
CC   having a condition characterised by unwanted angiogenesis. The method is
CC   useful for inhibiting angiogenesis associated with solid tumour growth,
CC   tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC   diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC   corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC   rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC   neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,
CC   wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC   hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC   acid of the invention
XX
SQ   Sequence 25 BP; 0 A; 0 C; 6 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         25 AAAAAAAAAAAAAAAAA 9


RESULT 2205
ABQ94378
ID   ABQ94378 standard; DNA; 25 BP.
XX
AC   ABQ94378;
XX
DT   28-OCT-2002  (first entry)
XX
DE   Tumour suppression-related oligonucleotide #29.
XX
KW   Tumour; cytostatic; antiviral; neuroprotective; nootropic; neuroleptic;
KW   tumour suppression; tumour reversion; apoptosis; viral resistance; human;
KW   viral infection; cell degeneration disease; neurodegeneration; ds;
KW   Alzheimer's disease; schizophrenia; immune disease; inflammatory disease.
XX
OS   Homo sapiens.
XX
PN   FR2819824-A1.
XX
PD   26-JUL-2002.
XX
PF   23-JAN-2001; 2001FR-00000899.
XX
PR   23-JAN-2001; 2001FR-00000899.
XX
PA   (MOLE-) MOLECULAR ENGINES LAB SA.
XX
PI   Telerman A,  Amson R,  Tuijnder M,  Susini L;
XX
DR   WPI; 2002-610803/66.
XX
PT   New nucleic acid implicated e.g. in tumor suppression, useful for
PT   diagnosis of tumors, viral infection and cellular degeneration and for
PT   drug screening.
XX
PS   Claim 1; Page 46; 623pp; French.
XX
CC   The present invention relates to novel human nucleic acid sequences (I).
CC   The present sequence is one such nucleic acid sequence. Expression of (I)
CC   are implicated in tumour suppression or reversion and apoptosis and viral
CC   resistance. (I) are useful as probes or primers for detecting,
CC   identifying, measuring and/or amplifying nucleic acid sequences, as
CC   antisense reagents and for recombinant production of polypeptides. (I),
CC   polypeptides (II) encoded by (I), vector containing (I), cells containing
CC   these vectors and antibodies (Ab) against (II) are all useful for
CC   treatment/prevention of viral, tumour and cell degeneration diseases
CC   (especially neurodegeneration, such as Alzheimer's disease and
CC   schizophrenia). Analysing the expression of (I) is also useful for
CC   diagnosis and/or prognosis of such diseases. Transgenic animals carrying
CC   (I) are used for studying the aetiology of these diseases (also immune
CC   and inflammatory diseases). Note: In the present specification, SEQ ID 1
CC   to 2280 are claimed in Claim 1, however only SEQ ID 1 to 2270 are shown
CC   in the specification
XX
SQ   Sequence 25 BP; 13 A; 3 C; 3 G; 6 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 2.3e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2774 TTGTTAGAATTGAAAAAAAAAAAAA 2798
              ||| | | ||||  ||||||||||||
Db          1 TTGATCGCATTGTCAAAAAAAAAAA 25


RESULT 2206
ABQ94374
ID   ABQ94374 standard; DNA; 25 BP.
XX
AC   ABQ94374;
XX
DT   28-OCT-2002  (first entry)
XX
DE   Tumour suppression-related oligonucleotide #25.
XX
KW   Tumour; cytostatic; antiviral; neuroprotective; nootropic; neuroleptic;
KW   tumour suppression; tumour reversion; apoptosis; viral resistance; human;
KW   viral infection; cell degeneration disease; neurodegeneration; ds;
KW   Alzheimer's disease; schizophrenia; immune disease; inflammatory disease.
XX
OS   Homo sapiens.
XX
PN   FR2819824-A1.
XX
PD   26-JUL-2002.
XX
PF   23-JAN-2001; 2001FR-00000899.
XX
PR   23-JAN-2001; 2001FR-00000899.
XX
PA   (MOLE-) MOLECULAR ENGINES LAB SA.
XX
PI   Telerman A,  Amson R,  Tuijnder M,  Susini L;
XX
DR   WPI; 2002-610803/66.
XX
PT   New nucleic acid implicated e.g. in tumor suppression, useful for
PT   diagnosis of tumors, viral infection and cellular degeneration and for
PT   drug screening.
XX
PS   Claim 1; Page 46; 623pp; French.
XX
CC   The present invention relates to novel human nucleic acid sequences (I).
CC   The present sequence is one such nucleic acid sequence. Expression of (I)
CC   are implicated in tumour suppression or reversion and apoptosis and viral
CC   resistance. (I) are useful as probes or primers for detecting,
CC   identifying, measuring and/or amplifying nucleic acid sequences, as
CC   antisense reagents and for recombinant production of polypeptides. (I),
CC   polypeptides (II) encoded by (I), vector containing (I), cells containing
CC   these vectors and antibodies (Ab) against (II) are all useful for
CC   treatment/prevention of viral, tumour and cell degeneration diseases
CC   (especially neurodegeneration, such as Alzheimer's disease and
CC   schizophrenia). Analysing the expression of (I) is also useful for
CC   diagnosis and/or prognosis of such diseases. Transgenic animals carrying
CC   (I) are used for studying the aetiology of these diseases (also immune
CC   and inflammatory diseases). Note: In the present specification, SEQ ID 1
CC   to 2280 are claimed in Claim 1, however only SEQ ID 1 to 2270 are shown
```

```
CC   in the specification
XX
SQ   Sequence 25 BP; 13 A; 3 C; 3 G; 6 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 2.3e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2774 TTGTTAGAATTGAAAAAAAAAAAAA 2798
              ||| | | ||||  ||||||||||||
Db          1 TTGATCGCATTGTCAAAAAAAAAAA 25


RESULT 2207
ABQ94375
ID   ABQ94375 standard; DNA; 25 BP.
XX
AC   ABQ94375;
XX
DT   28-OCT-2002  (first entry)
XX
DE   Tumour suppression-related oligonucleotide #26.
XX
KW   Tumour; cytostatic; antiviral; neuroprotective; nootropic; neuroleptic;
KW   tumour suppression; tumour reversion; apoptosis; viral resistance; human;
KW   viral infection; cell degeneration disease; neurodegeneration; ds;
KW   Alzheimer's disease; schizophrenia; immune disease; inflammatory disease.
XX
OS   Homo sapiens.
XX
PN   FR2819824-A1.
XX
PD   26-JUL-2002.
XX
PF   23-JAN-2001; 2001FR-00000899.
XX
PR   23-JAN-2001; 2001FR-00000899.
XX
PA   (MOLE-) MOLECULAR ENGINES LAB SA.
XX
PI   Telerman A,  Amson R,  Tuijnder M,  Susini L;
XX
DR   WPI; 2002-610803/66.
XX
PT   New nucleic acid implicated e.g. in tumor suppression, useful for
PT   diagnosis of tumors, viral infection and cellular degeneration and for
PT   drug screening.
XX
PS   Claim 1; Page 46; 623pp; French.
XX
CC   The present invention relates to novel human nucleic acid sequences (I).
CC   The present sequence is one such nucleic acid sequence. Expression of (I)
CC   are implicated in tumour suppression or reversion and apoptosis and viral
CC   resistance. (I) are useful as probes or primers for detecting,
CC   identifying, measuring and/or amplifying nucleic acid sequences, as
CC   antisense reagents and for recombinant production of polypeptides. (I),
CC   polypeptides (II) encoded by (I), vector containing (I), cells containing
CC   these vectors and antibodies (Ab) against (II) are all useful for
CC   treatment/prevention of viral, tumour and cell degeneration diseases
CC   (especially neurodegeneration, such as Alzheimer's disease and
CC   schizophrenia). Analysing the expression of (I) is also useful for
CC   diagnosis and/or prognosis of such diseases. Transgenic animals carrying
CC   (I) are used for studying the aetiology of these diseases (also immune
CC   and inflammatory diseases). Note: In the present specification, SEQ ID 1
CC   to 2280 are claimed in Claim 1, however only SEQ ID 1 to 2270 are shown
CC   in the specification
XX
SQ   Sequence 25 BP; 13 A; 3 C; 3 G; 6 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 2.3e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2774 TTGTTAGAATTGAAAAAAAAAAAAA 2798
              ||| | | ||||  ||||||||||||
Db          1 TTGATCGCATTGTCAAAAAAAAAAA 25


RESULT 2208
ABS76278
ID   ABS76278 standard; DNA; 25 BP.
XX
AC   ABS76278;
XX
DT   27-DEC-2002  (first entry)
XX
DE   Human PAPP-E exon 7 associated 25-mer SEQ ID 1804.
XX
KW   PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW   contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW   dysgenetic pregnancy; primer; ss.
XX
OS   Homo sapiens.
XX
PN   US2002102252-A1.
XX
PD   01-AUG-2002.
XX
PF   06-APR-2001; 2001US-00827998.
XX
PR   26-MAY-2000; 2000US-0207456P.
XX
PA   (GUYY/) GU Y.
PA   (SHAN/) SHANNON M E.
XX
PI   Gu Y,  Shannon ME;
XX
DR   WPI; 2002-697817/75.
XX
PT   New isolated nucleic acid encoding an isoform of human pregnancy
PT   associated plasma protein E, for preventing or aborting pregnancy.
XX
PS   Example 2; Page 312; 353pp; English.
XX
CC   This invention describes a novel isolated nucleic acid that encodes one
CC   of three new isoforms of human pregnancy associated plasma protein E,
CC   hPAPP-E. The products of the invention have abortive and contraceptive
CC   activity and can be used for gene therapy or in a vaccine. The nucleic
CC   acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC   used in pharmaceutical compositions or vaccines for preventing or
CC   aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC   dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC   the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC   antibodies can be used to assess the expression levels of PAPP-E isoform
CC   proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC   antenatally. This sequence represents an oligomer used in scanning the
CC   human PAPP-E genes described in the disclosure of the invention
XX
SQ   Sequence 25 BP; 1 A; 7 C; 7 G; 10 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 2.3e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2312 GCAATTTGTTGCTGCTTGTCACCCC 2336
              || | ||||||||||||||   |||
Db          1 GCCAGTTGTTGCTGCTTGTGTTCCC 25


RESULT 2209
ABS75770/c
ID   ABS75770 standard; DNA; 25 BP.
XX
AC   ABS75770;
XX
DT   27-DEC-2002  (first entry)
```

```
XX
DE   Human PAPP-Ea associated 25-mer SEQ ID 1296.
XX
KW   PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW   contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW   dysgenetic pregnancy; primer; ss.
XX
OS   Homo sapiens.
XX
PN   US2002102252-A1.
XX
PD   01-AUG-2002.
XX
PF   06-APR-2001; 2001US-00827998.
XX
PR   26-MAY-2000; 2000US-0207456P.
XX
PA   (GUYY/) GU Y.
PA   (SHAN/) SHANNON M E.
XX
PI   Gu Y,  Shannon ME;
XX
DR   WPI; 2002-697817/75.
XX
PT   New isolated nucleic acid encoding an isoform of human pregnancy
PT   associated plasma protein E, for preventing or aborting pregnancy.
XX
PS   Example 2; Page 245; 353pp; English.
XX
CC   This invention describes a novel isolated nucleic acid that encodes one
CC   of three new isoforms of human pregnancy associated plasma protein E,
CC   hPAPP-E. The products of the invention have abortive and contraceptive
CC   activity and can be used for gene therapy or in a vaccine. The nucleic
CC   acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC   used in pharmaceutical compositions or vaccines for preventing or
CC   aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC   dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC   the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC   antibodies can be used to assess the expression levels of PAPP-E isoform
CC   proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC   antenatally. This sequence represents an oligomer used in scanning the
CC   human PAPP-E genes described in the disclosure of the invention
XX
SQ   Sequence 25 BP; 16 A; 0 C; 9 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 2.3e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1770 CTTTTTTTTTTTGAACCCCATTCTT 1794
                ||||  |||||||    ||||  |||||
Db         25 CTTTCTTTTTTTTTCCCCCCTTCTT 1

RESULT 2210
ABS76277
ID   ABS76277 standard; DNA; 25 BP.
XX
AC   ABS76277;
XX
DT   27-DEC-2002  (first entry)
XX
DE   Human PAPP-E exon 7 associated 25-mer SEQ ID 1803.
XX
KW   PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW   contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW   dysgenetic pregnancy; primer; ss.
XX
OS   Homo sapiens.
XX
PN   US2002102252-A1.
XX
PD   01-AUG-2002.
XX
PF   06-APR-2001; 2001US-00827998.
XX
PR   26-MAY-2000; 2000US-0207456P.
XX
PA   (GUYY/) GU Y.
PA   (SHAN/) SHANNON M E.
XX
PI   Gu Y,  Shannon ME;
XX
DR   WPI; 2002-697817/75.
XX
PT   New isolated nucleic acid encoding an isoform of human pregnancy
PT   associated plasma protein E, for preventing or aborting pregnancy.
XX
PS   Example 2; Page 312; 353pp; English.
XX
CC   This invention describes a novel isolated nucleic acid that encodes one
CC   of three new isoforms of human pregnancy associated plasma protein E,
CC   hPAPP-E. The products of the invention have abortive and contraceptive
CC   activity and can be used for gené therapy or in a vaccine. The nucleic
CC   acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC   used in pharmaceutical compositions or vaccines for preventing or
CC   aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC   dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC   the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC   antibodies can be used to assess the expression levels of PAPP-E isoform
CC   proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC   antenatally. This sequence represents an oligomer used in scanning the
CC   human PAPP-E genes described in the disclosure of the invention
XX
SQ   Sequence 25 BP; 2 A; 6 C; 7 G; 10 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 2.3e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2311 AGCAATTTGTTGCTGCTTGTCACCC 2335
                ||| | |||||||||||||||   ||
Db          1 AGCCAGTTGTTGCTGCTTGTGTTCC 25

RESULT 2211
ADB04575
ID   ADB04575 standard; DNA; 25 BP.
XX
AC   ADB04575;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ7 scanning oligonucleotide SEQ ID 5561.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
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```
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 5561; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 25 BP; 4 A; 2 C; 3 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          1 CTTTTTTTTTTTTTTT 17


RESULT 2212
ADB04574
ID   ADB04574 standard; DNA; 25 BP.
XX
AC   ADB04574;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ7 scanning oligonucleotide SEQ ID 5560.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 5560; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 25 BP; 3 A; 2 C; 3 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          2 CTTTTTTTTTTTTTTT 18


RESULT 2213
ABV76902
ID   ABV76902 standard; DNA; 25 BP.
XX
AC   ABV76902;
XX
DT   12-FEB-2003  (first entry)
XX
DE   Inverse-PCR primer used to identify MudJ-fusion sequences.
XX
KW   Enterobacteriacea; Pseudomonad; cellulose; yhjONML operon;
KW   bacterial cellulosebiosynthesis; bcsABZc; bacterial cellulose synthesis;
KW   adrA gene; putative transmembrane protein; MudJ; PCR; primer; ss.
XX
OS   Synthetic.
XX
PN   WO200264817-A2.
XX
PD   22-AUG-2002.
XX
PF   08-FEB-2002; 2002WO-EP001360.
XX
PR   09-FEB-2001; 2001EP-00102809.
PR   12-DEC-2001; 2001EP-00129280.
XX
PA   (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
XX
PI   Roemling U,  Zogaj X,  Nimtz M;
XX
DR   WPI; 2003-058290/05.
XX
PT   Use of a bacteria comprising bcsABZc operon in their chromosome and
PT   expressing the adrA gene, for producing cellulose and for screening
PT   inhibitors of bacterial cellulose biosynthesis.
XX
PS   Disclosure; Page 24; 47pp; English.
XX
CC   The specification describes the use of a bacteria selected from
CC   Enterobacteriaceae and Pseudomonads for producing cellulose or for
CC   screening inhibitors of bacterial cellulosebiosynthesis. The bacteria
CC   comprise the bcsABZc (bacterial cellulose synthesis) operon (formerly
CC   yhjONML operon) in their chromosome and express the adrA gene (encoding
CC   putative transmembrane protein). The bacteria are useful for producing
CC   cellulose and for screening inhibitors of bacterial cellulose
CC   biosynthesis. Inverse PCR primers ABV76901-02 were used to identify MudJ-
CC   fusion sequences, in the course of the invention
XX
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```
SQ   Sequence 25 BP; 5 A; 7 C; 5 G; 8 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 2.3e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2613 AGAAAGCAATAACTTTGTCTCGTTC 2637
              ||   ||||||||||  ||||||||
Db          1 AGTGCGCAATAACTTGCTCTCGTTC 25


RESULT 2214
ACI00609/c
ID   ACI00609 standard; DNA; 25 BP.
XX
AC   ACI00609;
XX
DT   13-OCT-2003  (first entry)
XX
DE   Human microarray DNA oligonucleotide SEQ ID NO 600.
XX
KW   EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW   genetic variation; biallelic marker; polymorphism; human;
KW   cross-species comparison.
XX
OS   Homo sapiens.
XX
PN   US2003104410-A1.
XX
PD   05-JUN-2003.
XX
PF   15-MAR-2002; 2002US-00098263.
XX
PR   16-MAR-2001; 2001US-0276759P.
XX
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Mittmann MP;
XX
DR   WPI; 2003-567953/53.
XX
PT   New array of nucleic acid probes, useful for in situ hybridization, in
PT   Southern, Northern or dot-blot hybridization to identify or detect the
PT   sequence or specific mutations of any gene.
XX
PS   Claim 1; SEQ ID NO 600; 9pp; English.
XX
CC   The invention discloses a microarray comprising a plurality of nucleic
CC   acid probes including one of 2,018,500 fully defined sequences, or its
CC   perfect match, perfect mismatch, antisense match or antisense mismatch.
CC   Also disclosed is a method of gene expression analysis. The array is used
CC   in monitoring gene expression levels by hybridisation to a DNA library,
CC   in analysis of genetic variation or in hybridisation of tag-labelled
CC   compounds. The nucleic acid probes are specifically designed for analysis
CC   of at least one target sequence. The method of analysis comprises
CC   hybridising at least one or more nucleic acids to at least two or more
CC   nucleic acid probes and detecting the hybridisation. The nucleic acid
CC   probes are attached to a solid support. The analysis comprises monitoring
CC   gene expression levels, identifying biallelic markers or polymorphisms,
CC   or family members of a gene and a cross-species comparison. Each of the
CC   nucleic acids further comprises a tag sequence. The array of nucleic acid
CC   probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC   blot hybridisation to identify or detect the sequence or specific
CC   mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC   primer extensions or in screening cDNA or genomic libraries or subclones
CC   for additional subclones containing segments of DNA that have been
CC   isolated and previously sequenced. The sequence presented is one of the
CC   nucleic acid probes incorporated in the microarray. Note: The sequence
CC   data for this patent can also be obtained in electronic format directly
CC   from USPTO at seqdata.uspto.goc/sequence.html
XX
SQ   Sequence 25 BP; 2 A; 8 C; 6 G; 9 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 2.3e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1269 AAGACCGGACACCCCATGGGACCAG 1293
              |||||  ||||||  ||  |||||| |
Db         25 AAGACAGGACACGTCAAGGGACCTG 1


RESULT 2215
ACI03338/c
ID   ACI03338 standard; DNA; 25 BP.
XX
AC   ACI03338;
XX
DT   13-OCT-2003  (first entry)
XX
DE   Human microarray DNA oligonucleotide SEQ ID NO 3329.
XX
KW   EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW   genetic variation; biallelic marker; polymorphism; human;
KW   cross-species comparison.
XX
OS   Homo sapiens.
XX
PN   US2003104410-A1.
XX
PD   05-JUN-2003.
XX
PF   15-MAR-2002; 2002US-00098263.
XX
PR   16-MAR-2001; 2001US-0276759P.
XX
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Mittmann MP;
XX
DR   WPI; 2003-567953/53.
XX
PT   New array of nucleic acid probes, useful for in situ hybridization, in
PT   Southern, Northern or dot-blot hybridization to identify or detect the
PT   sequence or specific mutations of any gene.
XX
PS   Claim 1; SEQ ID NO 3329; 9pp; English.
XX
CC   The invention discloses a microarray comprising a plurality of nucleic
CC   acid probes including one of 2,018,500 fully defined sequences, or its
CC   perfect match, perfect mismatch, antisense match or antisense mismatch.
CC   Also disclosed is a method of gene expression analysis. The array is used
CC   in monitoring gene expression levels by hybridisation to a DNA library,
CC   in analysis of genetic variation or in hybridisation of tag-labelled
CC   compounds. The nucleic acid probes are specifically designed for analysis
CC   of at least one target sequence. The method of analysis comprises
CC   hybridising at least one or more nucleic acids to at least two or more
CC   nucleic acid probes and detecting the hybridisation. The nucleic acid
CC   probes are attached to a solid support. The analysis comprises monitoring
CC   gene expression levels, identifying biallelic markers or polymorphisms,
CC   or family members of a gene and a cross-species comparison. Each of the
CC   nucleic acids further comprises a tag sequence. The array of nucleic acid
CC   probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC   blot hybridisation to identify or detect the sequence or specific
CC   mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC   primer extensions or in screening cDNA or genomic libraries or subclones
CC   for additional subclones containing segments of DNA that have been
CC   isolated and previously sequenced. The sequence presented is one of the
CC   nucleic acid probes incorporated in the microarray. Note: The sequence
CC   data for this patent can also be obtained in electronic format directly
CC   from USPTO at seqdata.uspto.goc/sequence.html
XX
SQ   Sequence 25 BP; 3 A; 9 C; 5 G; 8 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 2.3e+03;
```

```
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1536 GGTTAGGAGAGTAGGGAAGGAACAG 1560
              ||||| || | |||||| ||| |||
Db         25 GGTTACGACAATAGGGACGGACCAG 1

RESULT 2216
ACI61004/c
ID   ACI61004 standard; DNA; 25 BP.
XX
AC   ACI61004;
XX
DT   13-OCT-2003  (first entry)
XX
DE   Human microarray DNA oligonucleotide SEQ ID NO 60995.
XX
KW   EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW   genetic variation; biallelic marker; polymorphism; human;
KW   cross-species comparison.
XX
OS   Homo sapiens.
XX
PN   US2003104410-A1.
XX
PD   05-JUN-2003.
XX
PF   15-MAR-2002; 2002US-00098263.
XX
PR   16-MAR-2001; 2001US-0276759P.
XX
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Mittmann MP;
XX
DR   WPI; 2003-567953/53.
XX
PT   New array of nucleic acid probes, useful for in situ hybridization, in
PT   Southern, Northern or dot-blot hybridization to identify or detect the
PT   sequence or specific mutations of any gene.
XX
PS   Claim 1; SEQ ID NO 60995; 9pp; English.
XX
CC   The invention discloses a microarray comprising a plurality of nucleic
CC   acid probes including one of 2,018,500 fully defined sequences, or its
CC   perfect match, perfect mismatch, antisense match or antisense mismatch.
CC   Also disclosed is a method of gene expression analysis. The array is used
CC   in monitoring gene expression levels by hybridisation to a DNA library,
CC   in analysis of genetic variation or in hybridisation of tag-labelled
CC   compounds. The nucleic acid probes are specifically designed for analysis
CC   of at least one target sequence. The method of analysis comprises
CC   hybridising at least one or more nucleic acids to at least two or more
CC   nucleic acid probes and detecting the hybridisation. The nucleic acid
CC   probes are attached to a solid support. The analysis comprises monitoring
CC   gene expression levels, identifying biallelic markers or polymorphisms,
CC   or family members of a gene and a cross-species comparison. Each of the
CC   nucleic acids further comprises a tag sequence. The array of nucleic acid
CC   probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC   blot hybridisation to identify or detect the sequence or specific
CC   mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC   primer extensions or in screening cDNA or genomic libraries or subclones
CC   for additional subclones containing segments of DNA that have been
CC   isolated and previously sequenced. The sequence presented is one of the
CC   nucleic acid probes incorporated in the microarray. Note: The sequence
CC   data for this patent can also be obtained in electronic format directly
CC   from USPTO at seqdata.uspto.goc/sequence.html
XX
SQ   Sequence 25 BP; 5 A; 8 C; 9 G; 3 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 2.3e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        572 GTGAGCGCCCGCAGGGATGCCTACC 596
              ||||||| |||| ||| | ||| ||
Db         25 GTGAGCGACCGCTGGGCTACCTTCC 1

RESULT 2217
ACI89380/c
ID   ACI89380 standard; DNA; 25 BP.
XX
AC   ACI89380;
XX
DT   14-OCT-2003  (first entry)
XX
DE   Human microarray DNA oligonucleotide SEQ ID NO 89371.
XX
KW   EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW   genetic variation; biallelic marker; polymorphism; human;
KW   cross-species comparison.
XX
OS   Homo sapiens.
XX
PN   US2003104410-A1.
XX
PD   05-JUN-2003.
XX
PF   15-MAR-2002; 2002US-00098263.
XX
PR   16-MAR-2001; 2001US-0276759P.
XX
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Mittmann MP;
XX
DR   WPI; 2003-567953/53.
XX
PT   New array of nucleic acid probes, useful for in situ hybridization, in
PT   Southern, Northern or dot-blot hybridization to identify or detect the
PT   sequence or specific mutations of any gene.
XX
PS   Claim 1; SEQ ID NO 89371; 9pp; English.
XX
CC   The invention discloses a microarray comprising a plurality of nucleic
CC   acid probes including one of 2,018,500 fully defined sequences, or its
CC   perfect match, perfect mismatch, antisense match or antisense mismatch.
CC   Also disclosed is a method of gene expression analysis. The array is used
CC   in monitoring gene expression levels by hybridisation to a DNA library,
CC   in analysis of genetic variation or in hybridisation of tag-labelled
CC   compounds. The nucleic acid probes are specifically designed for analysis
CC   of at least one target sequence. The method of analysis comprises
CC   hybridising at least one or more nucleic acids to at least two or more
CC   nucleic acid probes and detecting the hybridisation. The nucleic acid
CC   probes are attached to a solid support. The analysis comprises monitoring
CC   gene expression levels, identifying biallelic markers or polymorphisms,
CC   or family members of a gene and a cross-species comparison. Each of the
CC   nucleic acids further comprises a tag sequence. The array of nucleic acid
CC   probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC   blot hybridisation to identify or detect the sequence or specific
CC   mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC   primer extensions or in screening cDNA or genomic libraries or subclones
CC   for additional subclones containing segments of DNA that have been
CC   isolated and previously sequenced. The sequence presented is one of the
CC   nucleic acid probes incorporated in the microarray. Note: The sequence
CC   data for this patent can also be obtained in electronic format directly
CC   from USPTO at seqdata.uspto.goc/sequence.html
XX
SQ   Sequence 25 BP; 12 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 2.3e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2425 ACTGGTGCACTTCTTACGACTTTTT 2449
              | ||||| | ||||||| ||||| |
```

```
Db         25 ATTGGTGGATTTCTTACCACTTTAT 1


RESULT 2218
ACI62001
ID   ACI62001 standard; DNA; 25 BP.
XX
AC   ACI62001;
XX
DT   13-OCT-2003  (first entry)
XX
DE   Human microarray DNA oligonucleotide SEQ ID NO 61992.
XX
KW   EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW   genetic variation; biallelic marker; polymorphism; human;
KW   cross-species comparison.
XX
OS   Homo sapiens.
XX
PN   US2003104410-A1.
XX
PD   05-JUN-2003.
XX
PF   15-MAR-2002; 2002US-00098263.
XX
PR   16-MAR-2001; 2001US-0276759P.
XX
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Mittmann MP;
XX
DR   WPI; 2003-567953/53.
XX
PT   New array of nucleic acid probes, useful for in situ hybridization, in
PT   Southern, Northern or dot-blot hybridization to identify or detect the
PT   sequence or specific mutations of any gene.
XX
PS   Claim 1; SEQ ID NO 61992; 9pp; English.
XX
CC   The invention discloses a microarray comprising a plurality of nucleic
CC   acid probes including one of 2,018,500 fully defined sequences, or its
CC   perfect match, perfect mismatch, antisense match or antisense mismatch.
CC   Also disclosed is a method of gene expression analysis. The array is used
CC   in monitoring gene expression levels by hybridisation to a DNA library,
CC   in analysis of genetic variation or in hybridisation of tag-labelled
CC   compounds. The nucleic acid probes are specifically designed for analysis
CC   of at least one target sequence. The method of analysis comprises
CC   hybridising at least one or more nucleic acids to at least two or more
CC   nucleic acid probes and detecting the hybridisation. The nucleic acid
CC   probes are attached to a solid support. The analysis comprises monitoring
CC   gene expression levels, identifying biallelic markers or polymorphisms,
CC   or family members of a gene and a cross-species comparison. Each of the
CC   nucleic acids further comprises a tag sequence. The array of nucleic acid
CC   probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC   blot hybridisation to identify or detect the sequence or specific
CC   mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC   primer extensions or in screening cDNA or genomic libraries or subclones
CC   for additional subclones containing segments of DNA that have been
CC   isolated and previously sequenced. The sequence presented is one of the
CC   nucleic acid probes incorporated in the microarray. Note: The sequence
CC   data for this patent can also be obtained in electronic format directly
CC   from USPTO at seqdata.uspto.goc/sequence.html
XX
SQ   Sequence 25 BP; 4 A; 4 C; 6 G; 11 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 2.3e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1917 ATACCTTTTTTTTCAGTGTTAAGGT 1941
              | || | | ||||||||||| ||||
Db          1 AGACTTGTCTTTTCAGTGTTCAGGT 25


RESULT 2219
ACI30406/c
ID   ACI30406 standard; DNA; 25 BP.
XX
AC   ACI30406;
XX
DT   13-OCT-2003  (first entry)
XX
DE   Human microarray DNA oligonucleotide SEQ ID NO 30397.
XX
KW   EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW   genetic variation; biallelic marker; polymorphism; human;
KW   cross-species comparison.
XX
OS   Homo sapiens.
XX
PN   US2003104410-A1.
XX
PD   05-JUN-2003.
XX
PF   15-MAR-2002; 2002US-00098263.
XX
PR   16-MAR-2001; 2001US-0276759P.
XX
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Mittmann MP;
XX
DR   WPI; 2003-567953/53.
XX
PT   New array of nucleic acid probes, useful for in situ hybridization, in
PT   Southern, Northern or dot-blot hybridization to identify or detect the
PT   sequence or specific mutations of any gene.
XX
PS   Claim 1; SEQ ID NO 30397; 9pp; English.
XX
CC   The invention discloses a microarray comprising a plurality of nucleic
CC   acid probes including one of 2,018,500 fully defined sequences, or its
CC   perfect match, perfect mismatch, antisense match or antisense mismatch.
CC   Also disclosed is a method of gene expression analysis. The array is used
CC   in monitoring gene expression levels by hybridisation to a DNA library,
CC   in analysis of genetic variation or in hybridisation of tag-labelled
CC   compounds. The nucleic acid probes are specifically designed for analysis
CC   of at least one target sequence. The method of analysis comprises
CC   hybridising at least one or more nucleic acids to at least two or more
CC   nucleic acid probes and detecting the hybridisation. The nucleic acid
CC   probes are attached to a solid support. The analysis comprises monitoring
CC   gene expression levels, identifying biallelic markers or polymorphisms,
CC   or family members of a gene and a cross-species comparison. Each of the
CC   nucleic acids further comprises a tag sequence. The array of nucleic acid
CC   probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC   blot hybridisation to identify or detect the sequence or specific
CC   mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC   primer extensions or in screening cDNA or genomic libraries or subclones
CC   for additional subclones containing segments of DNA that have been
CC   isolated and previously sequenced. The sequence presented is one of the
CC   nucleic acid probes incorporated in the microarray. Note: The sequence
CC   data for this patent can also be obtained in electronic format directly
CC   from USPTO at seqdata.uspto.goc/sequence.html
XX
SQ   Sequence 25 BP; 10 A; 5 C; 4 G; 6 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 2.3e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2234 GTTCCCTTAAGGTACTGAAGCTTTA 2258
              |||   ||| |||||||| |||||
Db         25 GTTAGTTTACGGTACTGAACCTTTA 1


RESULT 2220
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```
ACK15478
ID   ACK15478 standard; DNA; 25 BP.
XX
AC   ACK15478;
XX
DT   14-OCT-2003  (first entry)
XX
DE   Human microarray DNA oligonucleotide SEQ ID NO 115459.
XX
KW   EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW   genetic variation; biallelic marker; polymorphism; human;
KW   cross-species comparison.
XX
OS   Homo sapiens.
XX
PN   US2003104410-A1.
XX
PD   05-JUN-2003.
XX
PF   15-MAR-2002; 2002US-00098263.
XX
PR   16-MAR-2001; 2001US-0276759P.
XX
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Mittmann MP;
XX
DR   WPI; 2003-567953/53.
XX
PT   New array of nucleic acid probes, useful for in situ hybridization, in
PT   Southern, Northern or dot-blot hybridization to identify or detect the
PT   sequence or specific mutations of any gene.
XX
PS   Claim 1; SEQ ID NO 115459; 9pp; English.
XX
CC   The invention discloses a microarray comprising a plurality of nucleic
CC   acid probes including one of 2,018,500 fully defined sequences, or its
CC   perfect match, perfect mismatch, antisense match or antisense mismatch.
CC   Also disclosed is a method of gene expression analysis. The array is used
CC   in monitoring gene expression levels by hybridisation to a DNA library,
CC   in analysis of genetic variation or in hybridisation of tag-labelled
CC   compounds. The nucleic acid probes are specifically designed for analysis
CC   of at least one target sequence. The method of analysis comprises
CC   hybridising at least one or more nucleic acids to at least two or more
CC   nucleic acid probes and detecting the hybridisation. The nucleic acid
CC   probes are attached to a solid support. The analysis comprises monitoring
CC   gene expression levels, identifying biallelic markers or polymorphisms,
CC   or family members of a gene and a cross-species comparison. Each of the
CC   nucleic acids further comprises a tag sequence. The array of nucleic acid
CC   probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC   blot hybridisation to identify or detect the sequence or specific
CC   mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC   primer extensions or in screening cDNA or genomic libraries or subclones
CC   for additional subclones containing segments of DNA that have been
CC   isolated and previously sequenced. The sequence presented is one of the
CC   nucleic acid probes incorporated in the microarray. Note: The sequence
CC   data for this patent can also be obtained in electronic format directly
CC   from USPTO at seqdata.uspto.goc/sequence.html
XX
SQ   Sequence 25 BP; 2 A; 9 C; 8 G; 6 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 2.3e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        541 GCCCCACCTCTCCGGGCTGGAGGCG 565
              | |||  |||||| ||||||| ||
Db          1 GTCCCGACTCTCCTGGCTGGAGTCG 25


RESULT 2221
ACI02702/c
ID   ACI02702 standard; DNA; 25 BP.
XX
AC   ACI02702;
XX
DT   13-OCT-2003  (first entry)
XX
DE   Human microarray DNA oligonucleotide SEQ ID NO 2693.
XX
KW   EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW   genetic variation; biallelic marker; polymorphism; human;
KW   cross-species comparison.
XX
OS   Homo sapiens.
XX
PN   US2003104410-A1.
XX
PD   05-JUN-2003.
XX
PF   15-MAR-2002; 2002US-00098263.
XX
PR   16-MAR-2001; 2001US-0276759P.
XX
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Mittmann MP;
XX
DR   WPI; 2003-567953/53.
XX
PT   New array of nucleic acid probes, useful for in situ hybridization, in
PT   Southern, Northern or dot-blot hybridization to identify or detect the
PT   sequence or specific mutations of any gene.
XX
PS   Claim 1; SEQ ID NO 2693; 9pp; English.
XX
CC   The invention discloses a microarray comprising a plurality of nucleic
CC   acid probes including one of 2,018,500 fully defined sequences, or its
CC   perfect match, perfect mismatch, antisense match or antisense mismatch.
CC   Also disclosed is a method of gene expression analysis. The array is used
CC   in monitoring gene expression levels by hybridisation to a DNA library,
CC   in analysis of genetic variation or in hybridisation of tag-labelled
CC   compounds. The nucleic acid probes are specifically designed for analysis
CC   of at least one target sequence. The method of analysis comprises
CC   hybridising at least one or more nucleic acids to at least two or more
CC   nucleic acid probes and detecting the hybridisation. The nucleic acid
CC   probes are attached to a solid support. The analysis comprises monitoring
CC   gene expression levels, identifying biallelic markers or polymorphisms,
CC   or family members of a gene and a cross-species comparison. Each of the
CC   nucleic acids further comprises a tag sequence. The array of nucleic acid
CC   probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC   blot hybridisation to identify or detect the sequence or specific
CC   mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC   primer extensions or in screening cDNA or genomic libraries or subclones
CC   for additional subclones containing segments of DNA that have been
CC   isolated and previously sequenced. The sequence presented is one of the
CC   nucleic acid probes incorporated in the microarray. Note: The sequence
CC   data for this patent can also be obtained in electronic format directly
CC   from USPTO at seqdata.uspto.goc/sequence.html
XX
SQ   Sequence 25 BP; 3 A; 8 C; 5 G; 9 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 2.3e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1535 AGGTTAGGAGAGTAGGGAAGGAACA 1559
              |||||| || | |||||| ||| ||
Db         25 AGGTTACGACAATAGGGACGGACCA 1


RESULT 2222
ACI83696/c
ID   ACI83696 standard; DNA; 25 BP.
XX
AC   ACI83696;
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XX
DT   14-OCT-2003  (first entry)
XX
DE   Human microarray DNA oligonucleotide SEQ ID NO 83687.
XX
KW   EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW   genetic variation; biallelic marker; polymorphism; human;
KW   cross-species comparison.
XX
OS   Homo sapiens.
XX
PN   US2003104410-A1.
XX
PD   05-JUN-2003.
XX
PF   15-MAR-2002; 2002US-00098263.
XX
PR   16-MAR-2001; 2001US-0276759P.
XX
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Mittmann MP;
XX
DR   WPI; 2003-567953/53.
XX
PT   New array of nucleic acid probes, useful for in situ hybridization, in
PT   Southern, Northern or dot-blot hybridization to identify or detect the
PT   sequence or specific mutations of any gene.
XX
PS   Claim 1; SEQ ID NO 83687; 9pp; English.
XX
CC   The invention discloses a microarray comprising a plurality of nucleic
CC   acid probes including one of 2,018,500 fully defined sequences, or its
CC   perfect match, perfect mismatch, antisense match or antisense mismatch.
CC   Also disclosed is a method of gene expression analysis. The array is used
CC   in monitoring gene expression levels by hybridisation to a DNA library,
CC   in analysis of genetic variation or in hybridisation of tag-labelled
CC   compounds. The nucleic acid probes are specifically designed for analysis
CC   of at least one target sequence. The method of analysis comprises
CC   hybridising at least one or more nucleic acids to at least two or more
CC   nucleic acid probes and detecting the hybridisation. The nucleic acid
CC   probes are attached to a solid support. The analysis comprises monitoring
CC   gene expression levels, identifying biallelic markers or polymorphisms,
CC   or family members of a gene and a cross-species comparison. Each of the
CC   nucleic acids further comprises a tag sequence. The array of nucleic acid
CC   probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC   blot hybridisation to identify or detect the sequence or specific
CC   mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC   primer extensions or in screening cDNA or genomic libraries or subclones
CC   for additional subclones containing segments of DNA that have been
CC   isolated and previously sequenced. The sequence presented is one of the
CC   nucleic acid probes incorporated in the microarray. Note: The sequence
CC   data for this patent can also be obtained in electronic format directly
CC   from USPTO at seqdata.uspto.goc/sequence.html
XX
SQ   Sequence 25 BP; 8 A; 9 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 2.3e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2343 CCCGTGGAGGTTCTGTATTTTAAGA 2367
             ||||||||| |||||| ||  |||
Db         25 CCCGTGGAGCTTCTGTTGTTGGAGA 1


RESULT 2223
ACK11064/c
ID   ACK11064 standard; DNA; 25 BP.
XX
AC   ACK11064;
XX
DT   14-OCT-2003  (first entry)
XX
DE   Human microarray DNA oligonucleotide SEQ ID NO 111045.
XX
KW   EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW   genetic variation; biallelic marker; polymorphism; human;
KW   cross-species comparison.
XX
OS   Homo sapiens.
XX
PN   US2003104410-A1.
XX
PD   05-JUN-2003.
XX
PF   15-MAR-2002; 2002US-00098263.
XX
PR   16-MAR-2001; 2001US-0276759P.
XX
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Mittmann MP;
XX
DR   WPI; 2003-567953/53.
XX
PT   New array of nucleic acid probes, useful for in situ hybridization, in
PT   Southern, Northern or dot-blot hybridization to identify or detect the
PT   sequence or specific mutations of any gene.
XX
PS   Claim 1; SEQ ID NO 111045; 9pp; English.
XX
CC   The invention discloses a microarray comprising a plurality of nucleic
CC   acid probes including one of 2,018,500 fully defined sequences, or its
CC   perfect match, perfect mismatch, antisense match or antisense mismatch.
CC   Also disclosed is a method of gene expression analysis. The array is used
CC   in monitoring gene expression levels by hybridisation to a DNA library,
CC   in analysis of genetic variation or in hybridisation of tag-labelled
CC   compounds. The nucleic acid probes are specifically designed for analysis
CC   of at least one target sequence. The method of analysis comprises
CC   hybridising at least one or more nucleic acids to at least two or more
CC   nucleic acid probes and detecting the hybridisation. The nucleic acid
CC   probes are attached to a solid support. The analysis comprises monitoring
CC   gene expression levels, identifying biallelic markers or polymorphisms,
CC   or family members of a gene and a cross-species comparison. Each of the
CC   nucleic acids further comprises a tag sequence. The array of nucleic acid
CC   probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC   blot hybridisation to identify or detect the sequence or specific
CC   mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC   primer extensions or in screening cDNA or genomic libraries or subclones
CC   for additional subclones containing segments of DNA that have been
CC   isolated and previously sequenced. The sequence presented is one of the
CC   nucleic acid probes incorporated in the microarray. Note: The sequence
CC   data for this patent can also be obtained in electronic format directly
CC   from USPTO at seqdata.uspto.goc/sequence.html
XX
SQ   Sequence 25 BP; 12 A; 6 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 2.3e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2341 TCCCCGTGGAGGTTCTGTATTTTAA 2365
              | | ||| |||||||||| | ||||
Db         25 TTCTCGTTGAGGTTCTGTGTATTAA 1


RESULT 2224
ACH03276
ID   ACH03276 standard; DNA; 25 BP.
XX
AC   ACH03276;
XX
DT   25-SEP-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #911.
```

```
XX
KW   Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW   antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW   psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW   inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS   Synthetic.
XX
PN   US2003050268-A1.
XX
PD   13-MAR-2003.
XX
PF   29-MAR-2002; 2002US-00112653.
XX
PR   29-MAR-2001; 2001US-0279642P.
XX
PA   (KRIE/) KRIEG A M.
PA   (BERG/) BERG D J.
XX
PI   Krieg AM,  Berg DJ;
XX
DR   WPI; 2003-521815/49.
XX
PT   Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT   allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT   disease by administering an immunostimulatory nucleic acid.
XX
PS   Disclosure; Page 33; 229pp; English.
XX
CC   The invention describes a method of treating non-allergic inflammatory
CC   disease comprising administering to a subject having or at risk of
CC   developing a non-allergic inflammatory disease an immunostimulatory
CC   nucleic acid for prevention or treatment of the disease. The method is
CC   useful for treating non-allergic inflammatory diseases, such as
CC   psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC   inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC   This sequence represents an immunostimulatory nucleic acid
XX
SQ   Sequence 25 BP; 0 A; 0 C; 6 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          9 TTTTTTTTTTTTTTTTT 25


RESULT 2225
ACH03276/c
ID   ACH03276 standard; DNA; 25 BP.
XX
AC   ACH03276;
XX
DT   25-SEP-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #911.
XX
KW   Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW   antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW   psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW   inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS   Synthetic.
XX
PN   US2003050268-A1.
XX
PD   13-MAR-2003.
XX
PF   29-MAR-2002; 2002US-00112653.
XX
PR   29-MAR-2001; 2001US-0279642P.
XX
PA   (KRIE/) KRIEG A M.
PA   (BERG/) BERG D J.
XX
PI   Krieg AM,  Berg DJ;
XX
DR   WPI; 2003-521815/49.
XX
PT   Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT   allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT   disease by administering an immunostimulatory nucleic acid.
XX
PS   Disclosure; Page 33; 229pp; English.
XX
CC   The invention describes a method of treating non-allergic inflammatory
CC   disease comprising administering to a subject having or at risk of
CC   developing a non-allergic inflammatory disease an immunostimulatory
CC   nucleic acid for prevention or treatment of the disease. The method is
CC   useful for treating non-allergic inflammatory diseases, such as
CC   psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC   inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC   This sequence represents an immunostimulatory nucleic acid
XX
SQ   Sequence 25 BP; 0 A; 0 C; 6 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         25 AAAAAAAAAAAAAAAAA 9


RESULT 2226
ADB37240
ID   ADB37240 standard; DNA; 25 BP.
XX
AC   ADB37240;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #854.
XX
KW   ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW   hypo-responsive subject; immunostimulatory.
XX
OS   Synthetic.
XX
PN   US2003087848-A1.
XX
PD   08-MAY-2003.
XX
PF   02-FEB-2001; 2001US-00776479.
XX
PR   03-FEB-2000; 2000US-0179991P.
XX
PA   (BRAT/) BRATZLER R L.
PA   (PETE/) PETERSEN D M.
PA   (FOUR/) FOURON Y.
XX
PI   Bratzler RL,  Petersen DM,  Fouron Y;
XX
DR   WPI; 2003-657977/62.
XX
PT   Treating and/or preventing allergy or asthma using an immunostimulatory
PT   nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS   Disclosure; Page 18; 221pp; English.
XX
CC   The invention relates to a method of treating or preventing allergy or
CC   asthma which comprises administering to a subject a poly-G nucleic acid
CC   in an aerosol formulation. The methods and compositions of the present
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CC   invention are useful for diagnosing and/or treating asthma and allergy
CC   especially in a hypo-responsive subject. The present sequence represents
CC   an immunostimulatory nucleic acid of the invention.
XX
SQ   Sequence 25 BP; 0 A; 0 C; 6 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          9 TTTTTTTTTTTTTTTTT 25


RESULT 2227
ADB37240/c
ID   ADB37240 standard; DNA; 25 BP.
XX
AC   ADB37240;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #854.
XX
KW   ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW   hypo-responsive subject; immunostimulatory.
XX
OS   Synthetic.
XX
PN   US2003087848-A1.
XX
PD   08-MAY-2003.
XX
PF   02-FEB-2001; 2001US-00776479.
XX
PR   03-FEB-2000; 2000US-0179991P.
XX
PA   (BRAT/) BRATZLER R L.
PA   (PETE/) PETERSEN D M.
PA   (FOUR/) FOURON Y.
XX
PI   Bratzler RL,  Petersen DM,  Fouron Y;
XX
DR   WPI; 2003-657977/62.
XX
PT   Treating and/or preventing allergy or asthma using an immunostimulatory
PT   nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS   Disclosure; Page 18; 221pp; English.
XX
CC   The invention relates to a method of treating or preventing allergy or
CC   asthma which comprises administering to a subject a poly-G nucleic acid
CC   in an aerosol formulation. The methods and compositions of the present
CC   invention are useful for diagnosing and/or treating asthma and allergy
CC   especially in a hypo-responsive subject. The present sequence represents
CC   an immunostimulatory nucleic acid of the invention.
XX
SQ   Sequence 25 BP; 0 A; 0 C; 6 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         25 AAAAAAAAAAAAAAAAA 9


RESULT 2228
AAT99265/c
ID   AAT99265 standard; DNA; 26 BP.
XX
AC   AAT99265;
XX
DT   15-APR-1998  (first entry)
XX
DE   Human PUR-alpha gene primer PDT-01.
XX
KW   PUR element; human; c-myc; inhibitor; hyperproliferative disease; ss;
KW   cancer; PCR; primer; amplification.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US5672479-A.
XX
PD   30-SEP-1997.
XX
PF   07-JUN-1995;   95US-00486421.
XX
PR   28-AUG-1992;   92US-00938189.
PR   02-FEB-1993;   93US-00014943.
PR   06-JUN-1995;   95US-00470911.
XX
PA   (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX
PI   Bergemann AD,  Johnson EM;
XX
DR   WPI; 1997-488859/45.
XX
PT   Assays for PUR protein ligands or modulators - using immobilised PUR
PT   protein or fragments, to treat hyper-proliferative diseases, e.g. cancer.
XX
PS   Disclosure; Col 9; 64pp; English.
XX
CC   The primers AAT99265-T99269 were used to PCR amplify and isolate the
CC   complete sequence of the human PUR-alpha gene (AAT99264). The PUR
CC   sequence can be used to identify chemical or biological compounds that
CC   bind to PUR or binding fragments of PUR. Inhibitors of PUR activity may
CC   be used to treat hyperproliferative diseases such as cancer
XX
SQ   Sequence 26 BP; 2 A; 2 C; 2 G; 20 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         26 AAAAAAAAAAAAAAAAA 10


RESULT 2229
AAV31721/c
ID   AAV31721 standard; DNA; 26 BP.
XX
AC   AAV31721;
XX
DT   24-SEP-1998  (first entry)
XX
DE   Nucleotide sequence of the PUR specific PCR primer.
XX
KW   PUR-alpha gene; inhibition; viral infection; cancer; PCR; primer;
KW   hyperproliferative disease; amplification; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US5756684-A.
XX
PD   26-MAY-1998.
XX
PF   06-JUN-1995;   95US-00470911.
XX
PR   28-AUG-1992;   92US-00938189.
```

PR 02-FEB-1993; 93US-00014943.
XX
PA (MOUN) MOUNT SINAI SCHOOL MEDICINE.
XX
PI Bergemann AD, Johnson EM;
XX
DR WPI; 1998-321632/28.
XX
PT PUR protein and its fragments - that inhibit PUR protein binding to PUR
PT element or other proteins.
XX
PS Disclosure; Col 9; 63pp; English.
XX
CC This is the nucleotide sequence of the PUR psecific PCR primer used for
CC amplification in the method of the invention, involving the use of the
CC PUR protein and its fragments, which inhibit PUR protein binding to PUR
CC element or other proteins. Inhibitors of PUR activity may be useful for
CC treating viral infections and hyperproliferative diseases such as cancer
XX
SQ Sequence 26 BP; 2 A; 2 C; 2 G; 20 T; 0 U; 0 Other;

Query Match 0.6%; Score 17; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAA 2802
||||||||||||||||||
Db 26 AAAAAAAAAAAAAAAAA 10

RESULT 2230
AAX04087/c
ID AAX04087 standard; DNA; 26 BP.
XX
AC AAX04087;
XX
DT 12-APR-1999 (first entry)
XX
DE PUR-alpha RACE reaction primer PDT-01.
XX
KW PUR element; PUR-alpha; hyperproliferative disease; cancer; human;
KW monoclonal antibody; identification; characterisation; RACE primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US5869622-A.
XX
PD 09-FEB-1999.
XX
PF 07-JUN-1995; 95US-00486809.
XX
PR 28-AUG-1992; 92US-00938189.
PR 02-FEB-1993; 93US-00014943.
PR 06-JUN-1995; 95US-00470911.
XX
PA (MOUN) MOUNT SINAI SCHOOL MEDICINE.
XX
PI Bergemann AD, Johnson EM;
XX
DR WPI; 1999-152881/13.
XX
PT Monoclonal antibody specific for PUR protein - useful for treating
PT cancer.
XX
PS Example; Col 9; 64pp; English.
XX
CC The present invention describes a monoclonal antibody that specifically
CC binds to an epitope of the PUR protein. Antibodies that bind to the PUR
CC protein and neutralise PUR activity may be used to treat
CC hyperproliferative diseases such as cancer. PUR antibodies may be used
CC diagnostically to detect aberrant expression of the PUR protein and/or
CC mutations in the PUR gene. The present sequence represents a PUR-alpha
CC RACE primer which is used in an example from the present invention
XX
SQ Sequence 26 BP; 2 A; 2 C; 2 G; 20 T; 0 U; 0 Other;

Query Match 0.6%; Score 17; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAA 2802
||||||||||||||||||
Db 26 AAAAAAAAAAAAAAAAA 10

RESULT 2231
AAS01630/c
ID AAS01630 standard; DNA; 26 BP.
XX
AC AAS01630;
XX
DT 18-JUL-2001 (first entry)
XX
DE Human CACNA1G R6 3'-target sequence for bisulfite PCR.
XX
KW Human; T-type calcium channel; CACNA1G; cytosine methylation; CpG island;
KW cellular proliferative disorder; colorectal cancer; age related disease;
KW apolipoprotein B; APOB; caudal type homeobox transcription factor 2;
KW CDX2; epidermal growth factor receptor; EGFR; fibrillin-1; FBN1;
KW G protein-coupled receptor 37; GPR37; heat shock 70kD protein 6; HSP70B';
KW HSPA6; RasGAP-related protein; IQGAP2; proteinase-activated receptor 2;
KW PAR2; paired-like homeodomain transcription factor 2; PITX2; klotho; KL;
KW patched A; patched B; PTCHA; PTCHB; syndecan 1; syndecan 4; SDC1; SDC4;
KW chromosome 17; ds.
XX
OS Homo sapiens.
XX
PN WO200119845-A1.
XX
PD 22-MAR-2001.
XX
PF 14-SEP-2000; 2000WO-US025479.
XX
PR 15-SEP-1999; 99US-00398522.
XX
PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI Issa J;
XX
DR WPI; 2001-244777/25.
XX
PT New nucleic acid molecule for use as a marker for screening cancer,
PT comprises the coding region for a T-type calcium channel and regulatory
PT sequences associated with the channel.
XX
PS Claim 20; Page 37; 125pp; English.
XX
CC The present sequence for human T-type calcium channel R6 3'-target
CC sequence (complementary to the 3'-bisulfite PCR primer) is used to study
CC the methylation state of R6 of CACNA1G which maps to chromosome 17. The
CC methylation state of specific regions within CpG islands associated with
CC the CACNA1G gene correlate with several cancerous phenotypes involving
CC various tissue and cell types. Since aberrant methylation of normally
CC unmethylated CpG islands is often observed in immortalised and
CC transformed cells, CACNA1G is implicated in cellular proliferative
CC disorders e.g. leukaemia, colorectal, lung, breast and other cancers. The
CC nucleic acid coding for CACNA1G is useful as a marker for screening
CC cancer and age related diseases. A diagnostic kit containing primers
CC (AAS01574-AAS01623) for amplification of a CpG-containing nucleic acid,
CC where the primer hybridises with a target polynucleotide sequence
CC (AAS01627-AAS01676), can be used for detecting aberrant methylation. The
CC CpG island sequences (AAS01677-AAS01692) are selected from genes encoding
CC CACNA1G, apolipoprotein B (APOB), caudal type homeobox transcription
CC factor 2 (CDX2), epidermal growth factor receptor (EGFR), fibrillin-1
CC (FBN1), G protein-coupled receptor 37 (GPR37), heat shock 70kD protein 6

```
CC   (HSP70B'; HSPA6), RasGAP-related protein (IQGAP2), klotho (KL),
CC   proteinase-activated receptor 2 (PAR2), paired-like homeodomain
CC   transcription factor 2 (PITX2), patched A and B (PTCHA; PTCHB) and
CC   syndecan 1 and 4 (SDC1; SDC4) or a MINT31 sequence
XX
SQ   Sequence 26 BP; 4 A; 0 C; 3 G; 18 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         23 AAAAAAAAAAAAAAAAA 7


RESULT 2232
AAC92118
ID   AAC92118 standard; DNA; 26 BP.
XX
AC   AAC92118;
XX
DT   19-MAR-2001  (first entry)
XX
DE   Human MLT gene intron-exon boundary #2.
XX
KW   Human; API2-MLT chimera; chimeric; apoptosis inhibitor 2; MLT; API2;
KW   mucosa-associated lymphoid tissue lymphoma associated translocation;
KW   chromosome 11 region q21-22.3; chromosome 18 region q21.1-22;
KW   molecular characterisation; chromosome translocation; carcinogenesis;
KW   fusion protein; malignancy; ss.
XX
OS   Homo sapiens.
XX
PN   WO200073500-A1.
XX
PD   07-DEC-2000.
XX
PF   26-MAY-2000; 2000WO-EP004796.
XX
PR   27-MAY-1999;   99EP-00201683.
XX
PA   (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
XX
PI   Baens M,  Marynen P,  Dierlamm J;
XX
DR   WPI; 2001-061556/07.
XX
PT   Determining if a tissue sample has a chromosome (11:18) translocation
PT   associated with malignancies by amplifying a nucleic acid sample using
PT   primers complementary to chromosome 11 region q21-22.3 and chromosome 18
PT   region q21.1-22.
XX
PS   Example 3; Page 22; 47pp; English.
XX
CC   The present invention describes a method for determining if a tissue
CC   sample comprises a cell with a chromosome (11:18) translocation
CC   associated with malignancies such as mucosa-associated lymphoid tissue
CC   (MALT) lymphomas. The method comprises subjecting a sample nucleic acid
CC   to amplification using primers complementary to sequences which are on
CC   chromosome 11 region q21-22.3 and on chromosome 18 region q21.1-22. The
CC   method can be used for determining if a tissue sample or analogue
CC   comprises a chromosome (11:18) translocation associated with malignancies
CC   such as mucosa-associated lymphoid tissue lymphomas. The nucleic acid or
CC   the antibody may be used as a probe for detection, for hybridisation to
CC   southern blot cell DNAs or for in situ hybridisation of cells, or for
CC   determining the presence of complementary DNA. The present sequence
CC   represents an intron-exon boundary oligonucleotide from the human MALT-
CC   lymphoma associated translocation (MLT) gene, which is used in an example
CC   from the present invention
XX
SQ   Sequence 26 BP; 6 A; 0 C; 3 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTA 17


RESULT 2233
AAT13051
ID   AAT13051 standard; DNA; 26 BP.
XX
AC   AAT13051;
XX
DT   25-MAR-2003  (revised)
DT   27-MAY-1996  (first entry)
XX
DE   cDNA primer.
XX
KW   Cotton; fibre; promoter; transgenic plant; crop improvement; primer;
KW   Gossypium; ss.
XX
OS   Synthetic.
XX
PN   US5495070-A.
XX
PD   27-FEB-1996.
XX
PF   18-MAY-1992;   92US-00885970.
XX
PR   04-OCT-1988;   88US-00253243.
PR   21-NOV-1990;   90US-00617239.
XX
PA   (CETU ) AGRACETUS INC.
XX
PI   John M;
XX
DR   WPI; 1996-139095/14.
XX
PT   New isolated fibre-specific promoters - used for introducing altered-
PT   fibre specific characteristics into plants, partic. cotton.
XX
PS   Example 1; Col 8; 48pp; English.
XX
CC   cDNA was prepd. from cotton fibre cell RNA using the primer given in
CC   AAT13051. cDNA libraries were produced and screened for fibre-specific
CC   clones (see AAT13033-50) and these were in turn used to screen genomic
CC   libraries to identify fibre-specific promoter sequences (see AAT13025-32
CC   and AAT13052-53). (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 26 BP; 2 A; 3 C; 3 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTTT 2180
              |||||||||||||||||
Db         10 CCTTTTTTTTTTTTTTT 26


RESULT 2234
AAT39393
ID   AAT39393 standard; DNA; 26 BP.
XX
AC   AAT39393;
XX
DT   25-MAR-2003  (revised)
DT   16-DEC-1996  (first entry)
XX
DE   Cotton fibre cDNA first strand synthesis primer.
XX
```

KW Cotton fibre; promoter; differential screening; leaf; ovule; root;
KW flower; PCR; polymerase chain reaction; homology; transgenic plant; ds.
XX
OS Synthetic.
XX
PN US5521078-A.
XX
PD 28-MAY-1996.
XX
PF 19-OCT-1994; 94US-00298687.
XX
PR 04-OCT-1988; 88US-00253243.
PR 21-NOV-1990; 90US-00617239.
PR 18-MAY-1992; 92US-00885970.
XX
PA (CETU) AGRACETUS INC.
XX
PI John M;
XX
DR WPI; 1996-267794/27.
XX
PT Isolation of fibre-specific cotton promoter sequences - using selected
PT DNA probes to screen genomic DNA fragments, for production of cotton
PT fibres with improved characteristics.
XX
PS Example; Col 23; 46pp; English.
XX
CC Cotton fibre cell-specific promoter sequences were isolated by
CC differential screening of a cotton plant cDNA library. Of 4788 clones
CC from a 10 day cell library screened with leaf cDNAs, 800 clones not
CC present in the leaf were isolated. These were screened with cDNAs from
CC ovule, root and flower mRNAs and resulted in 79 clones isolated. PCR
CC analysis was then used to remove cross-hybridising clones. This resulted
CC in the isolation of 18 cDNA clones specifically expressed in cotton fibre
CC cells (AAT30242-4 and AAT30253-67). These cDNAs were then used to screen
CC for homologous genomic sequences (AAT30245-53 and AAT30268) in order to
CC obtain the corresp. promoter sequences. This primer was used to generate
CC the first cDNA strand from mRNA isolated from the cotton fibre cells. The
CC promoters isolated from the fibre cell-specific clones can be used to
CC generate transgenic cotton plants and lines producing fibres having
CC altered quantity and quality. (Updated on 25-MAR-2003 to correct PF
CC field.)
XX
SQ Sequence 26 BP; 2 A; 3 C; 3 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 17; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2164 CCTTTTTTTTTTTTTTT 2180
              |||||||||||||||||
Db         10 CCTTTTTTTTTTTTTTT 26
```

RESULT 2235
AAT43363
ID AAT43363 standard; DNA; 26 BP.
XX
AC AAT43363;
XX
DT 11-MAR-1997 (first entry)
XX
DE Cotton fibre first strand cDNA primer.
XX
KW FbLate; promoter; fibre; transgenic plant; cotton; Gossypium hirsutum;
KW primer; ss.
XX
OS Synthetic.
XX
PN WO9639021-A1.
XX
PD 12-DEC-1996.
XX
PF 06-JUN-1996; 96WO-US009449.
XX
PR 06-JUN-1995; 95US-00467504.
XX
PA (MONS) MONSANTO CO.
XX
PI John ME;
XX
DR WPI; 1997-042726/04.
XX
PT Plant fibre-specific, developmentally regulated FbLate promoter - useful
PT for producing transgenic plants, esp. cotton, with altered fibre
PT properties.
XX
PS Example 2; Page 15; 79pp; English.
XX
CC A primer (AAT43363) was used for first strand cDNA synthesis from RNA
CC obtd. from fibre cells of 23 day-old Coker 312 or 10 day-old Sea Island
CC cotton bolls. The cDNA was used to construct a cDNA library from which
CC cDNA clones (see also AAT43361-62) were isolated that corresponded to RNA
CC prevalent in later fibre development. These clones were used to identify
CC the FbLate promoter (AAT43360)
XX
SQ Sequence 26 BP; 2 A; 3 C; 3 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 17; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2164 CCTTTTTTTTTTTTTTT 2180
              |||||||||||||||||
Db         10 CCTTTTTTTTTTTTTTT 26
```

RESULT 2236
AAT62627
ID AAT62627 standard; cDNA to mRNA; 26 BP.
XX
AC AAT62627;
XX
DT 25-MAR-2003 (revised)
DT 14-MAY-1997 (first entry)
XX
DE Primer for cotton fibre-specific cDNA amplification.
XX
KW cotton; fibre-specific; strength; transgenic plant; anthesis;
KW developmentally regulated; E6; H6; antisense; sense; primer; PCR; ss.
XX
OS Synthetic.
XX
PN US5597718-A.
XX
PD 28-JAN-1997.
XX
PF 20-SEP-1995; 95US-00530797.
XX
PR 04-OCT-1988; 88US-00253243.
PR 21-NOV-1990; 90US-00617239.
PR 18-OCT-1993; 93US-00138814.
XX
PA (CETU) AGRACETUS.
XX
PI Brill WJ, Umbeck PF, John ME;
XX
DR WPI; 1997-108326/10.
XX
PT Prodn. of transgenic cotton plants - by transformation with the H6 coding
PT sequence or E6 anti-sense sequence, produces fibre of altered strength.
XX
PS Example 1; Col 6; 33pp; English.
XX
CC AAT62627 is a primer used for first strand cDNA synthesis from mRNA
CC isolated from cotton fibre cells at different stages of development.

```
CC   Cotton fibre-specific cDNA clones (AAT62609-24) can be used to identify
CC   genomic clones by differential cDNA library screenings. Coding sequences
CC   from these isolated genes are used in sense or antisense orientation to
CC   alter the fibre characteristics, e.g. strength, of transgenic fibre-
CC   producing plants. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 26 BP; 2 A; 3 C; 3 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTT 2180
              ||||||||||||||||
Db         10 CCTTTTTTTTTTTTTT 26


RESULT 2237
AAT63663
ID   AAT63663 standard; DNA; 26 BP.
XX
AC   AAT63663;
XX
DT   25-MAR-2003  (revised)
DT   11-JUN-1997  (first entry)
XX
DE   Primer for cotton fibre-specific cDNA synthesis.
XX
KW   primer; PCR; polymerase chain reaction; cotton fibre; seed floss fibre;
KW   promoter; peroxidase; production; fibre strength; Sea Island;
KW   Gossypium sp; Coker; Kapok; G. barbadense; ss.
XX
OS   Synthetic.
XX
PN   US5608148-A.
XX
PD   04-MAR-1997.
XX
PF   25-JAN-1995;   95US-00378588.
XX
PR   30-SEP-1993;   93US-00130086.
XX
PA   (CETU ) AGRACETUS INC.
XX
PI   John ME;
XX
DR   WPI; 1997-164559/15.
XX
PT   Transgenic cotton plants with increased fibre strength - are transformed
PT   with construct containing peroxidase gene.
XX
PS   Disclosure; Col 31; 43pp; English.
XX
CC   This primer sequence was used for first strand cDNA synthesis of mRNA
CC   from cotton fibre-specific library. Cotton plants whose genome contains
CC   heterologous genetic construct comprising a seed floss fibre (SFF)-
CC   specific promoter isolated from cotton plants and a coding sequence
CC   encoding a peroxidase are useful for production of cotton with increased
CC   fibre strength. The peroxidase genes are over-expressed in fibre and not
CC   in other plant tissues where it would be harmful to the plant. (Updated
CC   on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 26 BP; 2 A; 3 C; 3 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTT 2180
              ||||||||||||||||
Db         10 CCTTTTTTTTTTTTTT 26


RESULT 2238
AAT70058
ID   AAT70058 standard; cDNA; 26 BP.
XX
AC   AAT70058;
XX
DT   25-MAR-2003  (revised)
DT   20-AUG-1997  (first entry)
XX
DE   Primer for cotton fibre specific cDNA amplification.
XX
KW   cotton; E6; fibre; promoter; transgenic plant; truncated;
KW   heterologous gene expression; primer; PCR; ss.
XX
OS   Synthetic.
XX
PN   US5620882-A.
XX
PD   15-APR-1997.
XX
PF   19-OCT-1994;   94US-00298829.
XX
PR   04-OCT-1988;   88US-00253243.
PR   21-NOV-1990;   90US-00617239.
PR   18-MAY-1992;   92US-00885970.
XX
PA   (CETU ) AGRACETUS INC.
XX
PI   John M;
XX
DR   WPI; 1997-235185/21.
XX
PT   DNA constructs contg. truncated promoter sequence - for fibre-specific
PT   gene expression in cotton plants.
XX
PS   Example 1; Col 8; 48pp; English.
XX
CC   AAT70058 is a primer used to synthesize first strand cDNA from mRNA
CC   isolated from cotton fibre cells at different stages of development.
CC   Claimed DNA constructs comprise a truncated promoter sequence (from one
CC   of AAT70031-38) that promotes preferential gene expression in plant fibre
CC   cells, a protein coding sequence not naturally associated with the
CC   promoter sequence and a 3' termination sequence. The DNA constructs are
CC   useful for expressing foreign genes in fibre-producing plants, esp. to
CC   produce transgenic cotton plants with varied cotton fibre characteristics
CC   and quality. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 26 BP; 2 A; 3 C; 3 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTT 2180
              ||||||||||||||||
Db         10 CCTTTTTTTTTTTTTT 26


RESULT 2239
AAZ59153/c
ID   AAZ59153 standard; DNA; 26 BP.
XX
AC   AAZ59153;
XX
DT   17-APR-2000  (first entry)
XX
DE   Oligonucleotide #10 for DNA determination method.
XX
KW   Oligonucleotide; restriction enzyme; PCR primer; amplification; template;
KW   vector; ss.
XX
OS   Synthetic.
XX
```

```
PN   JP11341986-A.
XX
PD   14-DEC-1999.
XX
PF   02-JUN-1998;   98JP-00152598.
XX
PR   02-JUN-1998;   98JP-00152598.
XX
PA   (HITA ) HITACHI LTD.
PA   (AMSH ) NYCOMED AMERSHAM PLC.
XX
DR   WPI; 2000-101695/09.
XX
PT   A process for preparation of a DNA sample - and a reagent for the
PT   preparation.
XX
PS   Example 1; Page 11; 16pp; Japanese.
XX
CC   This sequence represents an oligonucleotide used in a novel method for
CC   the direct and complete determination of long DNA sequences of
CC   restriction enzymes from PCR products. The method allows independent
CC   recognition of amplified DNA fragments at both ends and removal of one
CC   primer binding site can be carried out and leads to the following steps:
CC   (1) the resultant cleaved PCR fragment having the one primer binding site
CC   is used as a template for the simultaneous determination of the PCR
CC   fragment and the downstream fragment; (2) the fragments can be used for
CC   the determination of long DNA sequences; (3) the PCR amplification of 2
CC   primers provide replacements of the both ends with different restriction
CC   enzyme fragments; and (4) the above mentioned steps may give polarity of
CC   the fragment at both ends for integration in vectors and may be applied
CC   for preparation of samples
XX
SQ   Sequence 26 BP; 1 A; 1 C; 4 G; 18 T; 0 U; 2 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAA 2800
              |||||||||||||||||
Db         22 TGAAAAAAAAAAAAAAA 6


RESULT 2240
AAH40741/c
ID   AAH40741 standard; DNA; 26 BP.
XX
AC   AAH40741;
XX
DT   14-AUG-2001  (first entry)
XX
DE   SNP specific upper PCR primer SEQ ID 3537.
XX
KW   Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW   SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
KW   Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW   polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW   acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW   inflammation; forensic investigation; paternity analysis; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200129262-A2.
XX
PD   26-APR-2001.
XX
PF   13-OCT-2000; 2000WO-US028436.
XX
PR   15-OCT-1999;   99US-0160096P.
XX
PA   (ORCH-) ORCHID BIOSCIENCES INC.
XX
PI   Picoult-Newburg L,  Pohl M;
XX
DR   WPI; 2001-290930/30.
XX
PT   New genotyping oligonucleotide, useful for detecting the presence,
PT   absence or identity of single polynucleotide polymorphism in a nucleic
PT   acid sample.
XX
PS   Claim 1; Page 68; 83pp; English.
XX
CC   Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC   primer extension (SNPE) primers, and the sequences of regions flanking
CC   sites of single nucleotide polymorphisms SNPs. The present invention
CC   includes kits for determining the presence or absence of a SNP, using the
CC   oligonucleotides of the invention. The PCR primers are used to amplify a
CC   SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC   The oligonucleotides are useful for genotyping a nucleic acid sample by
CC   performing a single-nucleotide primer extension reaction. The
CC   oligonucleotides are useful for determining the presence, absence or
CC   identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC   assess by association analysis the genotype of an individual or group of
CC   individuals, having a pathological phenotypic trait suspected of being
CC   caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC   agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC   dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC   osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC   traits also include symptoms of or susceptibility to multifactorial
CC   disease of which a component is or may be genetic such as autoimmune
CC   diseases, including, rheumatoid arthritis, multiple sclerosis,
CC   inflammation, cancer, nervous system diseases and infection by pathogenic
CC   microorganism. The method is also useful in forensic investigations and
CC   paternity analysis. The present sequence represents a PCR primer specific
CC   for a human SNP containing DNA sequence
XX
SQ   Sequence 26 BP; 16 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 26;
  Best Local Similarity   80.0%;  Pred. No. 2.5e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTTTTAAC 2189
              ||||||| ||||  ||| ||| |||
Db         26 CTTTTTTGTTTTGATTTGTTTCAAC 2


RESULT 2241
ABL54492/c
ID   ABL54492 standard; DNA; 26 BP.
XX
AC   ABL54492;
XX
DT   12-AUG-2002  (first entry)
XX
DE   GPCR protein BG37 related primer #22.
XX
KW   Antirheumatic; Antiarthritic; Antiulcer; Antiinflammatory; Antiasthmatic;
KW   Antiallergic; Immunosuppressive; Cardiant; Rheumatoid arthritis;
KW   Stomach ulcer; Inflammatory bowel disease; Ischeamic heart disease;
KW   Cardiac arrhythmia; Hypertension; Hypotension; obesity; asthma; Allergy;
KW   Autoimmune disease; Guanosine triphospahte binding protein; BG37; GPCR;
KW   PCR; primer; ss.
XX
OS   Synthetic.
XX
PN   WO200240669-A1.
XX
PD   23-MAY-2002.
XX
PF   30-OCT-2001; 2001WO-JP009512.
XX
PR   17-NOV-2000; 2000JP-00351741.
PR   15-FEB-2001; 2001JP-00038619.
PR   16-MAR-2001; 2001JP-00077000.
XX
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PA   (BANY ) BANYU PHARM CO LTD.
XX
PI   Maruyama T,  Nakamura T,  Itadani H,  Tanaka K;
XX
DR   WPI; 2002-427094/45.
XX
PT   Guanosine triphosphate binding protein coupled receptor protein BG37,
PT   useful for screening potential signal transduction regulators having
PT   pharmaceutical use.
XX
PS   Example 8; Page 33; 92pp; Japanese.
XX
CC   This invention relates to DNA encoding a guanosine triphosphate binding
CC   protein coupled receptor (GPCR) protein (BG37). The GPCR BG37 protein is
CC   antirheumatic, antiarthritic, antiulcer, antiinflammatory, antiasthmatic,
CC   antiallergic, immunosuppressive and cardiant in its action. The protein
CC   is used in the prevention, treatment and diagnosis of diseases associated
CC   with GPCR signal transduction, such as rheumatoid arthritis, stomach
CC   ulcer, inflammatory bowel disease, ischeamic heart disease, cardiac
CC   arrhythmia, hypertension, hypotension, obesity, asthma, allergies, pain
CC   and autoimmune diseases. The present sequence represents a primer related
CC   to guanosine triphosphate binding protein coupled receptor protein BG37
CC   encoding sequence
XX
SQ   Sequence 26 BP; 6 A; 5 C; 9 G; 6 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 26;
  Best Local Similarity   80.0%;  Pred. No. 2.5e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        354 CCTACCAGCAGCTGGCCTACTCCCA 378
              ||||| |  |||||| |||||| ||
Db         25 CCTACTACTAGCTGGGCTACTCACA 1


RESULT 2242
ABK52620
ID   ABK52620 standard; DNA; 27 BP.
XX
AC   ABK52620;
XX
DT   27-AUG-2002  (first entry)
XX
DE   Minority genome method VFA-MUT-11 DNA sequence.
XX
KW   Minority genome method; viral quasi-species; majority genome;
KW   genetic diagnosis; viral infection; human immune deficiency virus;
KW   hepatitis B; hepatitis C; antiviral therapy; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1
FT                   /*tag=  a
FT                   /label= unknown
FT                   /note= "C6 aminolinker sequence"
XX
PN   WO200183815-A1.
XX
PD   08-NOV-2001.
XX
PF   27-APR-2001; 2001WO-ES000165.
XX
PR   27-APR-2000; 2000ES-00001068.
XX
PA   (CNSJ ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
XX
PI   Arias Esteban A,  Baranowski E,  Briones Llorente C;
PI   Domingo Solans E,  Escarmis Homs C,  Gomez Castilla J;
PI   Martin Ruiz- Jarabo C,  Parro Garcia V;
XX
DR   WPI; 2002-147445/19.
XX
PT   Detecting minority genomes in viral quasi-species, useful for identifying
PT   mutants responsible for drug resistance and to individualize therapy.
XX
PS   Example 1; Page 53; 107pp; Spanish.
XX
CC   The present invention relates to a new method for detecting minority
CC   genomes, present at less than 50%, in a population of nucleic acids of a
CC   viral quasi-species and having at least one mutation with respect to the
CC   majority genome. The invention can be used for genetic diagnosis of viral
CC   infections, especially human immune deficiency virus and hepatitis B or
CC   C, particularly to detect memory minority genomes that are implicated in
CC   failure of antiviral therapy, so the method may make possible design of
CC   therapies customised for individual patients. The present nucleic acid
CC   sequence represents the VFA-MUT-11 DNA sequence that was used in the
CC   methods of the invention
XX
SQ   Sequence 27 BP; 2 A; 4 C; 2 G; 18 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTAA 2188
              |||||||||||||||||
Db          2 TTTTTTTTTTTTTTTAA 18


RESULT 2243
AAT70106/c
ID   AAT70106 standard; DNA; 28 BP.
XX
AC   AAT70106;
XX
DT   24-SEP-1997  (first entry)
XX
DE   PolyTV primer 1.
XX
KW   primer; polymerase chain reaction; cDNA library; anchored end; PCSUB;
KW   lock-docking; screening; PCR-based cDNA subtractive cloning; ss.
XX
OS   Synthetic.
XX
PN   WO9640998-A1.
XX
PD   19-DEC-1996.
XX
PF   05-JUN-1996;   96WO-US008582.
XX
PR   07-JUN-1995;   95US-00481687.
XX
PA   (PION-) PIONEER HI-BRED INT INC.
XX
PI   Wang X,  Duvick JP,  Briggs SP;
XX
DR   WPI; 1997-087067/08.
XX
PT   Method for prodn. of cDNA libraries with anchored ends - useful for
PT   subtractive cloning of sequences of interest.
XX
PS   Claim 1; Page 26; 56pp; English.
XX
CC   The invention provides a PCR-based method for generating a full-length
CC   cDNA library with anchored ends. The method uses lock-docking primers
CC   (AAT70106-11), where one primer, poly TV (V = G,C or A) locks over the
CC   polyA tail of eukaryotic mRNA producing first strand synthesis and a
CC   second primer, polyGH (H = A, C or T) locks onto the polyC tail added by
CC   terminal deoxynucleotidyl transferase (TdT). In the final step, AAT70112-
CC   17 (polyAB and polyCD primers; B = G, T or C; D = G, A or T) are used to
CC   amplify the first strand and produce a cDNA library with anchored ends.
CC   cDNA libraries produced may be used to identify new (unique) nucleotide
CC   sequences from PCSUB (PCR-based cDNA subtractive) libraries. The new
CC   method produces discreet sized PCR products which would not necessarily
CC   require further subcloning/screening. The method also produces full-
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```
CC   length cDNA's obtainable from the libraries as opposed to specific cDNA
CC   clones, as produced by previously known methods. Other methods such as
CC   PCR and RACE require a knowledge of the target sequence to be amplified,
CC   by using the PCSUB method no previous knowledge is necessary
XX
SQ   Sequence 28 BP; 2 A; 4 C; 4 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAA 11


RESULT 2244
AAT70107/c
ID   AAT70107 standard; DNA; 28 BP.
XX
AC   AAT70107;
XX
DT   24-SEP-1997  (first entry)
XX
DE   PolyTV primer 2.
XX
KW   primer; polymerase chain reaction; cDNA library; anchored end; PCSUB;
KW   lock-docking; screening; PCR-based cDNA subtractive cloning; ss.
XX
OS   Synthetic.
XX
PN   WO9640998-A1.
XX
PD   19-DEC-1996.
XX
PF   05-JUN-1996;   96WO-US008582.
XX
PR   07-JUN-1995;   95US-00481687.
XX
PA   (PION-) PIONEER HI-BRED INT INC.
XX
PI   Wang X,  Duvick JP,  Briggs SP;
XX
DR   WPI; 1997-087067/08.
XX
PT   Method for prodn. of cDNA libraries with anchored ends - useful for
PT   subtractive cloning of sequences of interest.
XX
PS   Claim 1; Page 27; 56pp; English.
XX
CC   The invention provides a PCR-based method for generating a full-length
CC   cDNA library with anchored ends. The method uses lock-docking primers
CC   (AAT70106-11), where one primer, poly TV (V = G,C or A) locks over the
CC   polyA tail of eukaryotic mRNA producing first strand synthesis and a
CC   second primer, polyGH (H = A, C or T) locks onto the polyC tail added by
CC   terminal deoxynucleotidyl transferase (TdT). In the final step, AAT70112-
CC   17 (polyAB and polyCD primers; B = G, T or C; D = G, A or T) are used to
CC   amplify the first strand and produce a cDNA library with anchored ends.
CC   cDNA libraries produced may be used to identify new (unique) nucleotide
CC   sequences from PCSUB (PCR-based cDNA subtractive) libraries. The new
CC   method produces discreet sized PCR products which would not necessarily
CC   require further subcloning/screening. The method also produces full-
CC   length cDNA's obtainable from the libraries as opposed to specific cDNA
CC   clones, as produced by previously known methods. Other methods such as
CC   PCR and RACE require a knowledge of the target sequence to be amplified,
CC   by using the PCSUB method no previous knowledge is necessary
XX
SQ   Sequence 28 BP; 1 A; 4 C; 5 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAA 11


RESULT 2245
ABK52626/c
ID   ABK52626 standard; DNA; 28 BP.
XX
AC   ABK52626;
XX
DT   27-AUG-2002  (first entry)
XX
DE   Minority genome method VIH-MUT-12 DNA sequence.
XX
KW   Minority genome method; viral quasi-species; majority genome;
KW   genetic diagnosis; viral infection; human immune deficiency virus;
KW   hepatitis B; hepatitis C; antiviral therapy; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1
FT                   /*tag=  a
FT                   /label= unknown
FT                   /note= "C6 aminolinker sequence"
XX
PN   WO200183815-A1.
XX
PD   08-NOV-2001.
XX
PF   27-APR-2001; 2001WO-ES000165.
XX
PR   27-APR-2000; 2000ES-00001068.
XX
PA   (CNSJ ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
XX
PI   Arias Esteban A,  Baranowski E,  Briones Llorente C;
PI   Domingo Solans E,  Escarmis Homs C,  Gomez Castilla J;
PI   Martin Ruiz- Jarabo C,  Parro Garcia V;
XX
DR   WPI; 2002-147445/19.
XX
PT   Detecting minority genomes in viral quasi-species, useful for identifying
PT   mutants responsible for drug resistance and to individualize therapy.
XX
PS   Example 2; Page 55; 107pp; Spanish.
XX
CC   The present invention relates to a new method for detecting minority
CC   genomes, present at less than 50%, in a population of nucleic acids of a
CC   viral quasi-species and having at least one mutation with respect to the
CC   majority genome. The invention can be used for genetic diagnosis of viral
CC   infections, especially human immune deficiency virus and hepatitis B or
CC   C, particularly to detect memory minority genomes that are implicated in
CC   failure of antiviral therapy, so the method may make possible design of
CC   therapies customised for individual patients. The present nucleic acid
CC   sequence represents the VIH-MUT-12 DNA sequence that was used in the
CC   methods of the invention
XX
SQ   Sequence 28 BP; 3 A; 1 C; 4 G; 19 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 28;
  Best Local Similarity   80.0%;  Pred. No. 2.8e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAA 2804
              || || | | | ||||||||||||||
Db         28 GACTTTACACACAAAAAAAAAAAAA 4


RESULT 2246
AAQ49467/c
ID   AAQ49467 standard; DNA; 29 BP.
```

```
XX
AC   AAQ49467;
XX
DT   14-APR-1994  (first entry)
XX
DE   Oligo-dT primer "not1dt" to amplify human NK3R C-terminal clone.
XX
KW   human; neurokinin-3 receptor; NK3R; eledoisin; neurokinin B; tachykinin;
KW   enkephalin release; ss.
XX
OS   Synthetic.
XX
PN   GB2265375-A.
XX
PD   29-SEP-1993.
XX
PF   08-MAR-1993;   93GB-00004708.
XX
PR   16-MAR-1992;   92US-00851974.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Fong TM,  Huang RRC,  Strader CD;
XX
DR   WPI; 1993-305585/39.
XX
PT   New recombinant human neurokinin-receptor - used to identify binding
PT   ligands, antagonists and agonists of the receptor.
XX
PS   Example 1; Page 17; 46pp; English.
XX
CC   Degenerate PCR primers were designed based on the known sequence of rat
CC   NK3R central transmembrane core. The corresponding human cDNA sequence
CC   was obtained by amplification of human brain cDNA. New primers corresp.
CC   to the human sequence were designed and anchored PCR was performed using
CC   the human primer in the core region. A primary PCR was carried out using
CC   primers "not1dt" and "s1068" (AAQ49467 and AAQ49468, respectively) on
CC   template cDNA whose synthesis was initiated by "not1dt". After two
CC   further rounds of PCR using "not1dt", first with "s1106" (AAQ49469) and
CC   then with "s1137" (AAQ49470), a 600bp cDNA fragment which encodes the C-
CC   terminal region of human NK3R and the 3'-UTR was obtained and sequenced.
CC   The N-terminal coding region was similarly obtained. Finally a full-
CC   length cDNA (AAQ49461) was obtained in a single step using primers from
CC   the 5' and 3' untranslated regions. The human NK3R sequence will be
CC   useful for developing novel NK3 agonists and antagonists
XX
SQ   Sequence 29 BP; 0 A; 4 C; 4 G; 21 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         29 AAAAAAAAAAAAAAAAA 13


RESULT 2247
AAF74917
ID   AAF74917 standard; DNA; 29 BP.
XX
AC   AAF74917;
XX
DT   23-MAY-2001  (first entry)
XX
DE   CD40L poly-A tract sequence SEQ ID NO:14.
XX
KW   Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW   diagnosis; antiarthritic; antirheumatic; immunosuppressive;
KW   antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200119844-A1.
XX
PD   22-MAR-2001.
XX
PF   13-SEP-2000; 2000WO-US024966.
XX
PR   13-SEP-1999;   99US-0153625P.
XX
PA   (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
PI   Crow MK,  Li Y;
XX
DR   WPI; 2001-244776/25.
XX
PT   New altered CD40L promoter for use in the study, diagnosis and treatment
PT   of a variety of inflammatory disorders and autoimmune diseases, such as
PT   rheumatoid arthritis.
XX
PS   Example 1; Fig 3; 90pp; English.
XX
CC   The present invention describes an isolated, purified nucleic acid, which
CC   is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC   residues 331-455 of the sequence comprising 455 nucleotides given in
CC   AAF74905 where A in the wild type sequence at position 331 (corresponding
CC   to position -125) is replaced with C. (I) has antiarthritic,
CC   antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC   be used in gene therapy. (I) is useful in the study, diagnosis and
CC   treatment of inflammatory and autoimmune diseases, as well as diseases in
CC   which elevated expression of CD40L is a factor, e.g., rheumatoid
CC   arthritis. The present sequence represents a CD40L poly-A tract sequence
CC   which is used in an example from the present invention
XX
SQ   Sequence 29 BP; 22 A; 4 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 17;  DB 1;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAA 17


RESULT 2248
AAF74929
ID   AAF74929 standard; DNA; 29 BP.
XX
AC   AAF74929;
XX
DT   23-MAY-2001  (first entry)
XX
DE   CD40L poly-A tract sequence SEQ ID NO:26.
XX
KW   Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW   diagnosis; antiarthritic; antirheumatic; immunosuppressive;
KW   antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200119844-A1.
XX
PD   22-MAR-2001.
XX
PF   13-SEP-2000; 2000WO-US024966.
XX
PR   13-SEP-1999;   99US-0153625P.
XX
PA   (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
PI   Crow MK,  Li Y;
XX
DR   WPI; 2001-244776/25.
XX
```

PT New altered CD40L promoter for use in the study, diagnosis and treatment
PT of a variety of inflammatory disorders and autoimmune diseases, such as
PT rheumatoid arthritis.
XX
PS Example 1; Fig 3; 90pp; English.
XX
CC The present invention describes an isolated, purified nucleic acid, which
CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC residues 331-455 of the sequence comprising 455 nucleotides given in
CC AAF74905 where A in the wild type sequence at position 331 (corresponding
CC to position -125) is replaced with C. (I) has antiarthritic,
CC antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC be used in gene therapy. (I) is useful in the study, diagnosis and
CC treatment of inflammatory and autoimmune diseases, as well as diseases in
CC which elevated expression of CD40L is a factor, e.g., rheumatoid
CC arthritis. The present sequence represents a CD40L poly-A tract sequence
CC which is used in an example from the present invention
XX
SQ Sequence 29 BP; 22 A; 4 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 0.6%; Score 17; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAA 2802
||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAA 17

RESULT 2249
ABZ92865.
ID ABZ92865 standard; DNA; 20 BP.
XX
AC ABZ92865;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 8107; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 18 A; 0 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2781 AATTGAAAAAAAAAAAAAAA 2800
|| | ||||||||||||||||
Db 1 AAGTAAAAAAAAAAAAAAAA 20

RESULT 2250
ABZ85669
ID ABZ85669 standard; DNA; 20 BP.
XX
AC ABZ85669;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Claim 15; SEQ ID NO 911; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,

CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 0 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2185
||||||||||.|||||||.|
Db 1 TTTTTTTTTTCTTTTTTTCT 20

RESULT 2251
AAV12302/c
ID AAV12302 standard; DNA; 20 BP.
XX
AC AAV12302;
XX
DT 17-JUN-1998 (first entry)
XX
DE Ribonucleotide reductase R1 3'UTR fragment SEQ ID NO:46.
XX
KW Ribonucleotide reductase R1; 3'-untranslated region; 3'UTR; tumour;
KW housekeeping gene; identification; modulator; metastasis; neoplastic;
KW papilloma; atherosclerosis; angiogenesis; viral infection; ss.
XX
OS Homo sapiens.
XX
PN WO9800532-A2.
XX
PD 08-JAN-1998.
XX
PF 30-JUN-1997; 97WO-CA000454.
XX
PR 01-JUL-1996; 96US-0021152P.
XX
PA (WRIG/) WRIGHT J A.
PA (YOUN/) YOUNG A H.
XX
PI Wright JA, Young AH;
XX
DR WPI; 1998-086958/08.
XX
PT New oligo-nucleotide(s) complementary to untranslated regions of
PT housekeeping genes - are useful in, e.g. identifying modulators of tumour
PT growth/metastasis and inhibiting growth of neoplastic cells.
XX
PS Claim 4; Page 29; 64pp; English.
XX
CC The present sequence represents a 3'-untranslated region (3'UTR) fragment
CC of ribonucleotide reductase R1. The present invention describes: (1)
CC oligonucleotides (ON) comprising at least 7 consecutive nucleotides (nt)
CC or their analogues of a UTR of a housekeeping gene; (2) antisense ON
CC (AON) complementary to ON; (3) ribozymes (Rb) complementary or homologous
CC to ON, and able to cleave it; (4) DNA sequence encoding ON, OAN and Rb;
CC (5) an antibody (Ab) that binds to ON, OAN and Rb; (6) a nt probe ntP
CC that hybridise to ON, OAN and Rb. ON, AON, Rb and Ab are used to modulate
CC (especially inhibit) growth of tumour cells (especially neoplastic cells)
CC and to reduce their capacity for metastasis. The above may also be used
CC to treat benign proliferative disorders e.g. papillomas, atherosclerosis,
CC angiogenesis and viral infections, e.g. human immunodeficiency virus,
CC hepatitis or herpes. ON may further be used: (i) to identify modulators
CC of tumour growth/metastasis; (ii) to identify compounds (especially
CC potential antitumour agents) that inhibit or enhance interaction between
CC ON and its binding substances; (iii) as probes for detecting related
CC sequences, and (iv) to generate Ab, used for detection and quantification
CC of UTR especially for monitoring progress of cancer therapy. SON inhibit
CC tumorigenicity of neoplastic cells, particularly where these are
CC resistant to hydroxyurea
XX
SQ Sequence 20 BP; 17 A; 1 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2164 CCTTTTTTTTTTTTTTTTTT 2183
|.|||||||||.|||||||
Db 20 CGTTTTTTTTTTCTTTTTTT 1

RESULT 2252
AAV22586
ID AAV22586 standard; DNA; 20 BP.
XX
AC AAV22586;
XX
DT 08-JUL-1998 (first entry)
XX
DE Antisense oligonucleotide designed to target the R1 message.
XX
KW R1 subunit; ribonucleotide reductase; cell proliferation; tumour cell;
KW antisense; growth; inhibition; sensitivity; hydroxyurea;
KW chemotherapeutic drug; methotrexate; PALA; treatment; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9805769-A2.
XX
PD 12-FEB-1998.
XX
PF 01-AUG-1997; 97WO-CA000540.
XX
PR 02-AUG-1996; 96US-0023040P.
PR 07-MAR-1997; 97US-0039959P.
XX
PA (GENE-) GENESENSE TECHNOLOGIES INC.
XX
PI Wright JA, Young AH;
XX
DR WPI; 1998-145609/13.
XX
PT Antisense oligonucleotides to ribonucleotide reductase genes - used to
PT modulate tumour growth and inhibit tumour cell proliferation.
XX
PS Claim 8; Page 49; 79pp; English.
XX
CC AAV22531-89 represent antisense oligonucleotides which are targeted
CC against the mRNA of the R1 subunit sequence of ribonucleotide reductase.
CC Aberrant expression of the R2 gene, which encodes the second subunit of
CC the ribonucleotide reductase gene, can determine the malignant
CC characteristics of cells. Suppression of R2 and R1 gene expression was
CC found to reduce transformed properties of tumour cells. The antisense
CC oligonucleotides can be used for modulating tumour cell growth, or for
CC inhibiting tumour cell proliferation. They can also be used for
CC increasing the sensitivity of neoplastic cells to chemotherapeutic drugs
CC (especially to hydroxyurea, methotrexate (MTX), and PALA). The antisense
CC oligonucleotides may be used to treat proliferative disorders including

```
CC   leukaemias, lymphomas, sarcomas, melanomas, various other forms of
CC   cancer, papillomas, arthrosclerosis, psoriasis, polythemia, mastocytosis,
CC   autoimmune diseases, angiogenesis, bacterial infections and viral
CC   infections (including HIV hepatitis, or herpes infections)
XX
SQ   Sequence 20 BP; 0 A; 3 C; 1 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.5e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTT 2182
              ||| |||||||||| |||||
Db          1 TCCGTTTTTTTTTTCTTTTT 20


RESULT 2253
AAX18300
ID   AAX18300 standard; DNA; 20 BP.
XX
AC   AAX18300;
XX
DT   26-JUL-1999  (first entry)
XX
DE   PCR primer for telomerase coding sequence.
XX
KW   Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
KW   neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
KW   smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
KW   stem cell differentiation; organ regeneration; organ differentiation;
KW   PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9901560-A1.
XX
PD   14-JAN-1999.
XX
PF   01-JUL-1998;   98WO-US013835.
XX
PR   01-JUL-1997;   97US-0051410P.
PR   21-JUL-1997;   97US-0053018P.
PR   21-JUL-1997;   97US-0053329P.
PR   04-AUG-1997;   97US-0054642P.
PR   09-SEP-1997;   97US-0058287P.
XX
PA   (CAMB-) CAMBIA BIOSYSTEMS LLC.
XX
PI   Kilian A,  Bowtell D;
XX
DR   WPI; 1999-106060/09.
XX
PT   New isolated vertebrate telomerase genes - used to develop products for
PT   treating cancers or for organ regeneration, nerve cell or brain cell
PT   growth following injury or bone marrow transplantation.
XX
PS   Example 1; Page 42; 134pp; English.
XX
CC   This sequence is a PCR primer for DNA encoding a truncated human
CC   telomerase of the invention. Primers that amplify the telomerase coding
CC   sequence can be used in a method for diagnosing cancer in a patient. The
CC   telomerase can be used for detection, diagnosis and drug screening.
CC   Inhibitors of telomerase activity can be used to treat cancers such as
CC   melanomas, other skin cancers, neuroblastomas, breast carcinomas, colon
CC   carcinomas, leukaemias, lymphomas, osteosarcomas or smooth muscle cell
CC   hyperplasias or skin growths. Enhancers of telomerase may be used to
CC   stimulate stem cell proliferation and differentiation (expansion of
CC   haematopoietic stem cells could be administered in the bone marrow
CC   transplant context). As well, many tissues have stem cells. Proliferation
CC   of these cells may be useful in wound healing, hair growth, treatment of
CC   disease such as Wilm's tumour, organ regeneration or differentiation
CC   after injury or diseases, nerve cell or brain cell growth following
CC   injury
XX
SQ   Sequence 20 BP; 3 A; 5 C; 8 G; 4 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.5e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        789 CCTGTCAGAAGGAGCTGGTG 808
              |||| | ||||||||||||||
Db          1 CCTGCCTGAAGGAGCTGGTG 20


RESULT 2254
AAA94537
ID   AAA94537 standard; DNA; 20 BP.
XX
AC   AAA94537;
XX
DT   09-JAN-2001  (first entry)
XX
DE   Antisense oligonucleotide #20977 targeted to human G-alpha-S1.
XX
KW   G-alpha-S1; infection; inflammation; tumour; antisense; human;
KW   phosphorothioate; 2'-methoxyethyl; MOE; 5-methylcytidine;
KW   Gs-alpha short form; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Optionally the internucleotide linkages are
FT                   phosphorothioate"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "Optionally the nucleotides are 2'-methoxyethyl
FT                   and cytidine residues are 5-methylcytidines"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "Optionally the nucleotides are 2'-methoxyethyl
FT                   and cytidine residues are 5-methylcytidines"
XX
PN   US6110664-A.
XX
PD   29-AUG-2000.
XX
PF   25-JUN-1999;   99US-00344914.
XX
PR   25-JUN-1999;   99US-00344914.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM;
XX
DR   WPI; 2000-586346/55.
XX
PT   New antisense compounds for modulating the expression of G-alpha-S1,
PT   especially useful for diagnostics, therapeutics and prophylaxis, e.g. to
PT   prevent or delay infection, inflammation or tumor formation.
XX
PS   Claim 3; Col 40; 37pp; English.
XX
CC   The present invention relates to antisense compounds 8-30 bases long
CC   targeted to a coding region, a stop codon, or a 3' untranslated region of
CC   human G-alpha-S1 (see AAA94451). The antisense compounds specifically
CC   hybridize with and inhibit the expression of human G-alpha-S1. The
CC   antisense compounds are useful for diagnostics, therapeutics and
CC   prophylaxis, e.g. to prevent or delay infection, inflammation or tumour
CC   formation. Particularly, the antisense oligonucleotides are useful for
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CC   treating humans prone to a disease or condition associated with
CC   expression of G-alpha-S1. The present sequence an antisense
CC   oligonucleotide targeted to the 3' untranslated region of human G-alpha-
CC   S1
XX
SQ   Sequence 20 BP; 4 A; 2 C; 1 G; 13 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.5e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2264 ATATTTATTTCAGATGTTTC 2283
              ||||||||||||  ||||||
Db          1 ATATTTATTTCATTTGTTTC 20


RESULT 2255
AAA90815
ID   AAA90815 standard; DNA; 20 BP.
XX
AC   AAA90815;
XX
DT   20-DEC-2000  (first entry)
XX
DE   Ribonucleotide reductase R1 message antisense oligo AS-I-2769-20.
XX
KW   Antisense oligonucleotide; ribonucleotide reductase; R1 protein;
KW   R2 protein; tumour cell proliferation inhibition; cancer; cytostatic; ss.
XX
OS   Synthetic.
XX
PN   WO200047733-A1.
XX
PD   17-AUG-2000.
XX
PF   09-FEB-2000; 2000WO-CA000120.
XX
PR   11-FEB-1999;   99US-00249730.
XX
PA   (GENE-) GENESENSE TECHNOLOGIES INC.
XX
PI   Wright JA,  Young AH;
XX
DR   WPI; 2000-558216/51.
XX
PT   New antisense oligonucleotide, AS-I-618-20, is useful for inhibiting
PT   tumor cell growth.
XX
PS   Example 3; Page 32; 137pp; English.
XX
CC   The present sequence is an antisense oligonucleotide directed against the
CC   mRNA encoding the R1 component of mammalian ribonucleotide reductase.
CC   Ribonucleotide reductase catalyses the conversion of ribonucleotides to
CC   their corresponding deoxyribonucleotides and thus plays an important role
CC   in DNA synthesis and cell proliferation. Regulation of ribonucleotide
CC   reductase is altered in cultured malignant cells and increased levels of
CC   R2 protein and R2 mRNA have been found in pre-malignant and malignant
CC   tissues as compared to normal control tissue samples. The present
CC   antisense sequence is therefore useful for inhibiting tumourigenicity of
CC   neoplastic cells and inhibiting metastasis of tumour cells. It is also
CC   useful for increasing sensitivity of neoplastic cells to chemotherapeutic
CC   drugs, thus allowing chemotherapeutic treatments to be used in patients
CC   who have become resistant or less sensitive to chemotherapy. The sequence
CC   may be RNA or DNA and may comprise a modified backbone and/or nucleotide
CC   analogues
XX
SQ   Sequence 20 BP; 0 A; 3 C; 1 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.5e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTT 2182
              ||| ||||||||||| |||||
Db          1 TCCGTTTTTTTTTTCTTTTT 20


RESULT 2256
AAS05713
ID   AAS05713 standard; DNA; 20 BP.
XX
AC   AAS05713;
XX
DT   07-SEP-2001  (first entry)
XX
DE   Polypyrimidine Crick strand oligonucleotide.
XX
KW   reverse phase triplex forming oligonucleotide; RP-TFO;
KW   protected nucleic acid sequence; PNAS; single nucleotide polymorphism;
KW   SNP; short tandem repeat; cancer; Factor V Leiden SNP; ss.
XX
OS   Synthetic.
XX
PN   WO200132929-A1.
XX
PD   10-MAY-2001.
XX
PF   03-NOV-2000; 2000WO-US030534.
XX
PR   03-NOV-1999;   99US-0163356P.
PR   03-NOV-1999;   99US-0163416P.
PR   21-DEC-1999;   99US-0171348P.
PR   07-JUL-2000; 2000US-0216579P.
XX
PA   (CYGE-) CYGENE INC.
PA   (OSTE/) OSTE C C.
XX
PI   Oste CC,  Ramberg ER;
XX
DR   WPI; 2001-343488/36.
XX
PT   Analyzing target nucleic acid sequences, useful for population genetics,
PT   drug development and diagnosing cancer, comprises hybridizing triple
PT   forming oligonucleotide and probe to target sequence.
XX
PS   Example 2; Page 66; 141pp; English.
XX
CC   The sequence is a polypyrimidine oligonucleotide for binding a second
CC   reverse phase triplex forming oligonucleotide, RP-TFO, (3' to the SNP) to
CC   the target SNP used to analyse Factor V Leiden SNP using the method of
CC   the invention. The invention relates to analysing target nucleic acid
CC   sequences comprising restricting isolated DNA, hybridising at least one
CC   triplex forming oligonucleotide (TFO), adding a 3' to 5' exonuclease to
CC   form a protected nucleic acid sequence (PNAS) tail structure, hybridising
CC   the captured structure with a single nucleotide polymorphisms (SNP)
CC   identification probe and determining the SNP score. The methods can be
CC   used for analysing target nucleic acid sequences, especially genomic DNA
CC   sequences, to determine if they contain SNPs or short tandem repeats
CC   (STRs). The methods can be used to detect SNPs for use in population
CC   genetics, drug development, forensics, cancer, genetic disease research,
CC   genomic analysis, diagnostics and therapeutics in humans, plants and
CC   animals
XX
SQ   Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.5e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              |||||||||||||  || |||
Db          1 TTTTTTTTTTTTTCTTATTT 20


RESULT 2257
AAF83959
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```
ID   AAF83959 standard; DNA; 20 BP.
XX
AC   AAF83959;
XX
DT   06-AUG-2001  (first entry)
XX
DE   BAP28 gene fragment amplifying primer BAP28polyTcourt.
XX
KW   BAP28; prostate; tumour; cancer; diagnostic; genetic analysis; PCTA-1;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200100669-A2.
XX
PD   04-JAN-2001.
XX
PF   23-JUN-2000; 2000WO-IB001183.
XX
PR   25-JUN-1999;   99US-0141323P.
PR   18-JAN-2000; 2000US-0176880P.
XX
PA   (GEST ) GENSET.
XX
PI   Barry C,· Bougueleret L,  Chumakov I,  Cohen-Akenine A;
XX
DR   WPI; 2001-367032/38.
XX
PT   New BAP28 polynucleotides and polypeptides overexpressed in prostate
PT   cancer cells for diagnosing prostate tumors, e.g. by hybridization or
PT   polymerase chain reaction assays.
XX
PS   Example; Page 347; 349pp; English.
XX
CC   The invention is directed to BAP28 polypeptides, BAP28 polynucleotide
CC   sequences and regulatory region located at the 3' and 5' ends of the
CC   BAP28 coding region. The BAP28 polypeptides can be expressed by standard
CC   recombinant methodology. BAP28 polynucleotides and polypeptides have been
CC   found to be over expressed in prostate tumour cells, therefore levels of
CC   BAP28 expression and/or activity may be assayed (e.g. by polymerase chain
CC   reaction (PCR)) to diagnose patient suffering from or susceptible to
CC   prostate cancer. Antibodies specific for the BAP28 polypeptides are
CC   useful as diagnostic reagents. Biallelic markers of the BAP28 gene are
CC   useful in genetic analysis. Sequences AAF83934-963 represent primers for
CC   the BAP28 gene and PCTA-1 gene (the coding strand of PCTA-1 gene is on
CC   the opposite of the coding strand of BAP28)
XX
SQ   Sequence 20 BP; 2 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.5e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTTA 2187
              |||||||||||||||| | ||
Db          1 TTTTTTTTTTTTTTTGTATA 20


RESULT 2258
ABA91535/c
ID   ABA91535 standard; DNA; 20 BP.
XX
AC   ABA91535;
XX
DT   23-APR-2002  (first entry)
XX
DE   DNA oligonucleotide AGT02023 used to test RNase H cleavage.
XX
KW   Nucleic acid detection; probe; mismatch; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    11
FT                   /*tag=  a
FT                   /note= "mismatch to target DNA"
FT   misc_feature    13
FT                   /*tag=  b
FT                   /note= "mismatch to target DNA"
XX
PN   WO200206531-A2.
XX
PD   24-JAN-2002.
XX
PF   12-JUL-2001; 2001WO-US022166.
XX
PR   14-JUL-2000; 2000US-00616761.
PR   30-MAR-2001; 2001US-00823647.
XX
PA   (GENE-) APPLIED GENE TECHNOLOGIES INC.
XX
PI   Dattagupta N;
XX
DR   WPI; 2002-171819/22.
XX
PT   Probes for detecting target nucleotide sequence in sample, has sequence
PT   that forms hairpin structure having a double-stranded segment and single-
PT   stranded loop collectively forming region complementary to target
PT   sequence.
XX
PS   Example 5; Page 50; 72pp; English.
XX
CC   The present sequence is that of oligonucleotide AGT02023, which contains
CC   a single mismatch with a target DNA oligonucleotide (see ABA91531). It is
CC   one of a set of oligonucleotides (see ABA91532-37) containing
CC   mismatch(es) to the target DNA that were tested in a hybridisation/RNase
CC   H cleavage assay. The results showed that 2 mismatches between the target
CC   and the probe ablated RNase H cleavage. The invention provides probes for
CC   nucleic acid hybridisation. The probes form a hairpin structure
CC   comprising a double-stranded stem and a single-stranded loop, and are
CC   capable of both intramolecular and intermolecular hybridisation. The
CC   double-stranded stem may comprise a methylphosphonate DNA:RNA hybrid that
CC   is resistant to RNase H cleavage. When the probe hybridises with a target
CC   DNA, the RNA strand in the DNA:RNA duplex becomes sensitive to RNase H
CC   treatment and can be removed. Arrays and methods for nucleic acid
CC   hybridisation using the probes are provided
XX
SQ   Sequence 20 BP; 16 A; 0 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.5e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTT 2174
              |||||||| | |||||||||
Db         20 TTTTTTCACATTTTTTTTT 1


RESULT 2259
ABL94271
ID   ABL94271 standard; DNA; 20 BP.
XX
AC   ABL94271;
XX
DT   29-JUL-2002  (first entry)
XX
DE   Human C/EBP beta phosphorothioate antisense oligonucleotide, SEQ ID:37.
XX
KW   Human; C/EBP beta; CCAAT/enhancer-binding protein beta; C/EPB2; LAP;
KW   TCF5; CRP2; NFIL6; IL6DBP; NF-M; AGP/EBP; Apc/EBP; transcription factor;
KW   tissue development; cellular function; proliferation; differentiation;
KW   hormone responsiveness; oxidative stress response;
KW   IL-6 signalling mediator; interleukin-6; carbohydrate metabolism;
KW   immunity; Th1 response; female fertility; gluconeogenesis; ovarian;
KW   cancer; tumour formation; type II; diabetes; infection; inflammation;
KW   expression inhibition; phosphorothioate; antisense oligonucleotide; ss.
```

```
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate linkages"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-methoxyethyl (2'-MOE) nucleotides. All 2' MOE
FT                   cytosines are 5-methylcytosine"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-methoxyethyl (2'-MOE) nucleotides. All 2' MOE
FT                   cytosines are 5-methylcytosine"
XX
PN   US6271030-B1.
XX
PD   07-AUG-2001.
XX
PF   14-JUN-2000; 2000US-00593711.
XX
PR   14-JUN-2000; 2000US-00593711.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Monia BP,  Butler MM,  Wyatt J;
XX
DR   WPI; 2002-214451/27.
XX
PT   Novel antisense compound targeted to nucleic acids encoding human or
PT   mouse CCAAT/enhancer binding protein (C/EBP) beta, useful in vitro for
PT   inhibiting expression of human or mouse C/EBP beta in cells/tissues.
XX
PS   Example 15; Col 42; 69pp; English.
XX
CC   Sequences ABL94252-ABL94476 represent antisense oligonucleotides targeted
CC   to the human or mouse CCAAT/enhancer-binding protein alpha (C/EBP alpha)
CC   gene, which inhibit its expression. The antisense oligonucleotides were
CC   designed to target different regions of the human and/or mouse C/EBP
CC   alpha RNA, and were analysed for their effect on C/EBP alpha mRNA levels
CC   by quantitative real-time PCR. The C/EBP family of proteins are a family
CC   of transcription factors which regulate the expression of a wide range of
CC   genes that control normal tissue development, cellular function, cellular
CC   proliferation and functional differentiation. C/EBP beta (also known as
CC   C/EPB2, LAP, TCF5, CRP2, NFIL6, IL6DBP, NF-M, AGP/EBP and Apc/EBP)
CC   primarily regulates hormone responsiveness and oxidative stress responses
CC   and is a mediator of IL-6 (interleukin-6) signalling. C/EBP beta is
CC   thought to be involved in carbohydrate metabolism, immunity, the Th1
CC   response, female fertility and gluconeogenic pathways. C/EBP beta is
CC   expressed in the liver, lung, spleen, kidney, brain, and testis, with the
CC   highest expression found in the lung. It is also expressed at a higher
CC   level in malignant ovarian tissue compared with normal ovarian tissue,
CC   and its expression in pancreas is upregulated in response to chronically
CC   elevated levels of glucose, indicating that it is involved in the
CC   impairment of insulin secretion in type II diabetes. The oligonucleotides
CC   of the invention are useful for diagnosis, prevention and treatment of
CC   conditions associated with C/EBP beta expression, such as cancer
CC   (particularly ovarian cancer), tumour formation, diabetes (particularly
CC   type II diabetes), infection, or inflammation
XX
SQ   Sequence 20 BP; 0 A; 6 C; 14 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.5e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         47 GCGCGCGGCGGGGGCGGCGG 66
              ||| ||||||| ||||||||
Db          1 GCGGGCGGCGGCGGCGGCGG 20
```

```
RESULT 2260
ABZ89487/c
ID   ABZ89487 standard; DNA; 20 BP.
XX
AC   ABZ89487;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 4729; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 18 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.5e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||  ||
Db         20 TTTTTTTTTTTTTTTTGGTT 1
```

```
RESULT 2261
ABZ88564
ID   ABZ88564 standard; DNA; 20 BP.
XX
AC   ABZ88564;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 3806; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 17 A; 1 C; 2 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.5e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              || | ||||||||||||||||
Db          1 GACAGAAAAAAAAAAAAAAA 20
```

```
RESULT 2262
ABZ85532/c
ID   ABZ85532 standard; DNA; 20 BP.
XX
AC   ABZ85532;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Claim 15; SEQ ID NO 774; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 17 A; 2 C; 1 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.5e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTTAACT 2190
              ||||||||||||||||  ||
Db         20 TTTTTTTTTTTTTTTTGGCT 1
```

```
RESULT 2263
ABZ85535/c
ID   ABZ85535 standard; DNA; 20 BP.
XX
AC   ABZ85535;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Claim 15; SEQ ID NO 777; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 18 A; 0 C; 2 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.5e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              ||||||  ||||  ||||||||
Db         20 TTTTTTCTTTTCTTTTTTT 1
```

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RESULT 2264
AAT76021/c
ID   AAT76021 standard; DNA; 21 BP.
XX
AC   AAT76021;
XX
DT   16-SEP-1997  (first entry)
XX
DE   DEN-2 cloning/sequencing antisense primer, cD2-10261.
XX
KW   Dengue 2 virus; polyprotein; capsid; prM; M; E; NS1; NS2A; NS2B; NS3;
KW   NS4A; NS4B; NS5; PDK-53; quadravalent vaccine; immunity; serotype;
KW   chimeric DEN-2/1 virus; chimeric DEN-2/3 virus; chimeric DEN-2/4 virus;
KW   dengue fever; fatal dengue haemorrhagic fever; dengue shock syndrome;
KW   DHF; DSS; PCR; amplify; polymerase chain reaction; primer; ss.
XX
OS   Synthetic.
XX
PN   WO9640933-A1.
XX
PD   19-DEC-1996.
XX
PF   06-JUN-1996;   96WO-US009209.
XX
PR   07-JUN-1995;   95US-00483292.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA   (UYMA-) UNIV MAHIDOL AT SALAYA.
XX
PI   Bhamarapravati N,  Butrapet S,  Chang J,  Gubler DJ,  Halstead SB;
PI   Kinney R,  Trent DW;
XX
DR   WPI; 1997-052330/05.
XX
PT   PDK-53, a clone of infectious attenuated Dengue 2 virus strain 16681 -
PT   also chimeric DEN-2/1, DEN-2/3 and DEN-1/4 viruses, used as a
PT   quadravalent vaccine for protecting against Dengue virus infection.
XX
PS   Example; Page 104; 261pp; English.
XX
CC   The sequences given in AAT75909-T76029 are primers which were used in the
CC   amplification, cloning and sequencing of the Dengue-2 viral cDNA's of the
CC   invention. The Dengue 2 viral DNA encodes a polyprotein which comprises
CC   the capsid, prM, M, E, NS1, NS2A, NS2B, NS3, NS4A, NS4B and NS5 proteins.
CC   The quadravalent vaccine of the invention comprises an attenuated Dengue
CC   virus clone, PDK-53, and a chimeric DEN-2/1 virus, a chimeric DEN-2/3
CC   virus, and/or a chimeric DEN-2/4 virus. The new quadravalent vaccines are
CC   used to protect against infection by all four serotypes of dengue virus,
CC   DEN-1, DEN-2, DEN-3 and DEN-4, which can lead to dengue fever or fatal
CC   dengue haemorrhagic fever/dengue shock syndrome (DHF/DSS). Host cells are
CC   used to produce the recombinant protein products of the DNA constructs
CC   which are used in the vaccines
XX
SQ   Sequence 21 BP; 4 A; 7 C; 3 G; 7 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   90.0%;  Pred. No. 1.7e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2019 GTCCTCTGGTAGGAGGCAAA 2038
              |||||  ||||||  |||||||
Db         21 GTCCTGTGGTAGAAGGCAAA 2

RESULT 2265
AAX09559
ID   AAX09559 standard; DNA; 21 BP.
XX
AC   AAX09559;
XX
DT   24-MAR-1999  (first entry)
```

XX
DE Human biallelic polymorphic marker upstream primer #439.
XX
KW Polymorphism; biallelic; human; forensic; paternity testing; disease;
KW detection; phenotypic typing; characteristic; infection; hereditary;
KW autoimmune disease; cancer; inflammation; drug; therapy; medicament;
KW treatment; marker; primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9820165-A2.
XX
PD 14-MAY-1998.
XX
PF 05-NOV-1997; 97WO-US020313.
XX
PR 06-NOV-1996; 96US-0030455P.
XX
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
XX
PI Lander ES, Wang D, Hudson T;
XX
DR WPI; 1998-286974/25.
XX
PT New isolated nucleic acid segments from the human genome - used for
PT determining polymorphic forms for use in e.g. forensics, paternity
PT testing or phenotypic typing for disease.
XX
PS Claim 15; Page 204; 310pp; English.
XX
CC AAX09121-X10268 are allele-specific oligonucleotide primers used in the
CC isolation of various biallelic polymorphic markers found in the human
CC genome (represented in AAX10269-X12937). These primers can be used in a
CC method for determining polymorphic forms in an individual for use in e.g.
CC forensics, paternity testing or for phenotypic typing for diseases such
CC as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial
CC hypercholesterolemia, polycystic kidney disease, hereditary
CC spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary
CC haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos
CC syndrome, osteogenesis imperfecta, acute intermittent porphyria,
CC autoimmune diseases, inflammation, cancer, diseases of the nervous
CC system, infection by pathogenic microorganisms, and characteristics such
CC as longevity, appearance (e.g. baldness, obesity), strength, speed,
CC endurance, fertility, and susceptibility or receptivity to particular
CC drugs or therapeutic treatments. The isolated polymorphic nucleic acid
CC segments can also be used to produce medicaments for the treatment or
CC prophylaxis of such diseases
XX
SQ Sequence 21 BP; 5 A; 8 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 1.7e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1249 ATTCACAGAACTTCTCAGCC 1268
|| | ||||||||||||||||
Db 1 ATCCTCAGAACTTCTCAGCC 20

RESULT 2266
AAZ26235
ID AAZ26235 standard; DNA; 21 BP.
XX
AC AAZ26235;
XX
DT 30-NOV-1999 (first entry)
XX
DE Human polymorphic region 424.
XX
KW Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW cell viability; loss of heterozygosity; precancerous condition; ASI;
KW allele specific inhibitor; somatic cell; diagnosis; prevention;
KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW graft versus host disease; malignant cell removal; bone marrow; ss.
XX
OS Homo sapiens.
XX
PN WO9841648-A2.
XX
PD 24-SEP-1998.
XX
PF 19-MAR-1998; 98WO-US005419.
XX
PR 20-MAR-1997; 97US-0041057P.
XX
PA (VARI-) VARIAGENICS INC.
XX
PI Housman D, Ledley FD, Stanton VP;
XX
DR WPI; 1998-521232/44.
XX
PT Identifying target genes for allele-specific drugs - used for diagnosis,
PT prevention and treatment of, e.g. cancers, atherosclerotic plaque,
PT dysplastic lesions, endometriosis or graft versus host disease.
XX
PS Disclosure; Fig 7; 605pp; English.
XX
CC This invention describes a novel method for identifying an inhibitor
CC potentially useful for treatment of cancer, where the inhibitor is active
CC on a gene vital for cell growth or viability, and where the gene is
CC subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC used for preventing the development of cancer in a patient having a
CC precancerous condition, by administering to the patient a first allele
CC specific inhibitor (ASI) targeted to an allele of a first essential gene
CC present in cells of the precancerous condition, where the normal somatic
CC cells of the patient are heterozygous for the first gene, the inhibitor
CC is active on at least one but less than all allelic forms of the gene
CC present in a population and targets only one allelic form present in the
CC normal somatic cells, and the first gene. The products and methods can be
CC used in the diagnosis, prevention and treatment of LOH disorders, e.g.
CC cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
CC lesions, benign tumours, endometriosis, polycystic kidney disease, and
CC graft versus host disease. The method can also be used to remove
CC malignant cells from bone marrow transplants. AAZ25812-Z26825 represent
CC human polymorphic sites described in the method of the invention
XX
SQ Sequence 21 BP; 17 A; 0 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 1.7e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2779 AGAATTGAAAAAAAAAAAAA 2798
||| ||||||||||||||||
Db 2 AGAGATGAAAAAAAAAAAAA 21

RESULT 2267
AAH91826
ID AAH91826 standard; DNA; 21 BP.
XX
AC AAH91826;
XX
DT 09-OCT-2001 (first entry)
XX
DE Human inflammatory bowel disease associated polymorphic site #901.
XX
KW Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
KW chromosome 5q31-33; forensic test; gene therapy; ds.
XX
OS Homo sapiens.
XX

```
FH   Key             Location/Qualifiers
FT   misc_feature    9
FT                   /*tag=  a
FT                   /note= "SNP, optionally T or A at this position"
XX
PN   WO200142511-A2.
XX
PD   14-JUN-2001.
XX
PF   11-DEC-2000; 2000WO-US033632.
XX
PR   10-DEC-1999;   99US-0170257P.
PR   10-APR-2000; 2000US-0196046P.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA   (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.
XX
PI   Daly M,  Hudson TJ,  Lander ES,  Rioux J,  Siminovitch K;
XX
DR   WPI; 2001-367874/38.
XX
PT   Testing for the presence of polymorphisms associated with inflammatory
PT   bowel disease, using a hybridization assay.
XX
PS   Claim 1; Page 76; 463pp; English.
XX
CC   The present invention describes a method for detecting the presence of
CC   polymorphisms associated with inflammatory bowel diseases such as
CC   ulcerative colitis and Crohn's disease. The methods can be used to detect
CC   the presence of genetic polymorphisms associated with inflammatory bowel
CC   disease and correlating their occurrence with disease states. They may be
CC   used in this way for phenotypic correlations, forensics, paternity
CC   testing, medicine and genetic analysis. The present sequence is a
CC   polymorphic site described in the exemplification of the invention
XX
SQ   Sequence 21 BP; 1 A; 3 C; 0 G; 16 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity  85.7%;  Pred. No. 1.7e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2157 TTTTTCTCCTTTTTTTTTTTT 2177
              ||  |||| ||||||||||||
Db          1 TTCATCTCNTTTTTTTTTTTT 21


RESULT 2268
AAT78996
ID   AAT78996 standard; DNA; 22 BP.
XX
AC   AAT78996;
XX
DT   13-JAN-1998  (first entry)
XX
DE   Human Huntington's disease gene intron 1 3' acceptor site.
XX
KW   Huntington's disease; animal model; transgenic animal; human; therapy;
KW   drug screening; Hdh gene; ss.
XX
OS   Homo sapiens.
XX
PN   CA2178022-A.
XX
PD   02-DEC-1996.
XX
PF   03-JUN-1996;   96CA-02178022.
XX
PR   01-JUN-1995;   95US-00457273.
XX
PA   (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI   Hayden M,  Lin B,  Nasir J;
XX
DR   WPI; 1997-298677/28.
XX
PT   Mouse Huntington's Disease gene - useful for generating transgenic mice
PT   as a model of Huntington's Disease.
XX
PS   Disclosure; Page 60; 69pp; English.
XX
CC   This oligonucleotide comprises the 5' acceptor site of intron 1 of the
CC   human Huntington's disease (HD) gene. The splice site sequences for the
CC   first 5 exons of the mouse HD gene (see AAT78974) and the human HD gene
CC   were compared (see AAT78985-T79002). Targeted disruption of the murine HD
CC   gene, e.g. at exon 5, can be used to examine the function of the HD gene
CC   and its role in development. Transgenic mice can be used as models of HD
XX
SQ   Sequence 22 BP; 2 A; 3 C; 1 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 22;
  Best Local Similarity  90.0%;  Pred. No. 1.9e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTT 2182
              ||||| |||||||| |||||
Db          1 TCCTTCTTTTTTTTATTTTT 20


RESULT 2269
AAH37805
ID   AAH37805 standard; DNA; 23 BP.
XX
AC   AAH37805;
XX
DT   14-AUG-2001  (first entry)
XX
DE   SNP specific upper PCR primer SEQ ID 601.
XX
KW   Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW   SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
KW   Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW   polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW   acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW   inflammation; forensic investigation; paternity analysis; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200129262-A2.
XX
PD   26-APR-2001.
XX
PF   13-OCT-2000; 2000WO-US028436.
XX
PR   15-OCT-1999;   99US-0160096P.
XX
PA   (ORCH-) ORCHID BIOSCIENCES INC.
XX
PI   Picoult-Newburg L,  Pohl M;
XX
DR   WPI; 2001-290930/30.
XX
PT   New genotyping oligonucleotide, useful for detecting the presence,
PT   absence or identity of single polynucleotide polymorphism in a nucleic
PT   acid sample.
XX
PS   Claim 1; Page 53; 83pp; English.
XX
CC   Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC   primer extension (SNPE) primers, and the sequences of regions flanking
CC   sites of single nucleotide polymorphisms SNPs. The present invention
CC   includes kits for determining the presence or absence of a SNP, using the
CC   oligonucleotides of the invention. The PCR primers are used to amplify a
CC   SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC   The oligonucleotides are useful for genotyping a nucleic acid sample by
CC   performing a single-nucleotide primer extension reaction. The
CC   oligonucleotides are useful for determining the presence, absence or
```

CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a PCR primer specific
CC for a human SNP containing DNA sequence
XX
SQ Sequence 23 BP; 16 A; 1 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.8; DB 1; Length 23;
Best Local Similarity 90.0%; Pred. No. 2.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2784 TGAAAAAAAAAAAAAAAAAA 2803
|||| ||||||||||||||||
Db 1 TGAAGGAAAAAAAAAAAAAA 20

RESULT 2270
AAH37805/c
ID AAH37805 standard; DNA; 23 BP.
XX
AC AAH37805;
XX
DT 14-AUG-2001 (first entry)
XX
DE SNP specific upper PCR primer SEQ ID 601.
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW inflammation; forensic investigation; paternity analysis; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200129262-A2.
XX
PD 26-APR-2001.
XX
PF 13-OCT-2000; 2000WO-US028436.
XX
PR 15-OCT-1999; 99US-0160096P.
XX
PA (ORCH-) ORCHID BIOSCIENCES INC.
XX
PI Picoult-Newburg L, Pohl M;
XX
DR WPI; 2001-290930/30.
XX
PT New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample.
XX
PS Claim 1; Page 53; 83pp; English.
XX
CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a PCR primer specific
CC for a human SNP containing DNA sequence
XX
SQ Sequence 23 BP; 16 A; 1 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.8; DB 1; Length 23;
Best Local Similarity 90.0%; Pred. No. 2.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2164 CCTTTTTTTTTTTTTTTTT 2183
|||||||||||||||||| ||
Db 22 CCTTTTTTTTTTTTTTCCTT 3

RESULT 2271
ABN86902/c
ID ABN86902 standard; DNA; 24 BP.
XX
AC ABN86902;
XX
DT 23-JUL-2002 (first entry)
XX
DE Human macroprotein 21.78 PCR primer 2 SEQ ID NO:4.
XX
KW Human; macroprotein 21.78; embryo development teratogenesis; tumour;
KW PCR primer; ss.
XX
OS Homo sapiens.
XX
PN CN1331245-A.
XX
PD 16-JAN-2002.
XX
PF 30-JUN-2000; 2000CN-00116981.
XX
PR 30-JUN-2000; 2000CN-00116981.
XX
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-292882/34.
XX
PT New polypeptide-human macroprotein 21.78 and polynucleotide encoding it,
PT for treating diseases such as embryo development teratogenesis and tumor.
XX
PS Example 2; Page 19 (Disclosure); 35pp; Chinese.
XX
CC The present invention describes human macroprotein 21.78 (I). Also
CC described is a process for preparing (I) using DNA recombination
CC techniques. (I) and the polynucleotide sequence encoding it (II) can be
CC used in the treatment of diseases such as embryo development
CC teratogenesis and tumours. The present sequence represents a PCR primer
CC for (I), which is used in an example from the present invention
XX
SQ Sequence 24 BP; 0 A; 1 C; 2 G; 21 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.8; DB 1; Length 24;
Best Local Similarity 90.0%; Pred. No. 2.3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              |||||||||| ||||| ||
Db         24 GAAAAAAAAAACAAAAACAA 5


RESULT 2272
ABQ79564
ID   ABQ79564 standard; DNA; 24 BP.
XX
AC   ABQ79564;
XX
DT   25-NOV-2002  (first entry)
XX
DE   Forward primer for detecting T7 phage gene 10 inserts.
XX
KW   Protein identification; phage; intercellular; fibroblast; stem cell; PCR;
KW   primer; ss.
XX
OS   Synthetic.
XX
PN   WO200262965-A2.
XX
PD   15-AUG-2002.
XX
PF   06-FEB-2002; 2002WO-US005051.
XX
PR   06-FEB-2001; 2001US-0266662P.
XX
PA   (WISC ) WISCONSIN ALUMNI RES FOUND.
XX
PI   Thomson JA,  Xu R;
XX
DR   WPI; 2002-657535/70.
XX
PT   Identifying intercellular protein factors, e.g. intercellular factors
PT   expressed by fibroblasts that inhibit stem cell differentiation in
PT   culture, by employing a phage display technique using cDNA from the
PT   signaling cells.
XX
PS   Example; Page 9; 19pp; English.
XX
CC   The invention relates to identifying proteins, which function as
CC   intercellular signals between a signaling cell and affected cells. The
CC   method involves (a) inserting a cDNA library from the signaling cell into
CC   a phage; (b) incubating the phage with the affected cells; (c) washing
CC   phage that does not bind to the affected cells; (d) eluting the phage
CC   that does bind to the affected cells; and (e) sequencing the cDNA inserts
CC   in the bound phage to identify sequence information useful for
CC   characterizing a protein made by the signaling cell and recognized by a
CC   receptor in the affected cells. The method is useful for identifying
CC   intercellular protein factors, e.g. intercellular factors expressed by
CC   fibroblasts that act to inhibit the differentiation of stem cells in
CC   culture. The present sequence represents a PCR primer used for detecting
CC   T7 phage gene 10 inserts
XX
SQ   Sequence 24 BP; 7 A; 3 C; 10 G; 4 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 24;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1186 AGGACGAAATGAGATGGCAG 1205
              ||||||| |||||||||| |
Db          2 AGGACGAGATGAGATGGCTG 21


RESULT 2273
ABN85224/c
ID   ABN85224 standard; DNA; 24 BP.
XX
AC   ABN85224;
XX
DT   24-SEP-2002  (first entry)
XX
DE   Human translation initiation factor eIF4E binding protein 17.27 primer#2.
XX
KW   Human; translation initiation factor subunit eIF4E binding protein 17.27;
KW   embryo development malformation; tumour; diabetes; menoxenia;
KW   peptic ulcer; translation initiation factor; eIF4E; binding protein; PCR;
KW   primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1339492-A.
XX
PD   13-MAR-2002.
XX
PF   23-AUG-2000; 2000CN-00119722.
XX
PR   23-AUG-2000; 2000CN-00119722.
XX
PA   (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-464075/50.
XX
PT   New polypeptide-human translation initiation factor subunit eIF4E binding
PT   protein 17.27 for treating embryo development malformation, tumors,
PT   diabetes, menoxenia, and peptic ulcer.
XX
PS   Example 3; Page 20 (Disclosure); 33pp; Chinese.
XX
CC   The present invention relates to human translation initiation factor
CC   subunit eIF4E binding protein 17.27 (see ABB83427). The protein and its
CC   coding sequence are useful for treating various diseases, such as embryo
CC   development malformation, tumours, diabetes, menoxenia, peptic ulcer,
CC   etc. The present sequence is a PCR primer, which was used in an example
CC   from the invention
XX
SQ   Sequence 24 BP; 3 A; 0 C; 3 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 24;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAAA 2801
              ||| |||||||||||||| |
Db         21 ATTCAAAAAAAAAAAAAACA 2


RESULT 2274
ABL56666
ID   ABL56666 standard; DNA; 24 BP.
XX
AC   ABL56666;
XX
DT   30-JUL-2002  (first entry)
XX
DE   PCR primer #1 for human prolyl oligomeric peptidase 13.2 cDNA.
XX
KW   Human; prolyl oligomeric peptidase 13.2; enzyme; angiocardiopathy;
KW   nervous system retrograde disease; gene therapy; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200226990-A1.
XX
PD   04-APR-2002.
XX
PF   29-JUN-2001; 2001WO-CN001090.
XX
PR   30-JUN-2000; 2000CN-00116964.
XX
PA   (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
```

```
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-269651/31.
XX
PT   Prolyl oligomeric peptidase 13.2 polypeptide for diagnosing and treating
PT   angiocardiopathy and nervous system retrograde disease.
XX
PS   Example 2; Page 17; 35pp; Chinese.
XX
CC   PCR primers ABL56666-67 were used to amplify cDNA encoding human prolyl
CC   oligomeric peptidase 13.2. The polypeptide and polynucleotide are used in
CC   diagnosis and treatment of angiocardiopathy and nervous system retrograde
CC   disease. The polynucleotide may also be used for gene therapy
XX
SQ   Sequence 24 BP; 18 A; 3 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 24;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAA 2803
              | |||||||||||| ||||||
Db          5 TCAAAAAAAAAAAGAAAAAA 24


RESULT 2275
ABL56666/c
ID   ABL56666 standard; DNA; 24 BP.
XX
AC   ABL56666;
XX
DT   30-JUL-2002  (first entry)
XX
DE   PCR primer #1 for human prolyl oligomeric peptidase 13.2 cDNA.
XX
KW   Human; prolyl oligomeric peptidase 13.2; enzyme; angiocardiopathy;
KW   nervous system retrograde disease; gene therapy; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200226990-A1.
XX
PD   04-APR-2002.
XX
PF   29-JUN-2001; 2001WO-CN001090.
XX
PR   30-JUN-2000; 2000CN-00116964.
XX
PA   (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-269651/31.
XX
PT   Prolyl oligomeric peptidase 13.2 polypeptide for diagnosing and treating
PT   angiocardiopathy and nervous system retrograde disease.
XX
PS   Example 2; Page 17; 35pp; Chinese.
XX
CC   PCR primers ABL56666-67 were used to amplify cDNA encoding human prolyl
CC   oligomeric peptidase 13.2. The polypeptide and polynucleotide are used in
CC   diagnosis and treatment of angiocardiopathy and nervous system retrograde
CC   disease. The polynucleotide may also be used for gene therapy
XX
SQ   Sequence 24 BP; 18 A; 3 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 24;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTA 2187
              |||||| |||||||||||| |
Db         24 TTTTTTCTTTTTTTTTTGA 5


RESULT 2276
ADD19369
ID   ADD19369 standard; DNA; 24 BP.
XX
AC   ADD19369;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Salmo salar SNP OLA primer SEQ ID NO:4.
XX
KW   single nucleotide polymorphism; SNP; fish; Salmo salar;
KW   Orechromis niloticus; Atlantic halibut; microsatellite; cod;
KW   polymorphic site; seabass; salmonidae; Tilapia; rainbow trout; halibut;
KW   detection; primer; ss.
XX
OS   Synthetic.
OS   Salmo salar.
XX
PN   WO2003060160-A2.
XX
PD   24-JUL-2003.
XX
PF   17-JAN-2003; 2003WO-IB000112.
XX
PR   18-JAN-2002; 2002US-0349950P.
PR   16-AUG-2002; 2002US-0404200P.
XX
PA   (GENO-) GENOMAR ASA.
XX
PI   Lie O,  Slettan A,  Hoyum M,  Lingaas F;
XX
DR   WPI; 2003-627388/59.
XX
PT   Novel isolated nucleic acid molecule comprising single nucleotide
PT   polymorphism associated with fish, useful for forming PCR primers which
PT   are used for detecting single nucleotide polymorphisms in fish nucleic
PT   acids.
XX
PS   Claim 1; SEQ ID NO 4; 233pp; English.
XX
CC   The present invention describes an isolated nucleic acid (I) comprising a
CC   single nucleotide polymorphism (SNP) chosen from: (i) a nucleic acid of
CC   Salmo salar SNPs, Oreochromis niloticus SNPs or Atlantic halibut SNPs;
CC   and (ii) a nucleic acid having nucleotide sequence that hybridises to
CC   (i), or its complement under highly stringent hybridisation conditions.
CC   Also described: (1) an isolated oligonucleotide (II) comprising at least
CC   17 contiguous nucleotides of a nucleotide sequence of S. salar SNPs, O.
CC   niloticus SNPs, O. niloticus microsatellites, Atlantic halibut SNPs, cod
CC   polymorphic sites and seabass polymorphic sites, or their complement; (2)
CC   a primer pair (III) suitable for use in PCR, comprising two (II) capable
CC   of amplifying a nucleotide sequence chosen from S. salar SNPs and, O.
CC   niloticus SNPs, O. niloticus microsatellites, Atlantic halibut SNPs, cod
CC   polymorphic sites and seabass polymorphic sites; and determining (M1) the
CC   origin of fish sample comprising providing a parentage genotype database
CC   comprising a collection of candidate parent genotypes, where each of the
CC   candidate parent genotype represents a distinct origin, and comparing a
CC   sample genotype to the parentage genotype database, where a match between
CC   the sample genotype and one of the candidate parent genotype identifies
CC   to the origin of the sample. (M1) is useful for determining the origin of
CC   a fish sample such as family salmonidae, S. salar, Tilapia, O. niloticus,
CC   rainbow trout, halibut, seabass and Atlantic cod. (II) is useful for
CC   detecting nucleic acid molecule comprising SNP in a sample, which
CC   involves contacting the sample containing nucleic acids with one or more
CC   (II) derived from nucleotide sequence of S. salar SNPs and O. niloticus
CC   SNPs, and identifying nucleic acid that hybridises to (II). (II) is
CC   useful for detecting nucleic acid molecule comprising a polymorphic
CC   sequence in a sample, comprising contacting the sample containing nucleic
CC   acids with one or more (II) which is derived from O. niloticus
CC   microsatellite, O. niloticus SNPs, Atlantic halibut SNPs, cod polymorphic
CC   sites or seabass polymorphic sites, and identifying a nucleic acid that
```

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CC   hybridises to (II). (III) is useful for detecting nucleic acid molecule
CC   comprising a microsatellite sequence in sample. The present sequence is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 24 BP; 16 A; 1 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 24;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAA 2800
              ||||| |||||| |||||||
Db          2 AATTGGAAAAAACAAAAAAA 21


RESULT 2277
ADB04574/c
ID   ADB04574 standard; DNA; 25 BP.
XX
AC   ADB04574;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ7 scanning oligonucleotide SEQ ID 5560.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 5560; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 25 BP; 3 A; 2 C; 3 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 25;
  Best Local Similarity   90.0%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAA 2803
              | ||||||||||||||||| |
Db         20 TCAAAAAAAAAAAAAAAAGA 1


RESULT 2278
AAQ98161
ID   AAQ98161 standard; DNA; 25 BP.
XX
AC   AAQ98161;
XX
DT   05-FEB-1996  (first entry)
XX
DE   Hind III primer/adaptor.
XX
KW   Hind III primer/adaptor; random oligonucleotide identification;
KW   beta-galactosidase gene; E. coli; infectious diseases;
KW   herpes simplex virus; ss.
XX
OS   Synthetic.
XX
PN   WO9516054-A1.
XX
PD   15-JUN-1995.
XX
PF   02-DEC-1994;   94WO-US013884.
XX
PR   02-DEC-1993;   93US-00161281.
XX
PA   (MIRA/) MIRABELLI C K.
PA   (ECKE/) ECKER D J.
PA   (VICK/) VICKERS T A.
PA   (ROBE/) ROBERTSON D L.
XX
PI   Mirabelli CK,  Ecker DJ,  Vickers TA,  Robertson DL;
XX
DR   WPI; 1995-224334/29.
XX
PT   Identification of oligo:nucleotide(s) with a desired activity, e.g.
PT   activity against an infectious agent - by cloning vectors contg. randomly
PT   sequenced oligo:nucleotide(s) into cells and assaying for the desired
PT   phenotype.
XX
PS   Claim 25; Page 25; 53pp; English.
XX
CC   AAQ98161 is a random oligonucleotide Hind III primer/adaptor used in a
CC   new method for the identification of random oligonucleotides which
CC   inhibit the expression of a target gene, e.g. the beta-galactosidase gene
CC   in E. coli. Such random oligonucleotides may be used in the treatment of
CC   infectious diseases, pref. herpes simplex virus infection
XX
SQ   Sequence 25 BP; 2 A; 3 C; 3 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 25;
  Best Local Similarity   90.0%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTT 2184
              |||  ||||||||||||||||
Db          6 CTTGGTTTTTTTTTTTTTT 25


RESULT 2279
AAC66194
ID   AAC66194 standard; DNA; 25 BP.
XX
AC   AAC66194;
XX
DT   14-FEB-2001  (first entry)
XX
DE   PCR primer EcoR1-dt used in trypsin hL identification.
```

```
XX
KW   Human; trypsin hL; serine protease; lung disease model animal;
KW   PCR primer; ss.
XX
OS   Synthetic.
XX
PN   JP2000253887-A.
XX
PD   19-SEP-2000.
XX
PF   11-MAR-1999;   99JP-00065337.
XX
PR   11-MAR-1999;   99JP-00065337.
XX
PA   (TTPH-) TT PHARMA KK.
XX
DR   WPI; 2000-658814/64.
XX
PT   Novel gene encoding a serine protease and its protein used to screen for
PT   serine protease inhibitors and to prepare lung disease animal models.
XX
PS   Disclosure; Page 7-8; 17pp; Japanese.
XX
CC   Nucleotide sequence AAC66182 encodes human trypsin hL AAB35701, a serine
CC   protease. The invention relates to the human hL gene and protein
CC   sequences, to a recombinant vector containing the nucleotide sequence,
CC   and a host cell containing the vector. Human trypsin hL can be used for
CC   screening for serine protease inhibitors, in the preparation of a lung
CC   disease model animal, and for the development of an index marker of lung
CC   diseases caused by an anti-trypsin hL antibody. The present sequence
CC   represents a PCR primer used in the identification of trypsin hL
XX
SQ   Sequence 25 BP; 2 A; 2 C; 4 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 25;
  Best Local Similarity   90.0%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2160 TTCTCCTTTTTTTTTTTTT 2179
              ||| | ||||||||||||||
Db          6 TTCGCTTTTTTTTTTTTTT 25


RESULT 2280
AAC96039
ID   AAC96039 standard; DNA; 25 BP.
XX
AC   AAC96039;
XX
DT   26-FEB-2001  (first entry)
XX
DE   16s rRNA gene PCR primer #6.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 44; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 1 A; 5 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 25;
  Best Local Similarity   90.0%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1771 TTTTTTTTTTTGAACCCCAT 1790
              |||||||||||| ||||| |
Db          4 TTTTTTTTTTTGCACCCCTT 23


RESULT 2281
AAC95680
ID   AAC95680 standard; DNA; 25 BP.
XX
AC   AAC95680;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DPB1 gene PCR primer #15.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 38; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 4 A; 3 C; 4 G; 14 T; 0 U; 0 Other;
```

Query Match 0.6%; Score 16.8; DB 1; Length 25;
Best Local Similarity 90.0%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       2175 TTTTTTTTTTTTAACTTTGA 2194
              ||||||||||||||||  ||
Db          1 TTTTTTTTTTTTAACTACGA 20
```

RESULT 2282
AAC96070
ID AAC96070 standard; DNA; 25 BP.
XX
AC AAC96070;
XX
DT 26-FEB-2001 (first entry)
XX
DE 16s rRNA gene PCR primer #37.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 45; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 2 A; 2 C; 6 G; 15 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.8; DB 1; Length 25;
Best Local Similarity 90.0%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       2174 TTTTTTTTTTTTTAACTTTG 2193
              ||||||||||||||  | |||
Db          1 TTTTTTTTTTTTTAGCCTTG 20
```

RESULT 2283
AAC96447
ID AAC96447 standard; DNA; 25 BP.
XX
AC AAC96447;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA DQA1 gene PCR primer #49.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 51; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 2 A; 4 C; 3 G; 16 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.8; DB 1; Length 25;
Best Local Similarity 90.0%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       1922 TTTTTTTTCAGTGTTAAGGT 1941
              ||||||||||| ||| |||
Db          5 TTTTTTTTCAGTCTTACGGT 24
```

RESULT 2284
AAC96249
ID AAC96249 standard; DNA; 25 BP.
XX
AC AAC96249;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA DPA1 gene PCR primer #6.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.

```
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 48; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 3 A; 4 C; 2 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 25;
  Best Local Similarity   90.0%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTAACTT 2191
              ||||||||||||  | |||||
Db          1 TTTTTTTTTTTTGTCAACTT 20


RESULT 2285
AAC95664
ID   AAC95664 standard; DNA; 25 BP.
XX
AC   AAC95664;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DPA1 gene PCR primer #9.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 37; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 3 A; 4 C; 2 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 25;
  Best Local Similarity   90.0%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTAACTT 2191
              ||||||||||||  | |||||
Db          1 TTTTTTTTTTTTGTCAACTT 20


RESULT 2286
AAC96455
ID   AAC96455 standard; DNA; 25 BP.
XX
AC   AAC96455;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DQB1 gene PCR primer #7.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 51; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 4 A; 2 C; 5 G; 14 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 25;
  Best Local Similarity   90.0%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2175 TTTTTTTTTTTTAACTTTGA 2194
              ||||||||||||||||  ||
Db          1 TTTTTTTTTTTTAACTACGA 20


RESULT 2287
AAC96434
ID   AAC96434 standard; DNA; 25 BP.
```

XX
AC AAC96434;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA DQA1 gene PCR primer #36.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 51; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 4 A; 5 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.8; DB 1; Length 25;
Best Local Similarity 90.0%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       2173 TTTTTTTTTTTTTTAACTTT 2192
              |||||||||||| ||||| |
Db          1 TTTTTTTTTTTTATAACTCT 20
```

RESULT 2288
AAC96421/c
ID AAC96421 standard; DNA; 25 BP.
XX
AC AAC96421;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA DQA1 gene PCR primer #23.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 51; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 3 A; 5 C; 4 G; 13 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.8; DB 1; Length 25;
Best Local Similarity 90.0%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       2778 TAGAATTGAAAAAAAAAAAAA 2797
              | | ||||||||||||||||
Db         20 TGGGATTGAAAAAAAAAAAAA 1
```

RESULT 2289
AAC96251/c
ID AAC96251 standard; DNA; 25 BP.
XX
AC AAC96251;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA DPA1 gene PCR primer #8.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 48; 66pp; English.
XX

```
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 3 A; 3 C; 3 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 25;
  Best Local Similarity   90.0%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAA 2803
              || | ||||||||||||||||
Db         20 TGTACAAAAAAAAAAAAAAAA 1


RESULT 2290
AAC96448
ID   AAC96448 standard; DNA; 25 BP.
XX
AC   AAC96448;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DQA1 gene PCR primer #50.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 51; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 2 A; 3 C; 3 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 25;
  Best Local Similarity   90.0%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1922 TTTTTTTTCAGTGTTAAGGT 1941
              |||||||||||| ||| |||
Db          5 TTTTTTTTCAGTCTTATGGT 24


RESULT 2291
AAC95706/c
ID   AAC95706 standard; DNA; 25 BP.
XX
AC   AAC95706;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DQA1 gene PCR primer #3.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 38; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 5 A; 4 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 25;
  Best Local Similarity   90.0%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAAAA 2797
              || | ||||||||||||||||
Db         20 TAAACTTGAAAAAAAAAAAA 1


RESULT 2292
AAC95968/c
ID   AAC95968 standard; DNA; 25 BP.
XX
AC   AAC95968;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA HLA-B gene PCR primer #79.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
```

XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 43; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 2 A; 5 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.8; DB 1; Length 25;
Best Local Similarity 90.0%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2783 TTGAAAAAAAAAAAAAAAAA 2802
|||||| ||||||||||||
Db 20 TGGAAAAGAAAAAAAAAAAA 1

RESULT 2293
AAC96355
ID AAC96355 standard; DNA; 25 BP.
XX
AC AAC96355;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA DPB1 gene PCR primer #87.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 50; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 5 A; 2 C; 5 G; 13 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.8; DB 1; Length 25;
Best Local Similarity 90.0%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2175 TTTTTTTTTTTTAACTTTGA 2194
|||||||||||||||| | ||
Db 1 TTTTTTTTTTTTAACCTGGA 20

RESULT 2294
AAC96432/c
ID AAC96432 standard; DNA; 25 BP.
XX
AC AAC96432;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA DQA1 gene PCR primer #34.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 51; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 1 A; 5 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.8; DB 1; Length 25;
Best Local Similarity 90.0%; Pred. No. 2.4e+03;

```
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAA 2798
              || | ||||||||||||||||
Db         20 AGGAATGAAAAAAAAAAAAA 1


RESULT 2295
AAC96550/c
ID   AAC96550 standard; DNA; 25 BP.
XX
AC   AAC96550;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DRB345 gene PCR primer #21.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 53; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 0 A; 5 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match              0.6%;  Score 16.8;  DB 1;  Length 25;
  Best Local Similarity   90.0%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAA 2799
              |||  ||||||||||||||||
Db         20 GAAGAGAAAAAAAAAAAAAA 1


RESULT 2296
AAC96256
ID   AAC96256 standard; DNA; 25 BP.
XX
AC   AAC96256;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DPA1 gene PCR primer #13.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 48; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 3 A; 2 C; 3 G; 17 T; 0 U; 0 Other;

  Query Match              0.6%;  Score 16.8;  DB 1;  Length 25;
  Best Local Similarity   90.0%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTTA 2187
              |||||||||||||| ||| ||
Db          1 TTTTTTTTTTTTTGTTTGTA 20


RESULT 2297
ABS76271
ID   ABS76271 standard; DNA; 25 BP.
XX
AC   ABS76271;
XX
DT   27-DEC-2002  (first entry)
XX
DE   Human PAPP-E exon 7 associated 25-mer SEQ ID 1797.
XX
KW   PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW   contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW   dysgenetic pregnancy; primer; ss.
XX
OS   Homo sapiens.
XX
PN   US2002102252-A1.
XX
PD   01-AUG-2002.
XX
PF   06-APR-2001; 2001US-00827998.
XX
PR   26-MAY-2000; 2000US-0207456P.
XX
PA   (GUYY/) GU Y.
PA   (SHAN/) SHANNON M E.
XX
```

```
PI   Gu Y,  Shannon ME;
XX
DR   WPI; 2002-697817/75.
XX
PT   New isolated nucleic acid encoding an isoform of human pregnancy
PT   associated plasma protein E, for preventing or aborting pregnancy.
XX
PS   Example 2; Page 311; 353pp; English.
XX
CC   This invention describes a novel isolated nucleic acid that encodes one
CC   of three new isoforms of human pregnancy associated plasma protein E,
CC   hPAPP-E. The products of the invention have abortive and contraceptive
CC   activity and can be used for gene therapy or in a vaccine. The nucleic
CC   acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC   used in pharmaceutical compositions or vaccines for preventing or
CC   aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC   dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC   the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC   antibodies can be used to assess the expression levels of PAPP-E isoform
CC   proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC   antenatally. This sequence represents an oligomer used in scanning the
CC   human PAPP-E genes described in the disclosure of the invention
XX
SQ   Sequence 25 BP; 4 A; 5 C; 7 G; 9 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 25;
  Best Local Similarity   90.0%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2310 AAGCAATTTGTTGCTGCTTG 2329
              |||| | ||||||||||||||
Db          6 AAGCCAGTTGTTGCTGCTTG 25


RESULT 2298
ACD00129
ID   ACD00129 standard; DNA; 25 BP.
XX
AC   ACD00129;
XX
DT   28-JUL-2003  (first entry)
XX
DE   G-protein coupled receptor GPCR-A-1 analysis oligonucleotide #602.
XX
KW   Human; G-protein coupled receptor; GPCR-A-1; cancer; tumour;
KW   G-Protein-Agonist; G-Protein-Antagonist; gene therapy; cytostatic; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003031621-A2.
XX
PD   17-APR-2003.
XX
PF   11-OCT-2002; 2002WO-US032599.
XX
PR   12-OCT-2001; 2001US-0329000P.
XX
PA   (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
XX
PI   Zhang J;
XX
DR   WPI; 2003-381720/36.
XX
PT   New GPCR-A-1 nucleic acid and polypeptide, useful for diagnosing,
PT   investigating and/or treating disorders associated with aberrant
PT   expression or activity of GPCR-A-1, such as tumors and cancers.
XX
PS   Example 2; SEQ ID NO 626; 156pp; English.
XX
CC   The invention describes an isolated nucleic acid encoding a G protein
CC   coupled receptor (GPCR), mutations of which cause cancer, comprising a
CC   2225 or 1921 base pair sequence, or their degenerate variants, encoding a
CC   409 residue amino acid sequence, all given in the specification, with or
CC   without conservative amino acid substitutions, or complements of the
CC   sequence of them. The encoding nucleic acid is not more than 100 kbase in
CC   length. The methods and compositions of the present invention are useful
CC   for diagnosing, investigating and/or treating disorders associated with
CC   aberrant expression or activity of GPCR-A-1, such as tumours and cancers.
CC   This sequence represents an oligonucleotide used to analyse the gene
CC   encoding human G-protein coupled receptor GPCR-A-1
XX
SQ   Sequence 25 BP; 3 A; 4 C; 10 G; 8 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 25;
  Best Local Similarity   90.0%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2105 GGGGGCCTTCTGGTTTTAGG 2124
              |||| ||||||||| |||||
Db          6 GGGGACCTTCTGGTCTTAGG 25


RESULT 2299
ACD00135
ID   ACD00135 standard; DNA; 25 BP.
XX
AC   ACD00135;
XX
DT   28-JUL-2003  (first entry)
XX
DE   G-protein coupled receptor GPCR-A-1 analysis oligonucleotide #608.
XX
KW   Human; G-protein coupled receptor; GPCR-A-1; cancer; tumour;
KW   G-Protein-Agonist; G-Protein-Antagonist; gene therapy; cytostatic; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003031621-A2.
XX
PD   17-APR-2003.
XX
PF   11-OCT-2002; 2002WO-US032599.
XX
PR   12-OCT-2001; 2001US-0329000P.
XX
PA   (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
XX
PI   Zhang J;
XX
DR   WPI; 2003-381720/36.
XX
PT   New GPCR-A-1 nucleic acid and polypeptide, useful for diagnosing,
PT   investigating and/or treating disorders associated with aberrant
PT   expression or activity of GPCR-A-1, such as tumors and cancers.
XX
PS   Example 2; SEQ ID NO 632; 156pp; English.
XX
CC   The invention describes an isolated nucleic acid encoding a G protein
CC   coupled receptor (GPCR), mutations of which cause cancer, comprising a
CC   2225 or 1921 base pair sequence, or their degenerate variants, encoding a
CC   409 residue amino acid sequence, all given in the specification, with or
CC   without conservative amino acid substitutions, or complements of the
CC   sequence of them. The encoding nucleic acid is not more than 100 kbase in
CC   length. The methods and compositions of the present invention are useful
CC   for diagnosing, investigating and/or treating disorders associated with
CC   aberrant expression or activity of GPCR-A-1, such as tumours and cancers.
CC   This sequence represents an oligonucleotide used to analyse the gene
CC   encoding human G-protein coupled receptor GPCR-A-1
XX
SQ   Sequence 25 BP; 4 A; 5 C; 10 G; 6 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 25;
  Best Local Similarity   90.0%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2106 GGGGCCTTCTGGTTTTAGGA 2125
```

```
                ||| |||||||||| ||||||
Db            1 GGGACCTTCTGGTCTTAGGA 20
```

RESULT 2300
AAA07787
ID AAA07787 standard; DNA; 23 BP.
XX
AC AAA07787;
XX
DT 23-JUN-2000 (first entry)
XX
DE Structure of a fragment of duplex A target strand.
XX
KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; ss.
XX
OS Synthetic.
XX
PN WO200011013-A1.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US019029.
XX
PR 22-AUG-1998; 98US-0097712P.
XX
PA (UYNE-) UNIV NEBRASKA.
XX
PI Gold B;
XX
DR WPI; 2000-246530/21.
XX
PT Modified nucleomonomers, used in physiologically stable, non-toxic
PT oligomers used to inhibit expression of nucleic acids and in gene
PT regulation, antisense technology and diagnostics.
XX
PS Disclosure; Page 20; 42pp; English.
XX
CC The invention provides modified nucleomonomers of specified formula and
CC their pharmaceutically acceptable salts. The nucleomonomers are used as
CC monomers in oligomers, which are used in pharmaceutical compositions to
CC inhibit expression of nucleic acid molecules including DNA and RNA in
CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC infected cells. They are used in oligomers for gene regulation, antisense
CC technology, diagnostic applications to detect target sequences in
CC biological samples such as those containing pathogenic bacteria, fungi
CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC interleukins associated with pathological conditions such as inflammatory
CC conditions, cardiovascular disorders, immune reactions, cancer, viral
CC infections and bacterial infections (see AAA07786 for details of other
CC uses for which the oligomers are suitable for). Oligomers comprising the
CC nucleomonomers exhibit increased duplex DNA stability when hybridizing to
CC target nucleic acid sequences, are physiologically stable, non-toxic and
CC able to penetrate into cells while maintaining stringent base pair
CC fidelity for target DNA sequences. The oligomers demonstrate significant
CC single- or double-stranded target nucleic acid binding activity to form
CC duplexes, triplexes or other forms of stable association
XX
SQ Sequence 23 BP; 1 A; 2 C; 2 G; 18 T; 0 U; 0 Other;

```
  Query Match             0.6%;  Score 16.6;  DB 1;  Length 23;
  Best Local Similarity   82.6%;  Pred. No. 2.2e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTAA 2188
                ||  |||||||||||||||| | |
Db          1 TTGGTTTTTTTTTTTTTTTCTCA 23
```

RESULT 2301
AAA07786/c
ID AAA07786 standard; DNA; 23 BP.
XX
AC AAA07786;
XX
DT 23-JUN-2000 (first entry)
XX
DE Structure of a fragment of duplex A target strand.
XX
KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; ss.
XX
OS Synthetic.
XX
PN WO200011013-A1.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US019029.
XX
PR 22-AUG-1998; 98US-0097712P.
XX
PA (UYNE-) UNIV NEBRASKA.
XX
PI Gold B;
XX
DR WPI; 2000-246530/21.
XX
PT Modified nucleomonomers, used in physiologically stable, non-toxic
PT oligomers used to inhibit expression of nucleic acids and in gene
PT regulation, antisense technology and diagnostics.
XX
PS Disclosure; Page 20; 42pp; English.
XX
CC The invention provides modified nucleomonomers of specified formula and
CC their pharmaceutically acceptable salts. The nucleomonomers are used as
CC monomers in oligomers, which are used in pharmaceutical compositions to
CC inhibit expression of nucleic acid molecules including DNA and RNA in
CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC infected cells. They are used in oligomers for gene regulation, antisense
CC technology, diagnostic applications to detect target sequences in
CC biological samples such as those containing pathogenic bacteria, fungi
CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC interleukins associated with pathological conditions such as inflammatory
CC conditions, cardiovascular disorders, immune reactions, cancer, viral
CC infections and bacterial infections. The oligomers are suitable for use
CC in both in vivo and ex vivo therapeutic applications including treatment
CC of cells such as bone marrow or peripheral blood in conditions such as
CC leukemia or viral infections, genes as target for cancer treatments
CC including oncogenes such as ras, k-ras, bcl-2, c-myb, bcr, c-myc, c-abl
CC or overexpressed sequences such as mdm2, oncostatin M, interleukin 6
CC (Kaposi's sarcoma), HER-2 and translocations such as bcr/abl or RNAs
CC encoded by such genes, as well as viral gene sequences such as polymerase
CC or reverse transcriptase genes of cytomegalovirus, herpes simplex virus-1
CC or -2, HTLV-1, human immunodeficiency virus-1 or -2, hepatitis B virus,
CC human papilloma virus, varicella zoster virus, influenza virus or
CC rhinovirus. They can also be used to modulate inflammatory responses by
CC modulating expression of genes such as IL-1 receptor, IL-1, ICAM-1 or E-
CC selectin in mediating inflammation and modulation of cellular
CC proliferation in conditions such as arterial occlusion (restenosis) after
CC angioplasty by modulating the expression of growth or mitogenic factors
CC such as non-muscle myosin, myc, fos, PCNA, platelet-derived growth factor
CC or fibroblast growth factor or their receptors or cell proliferation
CC factor such as c-myb, other extracellular proliferation factors such as
CC transforming growth factor alpha, IL-6, approx.g-interferon, protein
CC kinase C for treatment of psoriasis or other conditions, and epithelial
CC growth factor, transforming growth factor or MHC alleges in autoimmune
CC disease. Oligomers comprising the nucleomonomers exhibit increased duplex
CC DNA stability when hybridizing to target nucleic acid sequences, are

```
CC   physiologically stable, non-toxic and able to penetrate into cells while
CC   maintaining stringent base pair fidelity for target DNA sequences. The
CC   oligomers demonstrate significant single- or double-stranded target
CC   nucleic acid binding activity to form duplexes, triplexes or other forms
CC   of stable association
XX
SQ   Sequence 23 BP; 18 A; 2 C; 2 G; 1 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 23;
  Best Local Similarity   82.6%;  Pred. No. 2.2e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTAA 2188
              ||  ||||||||||||||| | |
Db         23 TTGGTTTTTTTTTTTTTTTCTCA 1


RESULT 2302
AAX23577/c
ID   AAX23577 standard; DNA; 23 BP.
XX
AC   AAX23577;
XX
DT   18-JUN-1999  (first entry)
XX
DE   Deletion sequence oligonucleotide 30.
XX
KW   Deletion sequence oligonucleotide; sensor array; eukaryotic pathogen;
KW   probe; cellular adhesion modulator; cellular proliferation modulator;
KW   human retrovirus; human immunodeficiency virus; non-human retrovirus;
KW   HIV; primer; ss.
XX
OS   Synthetic.
XX
PN   WO9911820-A1.
XX
PD   11-MAR-1999.
XX
PF   01-SEP-1998;   98WO-US018084.
XX
PR   02-SEP-1997;   97US-00923771.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Chen D,  Srivatsa GS;
XX
DR   WPI; 1999-205198/17.
XX
PT   New compositions comprising sensor arrays made up of unique probe
PT   oligonucleotides - useful for characterizing a sample of target deletion
PT   oligonucleotides.
XX
PS   Example 9; Page 99; 163pp; English.
XX
CC   This invention describes a novel composition comprising a number of
CC   sensor arrays, where each array comprises a unique probe oligonucleotide,
CC   which is the reverse complement of part of a unique target
CC   oligonucleotide present in a mixture of target deletion sequence
CC   oligonucleotides. The compositions form a method for characterizing a
CC   sample of target deletion oligonucleotides which are labelled and
CC   hybridize with the probe oligonucleotides of the sensor arrays. Such
CC   oligonucleotides and their targets are represented in AAX23548-X23709.
CC   Oligonucleotides characterized by the method form pharmaceutical
CC   compositions that are useful for modulating cellular adhesion or
CC   proliferation, and being active against a eukaryotic pathogen, a human
CC   retrovirus, a human immunodeficiency virus (HIV), or a non-human
CC   retrovirus, including influenza virus, Epstein-Barr virus, Respiratory
CC   Syncytial Virus or cytomegalovirus (CMV). The compositions enable
CC   characterization of deletion sequence oligonucleotides having related,
CC   but different nucleobase sequences, and quantification of different
CC   species of deletion sequence ("target") oligonucleotides in a mixture.
CC   Also, if the specificity of the oligonucleotide's nucleobase sequence for
CC   its reverse complement is not modified, the method may be performed using
CC   oligodeoxynucleotides
XX
SQ   Sequence 23 BP; 4 A; 1 C; 3 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 23;
  Best Local Similarity   82.6%;  Pred. No. 2.2e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAAAAAAA 2800
              | |  || ||||||||||||||||
Db         23 TTGCCTTCAAAAAAAAAAAAAAA 1


RESULT 2303
ABN85224
ID   ABN85224 standard; DNA; 24 BP.
XX
AC   ABN85224;
XX
DT   24-SEP-2002  (first entry)
XX
DE   Human translation initiation factor eIF4E binding protein 17.27 primer#2.
XX
KW   Human; translation initiation factor subunit eIF4E binding protein 17.27;
KW   embryo development malformation; tumour; diabetes; menoxenia;
KW   peptic ulcer; translation initiation factor; eIF4E; binding protein; PCR;
KW   primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1339492-A.
XX
PD   13-MAR-2002.
XX
PF   23-AUG-2000; 2000CN-00119722.
XX
PR   23-AUG-2000; 2000CN-00119722.
XX
PA   (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-464075/50.
XX
PT   New polypeptide-human translation initiation factor subunit eIF4E binding
PT   protein 17.27 for treating embryo development malformation, tumors,
PT   diabetes, menoxenia, and peptic ulcer.
XX
PS   Example 3; Page 20 (Disclosure); 33pp; Chinese.
XX
CC   The present invention relates to human translation initiation factor
CC   subunit eIF4E binding protein 17.27 (see ABB83427). The protein and its
CC   coding sequence are useful for treating various diseases, such as embryo
CC   development malformation, tumours, diabetes, menoxenia, peptic ulcer,
CC   etc. The present sequence is a PCR primer, which was used in an example
CC   from the invention
XX
SQ   Sequence 24 BP; 3 A; 0 C; 3 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 24;
  Best Local Similarity   82.6%;  Pred. No. 2.4e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTAACTTT 2192
              | |||||||||||||| ||  ||
Db          2 TGTTTTTTTTTTTTTGAATGTT 24


RESULT 2304
AAT03687
ID   AAT03687 standard; DNA; 24 BP.
XX
AC   AAT03687;
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```
XX
DT   17-JUL-1996  (first entry)
XX
DE   Homopyrimidine probe for use in triplex-affinity capture method.
XX
KW   Probe; purification method; triplex-affinity capture; triple helix;
KW   specific binding pair; biotin; avidin; antigen; antibody; immobilisation;
KW   heterogenous mix; S.cerevisiae; ss.
XX
OS   Synthetic.
XX
PN   US5482836-A.
XX
PD   09-JAN-1996.
XX
PF   14-JAN-1993;   93US-00004552.
XX
PR   14-JAN-1993;   93US-00004552.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Smith CL,  Cantor CR,  Ito T;
XX
DR   WPI; 1996-076888/08.
XX
PT   Isolating particular double stranded DNA - by formation of a triple helix
PT   and sepn. using a specific molecular recognition system and a solid
PT   carrier.
XX
PS   Claim 8; Col 21; 20pp; English.
XX
CC   The oligonucleotides AAT03687-9 are examples of probes used in a novel
CC   DNA purification method designated triplex-affinity capture. The method
CC   comprises binding an oligonucleotide probe to a double-stranded target
CC   nucleic acid under conditions where a triple helix is formed. The probe
CC   is attached directly or indirectly to the one half of a specific binding
CC   pair e.g. biotin/avidin, antigen/antibody. The other half of the binding
CC   pair is attached to an immobilising agent e.g. a bead. After formation of
CC   the target-probe-binding pair-solid support complex, the target mol. can
CC   be recovered by separating the complex from the medium and separating the
CC   probe from the target nucleic acid. The method can be used to isolate
CC   very large specific intact double strand DNA from a heterogenous mix.
CC   This primer was used in conjunction with a S.cerevisiae strain contg. a
CC   triple helix sequence integrated into the LEU2 locus. Genomic DNA from
CC   the strain was cloned into the plasmid pTZ19RG, a derivative of pTZ19R
CC   contg. rare restriction endonuclease sites
XX
SQ   Sequence 24 BP; 0 A; 6 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 24;
  Best Local Similarity   82.6%;  Pred. No. 2.4e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTT 2177
              || |||||| |||| ||||| ||
Db          2 TTCTTTTCTTCTTTCTTTTTCTT 24


RESULT 2305
AAX09351
ID   AAX09351 standard; DNA; 24 BP.
XX
AC   AAX09351;
XX
DT   24-MAR-1999  (first entry)
XX
DE   Human biallelic polymorphic marker upstream primer #231.
XX
KW   Polymorphism; biallelic; human; forensic; paternity testing; disease;
KW   detection; phenotypic typing; characteristic; infection; hereditary;
KW   autoimmune disease; cancer; inflammation; drug; therapy; medicament;
KW   treatment; marker; primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9820165-A2.
XX
PD   14-MAY-1998.
XX
PF   05-NOV-1997;   97WO-US020313.
XX
PR   06-NOV-1996;   96US-0030455P.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
PI   Lander ES,  Wang D,  Hudson T;
XX
DR   WPI; 1998-286974/25.
XX
PT   New isolated nucleic acid segments from the human genome - used for
PT   determining polymorphic forms for use in e.g. forensics, paternity
PT   testing or phenotypic typing for disease.
XX
PS   Claim 15; Page 76; 310pp; English.
XX
CC   AAX09121-X10268 are allele-specific oligonucleotide primers used in the
CC   isolation of various biallelic polymorphic markers found in the human
CC   genome (represented in AAX10269-X12937). These primers can be used in a
CC   method for determining polymorphic forms in an individual for use in e.g.
CC   forensics, paternity testing or for phenotypic typing for diseases such
CC   as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC   dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial
CC   hypercholesterolemia, polycystic kidney disease, hereditary
CC   spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary
CC   haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos
CC   syndrome, osteogenesis imperfecta, acute intermittent porphyria,
CC   autoimmune diseases, inflammation, cancer, diseases of the nervous
CC   system, infection by pathogenic microorganisms, and characteristics such
CC   as longevity, appearance (e.g. baldness, obesity), strength, speed,
CC   endurance, fertility, and susceptibility or receptivity to particular
CC   drugs or therapeutic treatments. The isolated polymorphic nucleic acid
CC   segments can also be used to produce medicaments for the treatment or
CC   prophylaxis of such diseases
XX
SQ   Sequence 24 BP; 1 A; 5 C; 2 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 24;
  Best Local Similarity   82.6%;  Pred. No. 2.4e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTTTTTTTT 2178
              ||| |||||| || |||| ||||
Db          1 TTTATTCTCCCTTGTTTTCTTTT 23


RESULT 2306
AAF84874
ID   AAF84874 standard; cDNA; 24 BP.
XX
AC   AAF84874;
XX
DT   09-JUL-2001  (first entry)
XX
DE   Sequence of the acceptor site of intron/exon border of exon 5.
XX
KW   Human; SPG4 gene; spastin; PSF-AD; gene therapy; probe;
KW   autosomal dominant familial spastic paraplegia; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   FR2798138-A1.
XX
PD   09-MAR-2001.
XX
PF   03-SEP-1999;   99FR-00011097.
```

XX
PR 03-SEP-1999; 99FR-00011097.
XX
PA (CNRS) CNRS CENT NAT RECH SCI.
XX
PI Weissenbach J, Hazan J;
XX
DR WPI; 2001-283966/30.
XX
PT New human nucleic acid from the SPG4 gene, useful e.g. for diagnosis of
PT autosomal dominant familial spastic paraplegia and in drug screening.
XX
PS Claim 6; Page 30; 145pp; French.
XX
CC AAF84871-AAF84902 represent the acceptor and donor sites of the
CC intron/exon and exon/intron borders of the human SPG4 gene. The SPG4 gene
CC encodes a spastin polypeptide. The sequences may be used as PCR primers
CC and probes. Mutations in the SPG4 gene are responsible for autosomal
CC dominant familial spastic paraplegia. SPG4 polynucleotides, and their
CC fragments, are used to screen DNA banks for sequences that encode spastin
CC (particularly sequences in other mammals, specifically mice); to identify
CC SPG4 mutations, or other genetic anomalies, particularly for diagnosis of
CC autosomal dominant familial spastic paraplegia (PSF-AD); to identify
CC promoters and other regulatory elements of the SPG4 gene; for detection
CC and amplification; for recombinant production of spastin; and for
CC diagnostic genotyping of PSF-AD
XX
SQ Sequence 24 BP; 6 A; 4 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.6; DB 1; Length 24;
Best Local Similarity 82.6%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1789 ATTCTTTCCTTCTCTGAAAGTGG 1811
|| | ||||||| || ||||||||
Db 1 ACTTTTTCCTTGTCAGAAAGTGG 23

RESULT 2307
ABA95669/c
ID ABA95669 standard; DNA; 24 BP.
XX
AC ABA95669;
XX
DT 25-MAR-2002 (first entry)
XX
DE Human zinc finger protein 13 PCR primer #1.
XX
KW Human; zinc finger protein 13; cytostatic; haemostatic; virucide;
KW immunomodulatory; antiinflammatory; gene therapy; tumour; haemopathy;
KW HIV infection; immunological disease; inflammation; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200192325-A1.
XX
PD 06-DEC-2001.
XX
PF 21-MAY-2001; 2001WO-CN000832.
XX
PR 24-MAY-2000; 2000CN-00115827.
XX
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-090035/12.
XX
PT Human zinc-finger protein 13 and encoding polynucleotide, used in
PT diagnosis and treatment of malignant tumors, hemopathy, human
PT immunodeficiency virus infection, immunological diseases and
PT inflammation.
XX
PS Example 2; Page 16; 34pp; Chinese.
XX
CC The present invention relates to human zinc finger protein 13 (see
CC AAM48275). The zinc finger protein and its coding sequence are useful in
CC the diagnosis and treatment of malignant tumours, haemopathy, HIV
CC infection, immunological diseases and various inflammations. The present
CC sequence is a PCR primer, which was used in an example from the present
CC invention
XX
SQ Sequence 24 BP; 6 A; 5 C; 12 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.6; DB 1; Length 24;
Best Local Similarity 82.6%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 246 CGCGGGTCCCCCACCTCTCCTCC 268
|||||| | || ||||||||||
Db 23 CGCGGGGTCACCTCCTCTCCTCC 1

RESULT 2308
AAL42406
ID AAL42406 standard; DNA; 24 BP.
XX
AC AAL42406;
XX
DT 28-JUN-2002 (first entry)
XX
DE Human ORC413-64 PCR primer 2.
XX
KW Human; ss; replication initiation recognition complex subunit; ORC413.64;
KW cancer; HIV; PCR; primer.
XX
OS Homo sapiens.
XX
PN CN1327995-A.
XX
PD 26-DEC-2001.
XX
PF 12-JUN-2000; 2000CN-00116447.
XX
PR 12-JUN-2000; 2000CN-00116447.
XX
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-270050/32.
XX
PT New polypeptide-replication initiation recognition complex subunit
PT ORC413.64 for treating diseases such as cancer, and human
PT immunodeficiency virus infection.
XX
PS Example 2; Page 18 (Disclosure); 34pp; Chinese.
XX
CC The invention comprises the amino acid and nucleotide sequences of the
CC human replication initiation recognition complex subunit ORC413.64. The
CC ORC413.64 nucleotide and protein sequences of the invention are useful
CC for treating diseases such as cancer and HIV. The present DNA sequence
CC represents a PCR primer specific for the gene sequence of the human
CC replication initiation recognition complex subunit ORC413.64
XX
SQ Sequence 24 BP; 1 A; 4 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.6; DB 1; Length 24;
Best Local Similarity 82.6%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2158 TTTTCTCCTTTTTTTTTTTTTTT 2180
||| ||||||||| |||||||
Db 1 TTTCTTCCTTTTTTGATTTTTTT 23

```
RESULT 2309
ABV76657
ID   ABV76657 standard; DNA; 24 BP.
XX
AC   ABV76657;
XX
DT   21-FEB-2003  (first entry)
XX
DE   Human EGF receptor protein 10.12 RT-PCR primer, SEQ ID NO:3.
XX
KW   Human; epidermal growth factor receptor protein 10.12;
KW   EGF receptor protein 10.12; recombinant production; gene therapy;
KW   malignant tumour; cancer; blood disease; human immunodeficiency virus;
KW   HIV infection; immune disorder; inflammatory condition; cytostatic;
KW   antiinflammatory; immunomodulator; reverse transcription-PCR; RT-PCR;
KW   primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1358749-A.
XX
PD   17-JUL-2002.
XX
PF   13-DEC-2000; 2000CN-00127861.
XX
PR   13-DEC-2000; 2000CN-00127861.
XX
PA   (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-733538/80.
XX
PT   Novel polypeptide-human epidermal growth factor 10.12 the polynucleotide
PT   for encoding the polypeptide.
XX
PS   Example 2; Page 16 (Disclosure); 32pp; Chinese.
XX
CC   The invention relates to human epidermal growth factor (EGF) receptor
CC   protein 10.12 (ABB99979) and nucleic acids encoding it (ABV76656). The
CC   protein has a molecular weight of 10.12 kD. The invention also relates to
CC   a method for the recombinant production of the protein, an antagonist of
CC   the protein, and the use of the protein, gene and antagonist in
CC   therapeutic applications. EGF receptor protein 10.12 can be used in the
CC   treatment of a variety of diseases such as malignant tumours, blood
CC   diseases, HIV (human immunodeficiency virus) infection, immune disorders
CC   and inflammatory conditions. Sequences ABV76657-ABV76658 represent
CC   reverse transcription-PCR (RT-PCR) primers used in an exemplification of
CC   the invention to isolate human EGF receptor protein 10.12 cDNA
XX
SQ   Sequence 24 BP; 4 A; 4 C; 12 G; 4 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 24;
  Best Local Similarity   82.6%;  Pred. No. 2.4e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        111 GGGGCTGGGGGGATCCTGGATTT 133
              ||||| || |||| |||||| ||
Db          1 GGGGCAGGAGGGAGCCTGGACTT 23


RESULT 2310
AAS18179/c
ID   AAS18179 standard; DNA; 24 BP.
XX
AC   AAS18179;
XX
DT   09-APR-2002  (first entry)
XX
DE   Human proliferating cell nuclear antigen (PCNA) 13 RT-PCR primer #2.
XX
KW   Human; proliferating cell nuclear antigen 13; PCNA 13; malignant tumour;
KW   cancer; haemopathy; HIV infection; human immunodeficiency virus; ss;
KW   inflammation; transfusion reaction; graft immune rejection; gene chip;
KW   development disease; microarray; nucleic acid hybridisation; haemostatic;
KW   cytostatic; virucide; immunomodulatory; antiinflammatory; RT-PCR; primer;
KW   hereditary disease.
XX
OS   Homo sapiens.
XX
PN   WO200190169-A1.
XX
PD   29-NOV-2001.
XX
PF   14-MAY-2001; 2001WO-CN000787.
XX
PR   19-MAY-2000; 2000CN-00115755.
XX
PA   (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-106182/14.
XX
PT   Human proliferating cell nuclear antigen 13 and encoded polynucleotide,
PT   used in diagnosis and treatment of malignant tumors, hemopathy, human
PT   immunodeficiency virus infection, immunological diseases and
PT   inflammation.
XX
PS   Example 3; Page 12; 35pp; Chinese.
XX
CC   The invention relates to an isolated polypeptide of human proliferating
CC   cell nuclear antigen (PCNA) 13. This polypeptide and its related
CC   polynucleotide are applicable in diagnosis and treatment of tumours,
CC   transfusion reaction, haemopathy, graft immune rejection, development
CC   disease, hereditary disease, HIV infection and inflammation. Regulators
CC   of the polypeptide activity or expression that can mimic, promote,
CC   antagonise or inhibit human PCNA 13 can be used for this purpose, and
CC   also an antibody that binds specifically to the polypeptide. A method for
CC   detecting diseases or disease susceptibility relating to the polypeptide
CC   involves measuring the expression dose of the polypeptide, determining
CC   the polypeptide activity, or detecting the polypeptide expression dose
CC   caused by the polynucleotide that has abnormal activity due to a
CC   polynucleotide mutation. The polynucleotide can be used to supply primers
CC   for nucleic acid amplification and probes for hybridisation reactions, or
CC   in producing gene chips or microarrays. This sequence represents a
CC   reverse-transcription PCR (RT-PCR) primer used for isolation of cDNA
CC   encoding human PCNA 13
XX
SQ   Sequence 24 BP; 4 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 24;
  Best Local Similarity   82.6%;  Pred. No. 2.4e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAAAAA 2804
              || |||||| |||| |||| |||
Db         24 ATGGAAAAATAAAATAAAATAAA 2


RESULT 2311
ABN86867
ID   ABN86867 standard; DNA; 24 BP.
XX
AC   ABN86867;
XX
DT   23-JUL-2002  (first entry)
XX
DE   Human macroprotein 11.88 PCR primer 2 SEQ ID NO:4.
XX
KW   Human; macroprotein 11.88; embryo development disorder; tumour;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1331201-A.
```

XX
PD 16-JAN-2002.
XX
PF 30-JUN-2000; 2000CN-00116908.
XX
PR 30-JUN-2000; 2000CN-00116908.
XX
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-292867/34.
XX
PT Polypeptide-human macroprotein 11.88 and polynucleotide for coding it.
XX
PS Example 2; Page 19 (Disclosure); 34pp; Chinese.
XX
CC The present invention describes human macroprotein 11.88 (I). Also
CC described is a process for preparing (I) using DNA recombination
CC techniques. (I) and the polynucleotide encoding it can be used in the
CC treatment of diseases such as embryo development disorders and tumours.
CC The present sequence represents a PCR primer for human macroprotein
CC 11.88, which is used in an example from the present invention
XX
SQ Sequence 24 BP; 4 A; 0 C; 3 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.6; DB 1; Length 24;
Best Local Similarity 82.6%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTTAA 2188
|||||||||||| ||| ||||
Db 1 TTTTTTTTTTTGGGTTTATTAA 23

RESULT 2312
ABL55230/c
ID ABL55230 standard; DNA; 24 BP.
XX
AC ABL55230;
XX
DT 14-JUN-2002 (first entry)
XX
DE Pax protein 11 RT-PCR primer, SEQ ID NO:3.
XX
KW Pax protein 11; human; recombinant production; malignant tumour; cancer;
KW blood disease; HIV infection; human immunodeficiency virus;
KW immune disorder; inflammatory condition; cytostatic; gene therapy;
KW anti-HIV; antiinflammatory; immunomodulator; reverse transcription-PCR;
KW RT-PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN CN1329025-A.
XX
PD 02-JAN-2002.
XX
PF 21-JUN-2000; 2000CN-00116687.
XX
PR 21-JUN-2000; 2000CN-00116687.
XX
PA (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-305398/35.
XX
PT A novel polypeptide-Pax protein 11 and polynucleotide for coding this
PT polypeptide.
XX
PS Example 2; Page 16 (Disclosure); 32pp; Chinese.
XX
CC The invention relates to pax protein 11 (AAM49189) and to nucleic acids
CC encoding it (ABL55229). The protein has a molecular weight of 11 kD. The
CC invention also relates to a method for the recombinant production of the
CC protein, an antagonist of the protein, and the use of the protein, gene
CC and antagonist in therapeutic applications. Pax protein 11 can be used in
CC the treatment of a variety of diseases such as malignant tumours, blood
CC diseases, HIV (human immunodeficiency virus) infection, immune disorders
CC and inflammatory conditions. Sequences ABL55230-ABL55231 represent
CC reverse transcription-PCR (RT-PCR) primers used in an exemplification of
CC the invention to isolate human pax protein 11 cDNA
XX
SQ Sequence 24 BP; 19 A; 4 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.6; DB 1; Length 24;
Best Local Similarity 82.6%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2163 TCCTTTTTTTTTTTTTTTTTTT 2185
| |||||||| ||| ||||| ||
Db 24 TTCTTTTTTTGTTTGTTTTTGTT 2

RESULT 2313
AAL51806
ID AAL51806 standard; DNA; 24 BP.
XX
AC AAL51806;
XX
DT 24-APR-2003 (first entry)
XX
DE Short chain dehydrogenase 9-35 PCR primer #2.
XX
KW PCR; primer; ss; short chain dehydrogenase; 9.35; cancer; HIV.
XX
OS Unidentified.
XX
PN CN1363664-A.
XX
PD 14-AUG-2002.
XX
PF 05-JAN-2001; 2001CN-00105049.
XX
PR 05-JAN-2001; 2001CN-00105049.
XX
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-751778/82.
XX
PT Polypeptide-short-chain dehydrogenase 9.35 and polynucleotide for coding
PT it.
XX
PS Example 2; Page 17 (Disclosure); 32pp; Chinese.
XX
CC The invention comprises the amino acid and coding sequence of a short
CC chain dehydrogenase 9.35. The DNA and protein sequences of the invention
CC are useful for treating cancer and HIV infection. The present DNA
CC sequence represents a PCR primer for the short chain dehydrogenase 9.35
CC gene
XX
SQ Sequence 24 BP; 2 A; 3 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.6; DB 1; Length 24;
Best Local Similarity 82.6%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2174 TTTTTTTTTTTTTAACTTTGAAA 2196
|||||||||||| ||||| |
Db 1 TTTTTTTTTTTTCCTTTTGAGA 23

RESULT 2314
ABQ79142/c

```
ID   ABQ79142 standard; DNA; 24 BP.
XX
AC   ABQ79142;
XX
DT   15-NOV-2002  (first entry)
XX
DE   Primer #2 related to human eukaryotic initial factor -2 protein.
XX
KW   Human; eukaryotic initial factor -2; (eIF-2); tumour; virus infection;
KW   development disorder; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1340547-A.
XX
PD   20-MAR-2002.
XX
PF   31-AUG-2000; 2000CN-00119830.
XX
PR   31-AUG-2000; 2000CN-00119830.
XX
PA   (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-436441/47.
XX
PT   Polypeptide-human eukaryotic initiation factor-2 (eIF-2)-associated
PT   protein 74.14 and polynucleotide encoding it.
XX
PS   Example 2; Page 18 (Disclosure); 36pp; Chinese.
XX
CC   This invention relates to a novel polypeptide-human eukaryotic initial
CC   factor -2 (eIF-2)-associated protein 74.14 and the application of the
CC   polypeptide in treating diseases such as tumours, virus infection
CC   abnormalities and development disorders. The present sequence represents
CC   a primer related to the novel human eukaryotic initial factor -2 (eIF-2)-
CC   associated protein
XX
SQ   Sequence 24 BP; 4 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 24;
  Best Local Similarity   82.6%;  Pred. No. 2.4e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||||| |||||| ||||| ||
Db         24 AATGAAATAAAAAATAAAAATAA 2

RESULT 2315
ABS56172/c
ID   ABS56172 standard; DNA; 24 BP.
XX
AC   ABS56172;
XX
DT   30-JAN-2003  (first entry)
XX
DE   PCR primer #4 for DNA encoding human CIS3.
XX
KW   Human; effectiveness of interferon treatment; hepatitis C patient;
KW   JAK-combined protein; CIS3; hepatocyte sample; hepatotropic;
KW   antiinflammatory; virucide; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2002125683-A.
XX
PD   08-MAY-2002.
XX
PF   27-OCT-2000; 2000JP-00329615.
XX
PR   27-OCT-2000; 2000JP-00329615.
XX
PA   (TOKR-) ZH TOKYOTO RINSHO IGAKU SOGO KENKYUSHO.
PA   (YABA/) YABASHI H.
PA   (CHUS ) CHUGAI PHARM CO LTD.
PA   (SRLS-) SRL KK.
XX
DR   WPI; 2003-049086/05.
XX
PT   Estimation of effectiveness of interferon.
XX
PS   Claim 14; Page 7; 17pp; Japanese.
XX
CC   The present invention relates to a method for estimating the
CC   effectiveness of interferon treatment. The method comprises administering
CC   interferon to a hepatitis C patient in which the expression amount of at
CC   least one of the JAK-combined protein gene or the CIS3 gene in the
CC   hepatocyte sample is measured. The method employs primers and probes
CC   which are disclosed in the specification. The method is useful for
CC   estimating the effectiveness of interferon treatment in a hepatitis C
CC   patient. The present sequence represents a PCR primer used in the method
CC   of the present invention
XX
SQ   Sequence 24 BP; 4 A; 6 C; 8 G; 6 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 24;
  Best Local Similarity   82.6%;  Pred. No. 2.4e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        656 AACCTGGGGCTCCACGACATGCC 678
              || |||| || |||| |||||||
Db         24 AAGCTGGTGCACCACTACATGCC 2

RESULT 2316
AAC96201
ID   AAC96201 standard; DNA; 25 BP.
XX
AC   AAC96201;
XX
DT   26-FEB-2001  (first entry)
XX
DE   16s rRNA gene PCR primer #168.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 47; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
```

```
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 1 A; 3 C; 3 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTTAACTTTG 2193
                ||||||||||||||| |   |||
Db          1 TTTTTTTTTTTTTTTCAGTCTTG 23


RESULT 2317
AAC96219
ID   AAC96219 standard; DNA; 25 BP.
XX
AC   AAC96219;
XX
DT   26-FEB-2001  (first entry)
XX
DE   16s rRNA gene PCR primer #186.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 47; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 1 A; 5 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1771 TTTTTTTTTTTGAACCCCATTCT 1793
                ||||||||||   ||||||| |
Db          3 TTTTTTTTTTTTCCCCCATTGT 25


RESULT 2318
AAC95968
ID   AAC95968 standard; DNA; 25 BP.
XX
AC   AAC95968;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA HLA-B gene PCR primer #79.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 43; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 2 A; 5 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTAACT 2190
                ||||||||||||| ||||  | ||
Db          1 TTTTTTTTTTTTCTTTTCCACCT 23


RESULT 2319
AAQ55856
ID   AAQ55856 standard; DNA; 25 BP.
XX
AC   AAQ55856;
XX
DT   25-MAR-2003  (revised)
DT   25-JUL-1994  (first entry)
XX
DE   Fragile X probe.
XX
KW   FC; foetal cells; marker; probe; hybridise; denature; dye; label;
KW   fluroescent; kit; detection; haemoglobin; rhesus; gamma globulin; NR;
KW   nitrogen reductase; ss.
XX
OS   Homo sapiens.
XX
PN   WO9402646-A1.
```

```
XX
PD   03-FEB-1994.
XX
PF   19-JUL-1993;   93WO-US006828.
XX
PR   17-JUL-1992;   92US-00915965.
XX
PA   (RERE-) RES DEV FOUND.
XX
PI   Asgari M,  Prashad N,  Cubbage ML,  Ju S,  Blick M,  Bresser J;
XX
DR   WPI; 1994-048903/06.
XX
PT   Identifying foetal cells, conc. from maternal blood, using specific
PT   marker - e.g. surface antigen, before in situ hybridisation of target
PT   nucleic acid to detect viral infection, genetic abnormality, etc.
XX
PS   Disclosure; Page 73; 109pp; English.
XX
CC   Probes (AAQ55857-873) detect regions of 3 fragments of the HUMGLBN gene
CC   (AAQ64058). Bases 1-91 correspond to bases 2179-2269 of HUMGLBN, bases 92
CC   -314 are from 2393-2615 of HUMGLBN and bases 315-443 are from 3502-3630
CC   of HUMGLBN. The probes (AAQ55854-55) were used as control, positive and
CC   negative genetic testing probes. Probe (AAQ55856) was used to detect the
CC   fragile X condition (Example 14) (Updated on 25-MAR-2003 to correct PN
CC   field.)
XX
SQ   Sequence 25 BP; 0 A; 9 C; 16 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGCAGACGC 73
              ||||||| ||||||||| |  ||
Db          3 GCGGCGGCGGCGGCGGCGGCGGC 25


RESULT 2320
AAQ85271
ID   AAQ85271 standard; DNA; 25 BP.
XX
AC   AAQ85271;
XX
DT   25-MAR-2003  (revised)
DT   24-AUG-1995  (first entry)
XX
DE   Probe for Fragile X condition.
XX
KW   Prenatal diagnosis; fragile X; probe; ss.
XX
OS   Synthetic.
XX
PN   WO9503431-A1.
XX
PD   02-FEB-1995.
XX
PF   19-JUL-1994;   94WO-US008342.
XX
PR   19-JUL-1993;   93US-00094710.
XX
PA   (APRO-) APROGENEX INC.
XX
PI   Bresser J,  Weber WD,  Ryusaki T,  Prashad N,  Cubbage ML,  Blick M;
PI   Asgari M,  Poindexter BJ;
XX
DR   WPI; 1995-075255/10.
XX
PT   Identifying foetal cells in samples contg. maternal cells - used for
PT   monitoring foetus status, identifying sex or detecting genetic
PT   abnormalities or viral infection.
XX
PS   Example; Page 75; 115pp; English.
XX
CC   In the example, Fragile X Chromosome is identified in amniocytes and in
CC   peripheral blood mononuclear cells. The 5' aminohexyl oligos is coupled
CC   to the fluorescent dye fluroescein. When an amplification of the CGG DNA
CC   fragment (of the X chromosome in Xq27.3) is present, there is an increase
CC   in the intensity of the signal. (Updated on 25-MAR-2003 to correct PN
CC   field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 25 BP; 0 A; 9 C; 16 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGCAGACGC 73
              ||||||| ||||||||| |  ||
Db          3 GCGGCGGCGGCGGCGGCGGCGGC 25


RESULT 2321
AAV81177/c
ID   AAV81177 standard; DNA; 25 BP.
XX
AC   AAV81177;
XX
DT   09-MAR-1999  (first entry)
XX
DE   Antisense fragment inserted in msDNA.
XX
KW   Retron; msDNA; branched RNA-linked multicopy single-stranded DNA; msr;
KW   msd; reverse transcriptase; genetic element; msDNA hybrid; inhibit;
KW   alter; protein expression; antisense; ss.
XX
OS   Synthetic.
XX
PN   US5849563-A.
XX
PD   15-DEC-1998.
XX
PF   25-JUL-1995;   95US-00507634.
XX
PR   24-FEB-1989;   89US-00315316.
PR   24-FEB-1989;   89US-00315427.
PR   24-FEB-1989;   89US-00315432.
PR   02-MAY-1990;   90US-00517946.
PR   02-MAY-1990;   90US-00518749.
PR   30-AUG-1991;   91US-00753110.
XX
PA   (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX
PI   Miyata S,  Inouye M,  Ohshima A,  Inouye S;
XX
DR   WPI; 1999-069740/06.
XX
PT   Vectors for expression of hybrid RNA-DNA molecules - and hybrid RNA-DNA
PT   molecules containing foreign nucleic acid fragment.
XX
PS   Example 4; Col 21; 39pp; English.
XX
CC   The invention relates to an expression vector containing a retron for
CC   msDNA (branched RNA-linked multicopy single-stranded DNA structure)
CC   synthesis. The retron is a genetic element that contains msr and msd
CC   coding regions of the msDNA and a gene encoding a reverse transcriptase,
CC   where msd is a gene coding for the DNA portion of a msDNA molecule and
CC   msr is a gene coding the RNA portion of a msDNA molecule. The msDNA
CC   hybrid molecule comprises a branched single-stranded RNA portion that
CC   is:(a) covalently linked to a single-stranded DNA portion by a 2',5-
CC   phosphodiester bond between the 2'-OH group of an internal rG residue and
CC   the 5'-phosphate of the DNA portion and (b) noncovalently linked to the
CC   DNA portion by base pairing between complementary 3' ends of the RNA and
CC   DNA portions, where the msDNA contains a stable stem-loop structure in
CC   the RNA and/or DNA portion and contains a foreign nucleic acid fragment.
CC   msDNA molecules containing antisense DNA can be used to inhibit or alter
```

```
CC   the expression of undesirable proteins. The present sequence represents
CC   an antisense fragment inserted into a msDNA
XX
SQ   Sequence 25 BP; 7 A; 5 C; 1 G; 12 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2531 ATATACAGGGTATTAAGAATTAA 2553
                || || |||||||||| ||| ||
Db         24 ATCTAGAGGGTATTAATAATGAA 2


RESULT 2322
AAX07505
ID   AAX07505 standard; DNA; 25 BP.
XX
AC   AAX07505;
XX
DT   08-JUN-1999  (first entry)
XX
DE   Synthetic IDDMK1.2-22 PCR primer.
XX
KW   IDDM; insulin-dependent diabetes mellitus; endogenous retrovirus; SAg;
KW   superantigen; provirus; autoimmune disease; type 1 diabetes; diagnosis;
KW   PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   EP893691-A1.
XX
PD   27-JAN-1999.
XX
PF   23-JUL-1997;   97EP-00401773.
XX
PR   23-JUL-1997;   97EP-00401773.
XX
PA   (MACH/) MACH B F.
XX
PI   Conrad B,  Mach B;
XX
DR   WPI; 1999-097928/09.
XX
PT   Diagnosing human autoimmune disease by detecting retrovirus with
PT   superantigen activity - new retrovirus associated with type 1 diabetes,
PT   its proviral DNA, and related vectors, transformed cells, proteins,
PT   antibodies and specific binding agents, used for treating or preventing
PT   autoimmune disease.
XX
PS   Example; Page 34; 92pp; English.
XX
CC   The sequence is that of an insulin-dependent diabetes mellitus associated
CC   human endogenous retrovirus (IDDMK1.2-22) PCR primer. The retrovirus has
CC   Superantigen (SAg) activity. It can be used as part of a method is
CC   specifically used to diagnose type 1 diabetes mellitus. Modified proteins
CC   expressed by the retroviral sequence (without SAg activity but still able
CC   to induce an immune response) are useful in vaccines to treat or prevent
CC   SAg-related autoimmune disease; nucleic acid sequences encoding
CC   (modified) SAg can be used similarly to treat such diseases. Retroviral-
CC   encoded SAg are important in pathogenesis of autoimmune disease, probably
CC   by activating autoreactive T cells. The method is very specific (it can
CC   differentiate between expressed and non-expressed viral nucleic acids)
CC   and can be used even where the pathogen is an ubiquitous endogenous
CC   retrovirus. Blood or plasma samples can be tested without extensive
CC   preparation and diagnosis can be made before clinical signs are apparent,
CC   allowing early intervention before severe tissue damage has occurred
XX
SQ   Sequence 25 BP; 4 A; 4 C; 3 G; 14 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1951 TTTTTGTGTCCGCTAAATATTTA 1973
              |||||| |||| || | |||||||
Db          1 TTTTTGAGTCCCCTTAGTATTTA 23


RESULT 2323
AAX07482
ID   AAX07482 standard; DNA; 25 BP.
XX
AC   AAX07482;
XX
DT   08-JUN-1999  (first entry)
XX
DE   Synthetic IDDMK1.2-22 poly(A) specific primer.
XX
KW   IDDM; insulin-dependent diabetes mellitus; endogenous retrovirus; SAg;
KW   superantigen; provirus; autoimmune disease; type 1 diabetes; diagnosis;
KW   primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   EP893691-A1.
XX
PD   27-JAN-1999.
XX
PF   23-JUL-1997;   97EP-00401773.
XX
PR   23-JUL-1997;   97EP-00401773.
XX
PA   (MACH/) MACH B F.
XX
PI   Conrad B,  Mach B;
XX
DR   WPI; 1999-097928/09.
XX
PT   Diagnosing human autoimmune disease by detecting retrovirus with
PT   superantigen activity - new retrovirus associated with type 1 diabetes,
PT   its proviral DNA, and related vectors, transformed cells, proteins,
PT   antibodies and specific binding agents, used for treating or preventing
PT   autoimmune disease.
XX
PS   Claim 9; Page 52; 92pp; English.
XX
CC   The sequence is that of an insulin-dependent diabetes mellitus associated
CC   human endogenous retrovirus (IDDMK1.2-22) poly(A) specific primer. The
CC   retrovirus has Superantigen (SAg) activity. It can be used as part of a
CC   method is specifically used to diagnose type 1 diabetes mellitus.
CC   Modified proteins expressed by the retroviral sequence (without SAg
CC   activity but still able to induce an immune response) are useful in
CC   vaccines to treat or prevent SAg-related autoimmune disease; nucleic acid
CC   sequences encoding (modified) SAg can be used similarly to treat such
CC   diseases. Retroviral-encoded SAg are important in pathogenesis of
CC   autoimmune disease, probably by activating autoreactive T cells. The
CC   method is very specific (it can differentiate between expressed and non-
CC   expressed viral nucleic acids) and can be used even where the pathogen is
CC   an ubiquitous endogenous retrovirus. Blood or plasma samples can be
CC   tested without extensive preparation and diagnosis can be made before
CC   clinical signs are apparent, allowing early intervention before severe
CC   tissue damage has occurred
XX
SQ   Sequence 25 BP; 4 A; 4 C; 3 G; 14 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1951 TTTTTGTGTCCGCTAAATATTTA 1973
              |||||| |||| || | |||||||
Db          1 TTTTTGAGTCCCCTTAGTATTTA 23
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RESULT 2324
AAX05267
ID   AAX05267 standard; DNA; 25 BP.
XX
AC   AAX05267;
XX
DT   14-APR-1999  (first entry)
XX
DE   Fragile X chromosome detecting probe.
XX
KW   Genetic testing; foetal cell; maternal; blood; pregnant; hybridisation;
KW   detection; HIV, hepatitis virus; herpes virus; chromosomal abnormality;
KW   probe; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US5858649-A.
XX
PD   12-JAN-1999.
XX
PF   31-DEC-1996;   96US-00775609.
XX
PR   17-JUL-1992;   92US-00915765.
PR   19-JUL-1993;   93US-00094710.
PR   19-JUL-1994;   94WO-US008342.
PR   17-JAN-1995;   95US-00374144.
XX
PA   (APRO-) APROGENEX INC.
XX
PI   Blick M,  Cubbage ML,  Bresser J,  Prashad N,  Asgari M;
XX
DR   WPI; 1999-152096/13.
XX
PT   Method for distinguishing foetal cells from adult cells in blood - based
PT   on amplification and detection of mRNA selectively expressed in foetal
PT   cells.
XX
PS   Example 4, 14; Col 49; 49pp; English.
XX
CC   The invention relates to a method of enriching foetal cells from maternal
CC   blood and for identifying such foetal cells. Foetal cells can be
CC   distinguished from adult cells in a blood specimen by (a) treating a
CC   blood specimen from a pregnant female to yield a mixture of cells
CC   comprising foetal cells and adult cells; (b) amplifying one or more mRNAs
CC   within the cells, the mRNAs being selectively expressed in target foetal
CC   cells to be distinguished but not expressed in adult blood cells; (c)
CC   performing in situ hybridisation on the cells under hybridising
CC   conditions suitable to maintain cell membranes in a substantially intact
CC   state and with a hybridisation medium comprising a detectably labelled
CC   probe complementary to the amplified mRNA that is selectively expressed
CC   in the target foetal cells but not expressed in adult blood cells; (d)
CC   removing the hybridisation medium and unhybridised probe from the mixture
CC   of cells to yield hybridised cells, and (e) detecting the labelled probe
CC   remaining in the hybridised cells; whereby cells in which the labelled
CC   probe is detected are identified as the target foetal cells; A second
CC   method for determining the presence of a target nucleotide sequence in
CC   individual foetal cells present in a cellular specimen is also provided.
CC   The methods (especially the second) is useful for detecting HIV,
CC   hepatitis viruses or herpes viruses in foetal cells, or for detecting
CC   chromosomal abnormalities in foetal cells. The present sequence
CC   represents a probe used for the detection of the Fragile X chromosome in
CC   amniocytes and in peripheral blood mononuclear cells
XX
SQ   Sequence 25 BP; 0 A; 9 C; 16 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGCAGACGC 73
              ||||||| |||||||||  |  ||
Db          3 GCGGCGGCGGCGGCGGCGGCGGC 25


RESULT 2325
AAX07199
ID   AAX07199 standard; DNA; 25 BP.
XX
AC   AAX07199;
XX
DT   21-MAY-1999  (first entry)
XX
DE   IDDM-associated retrovirus polyA specific probe.
XX
KW   HERV; IDDKK1.2-22; superantigen; SAg; antigen; IDDM;
KW   insulin-dependent diabetes mellitus; autoimmune disease; diagnosis;
KW   therapy; vaccine; probe; PCR; primer; ss.
XX
OS   Synthetic.
OS   Human endogenous retrovirus.
XX
PN   WO9905527-A2.
XX
PD   04-FEB-1999.
XX
PF   22-JUL-1998;   98WO-EP004926.
XX
PR   22-JUL-1997;   97EP-00112482.
PR   23-JUL-1997;   97EP-00401773.
XX
PA   (MEDI-) MEDIGEN SA.
XX
PI   Conrad B,  Mach B;
XX
DR   WPI; 1999-143118/12.
XX
PT   New isolated human endogenous retrovirus - used to develop products for
PT   the diagnosis, prevention and treatment of autoimmune disease,
PT   particularly insulin dependent diabetes mellitus.
XX
PS   Claim 8; Page 90; 165pp; English.
XX
CC   This oligonucleotide is specific to the polyA signal present in the 3' R-
CC   poly(A) sequences at the 3' extremity of IDDMK1.2-22, a newly identified
CC   human endogenous retrovirus (HERV) that is the source of superantigen
CC   (SAg) activity in insulin-dependent diabetes mellitus (IDDM) patients. It
CC   can be used as a probe or primer (claimed) in a method for the diagnosis
CC   of a human autoimmune disease. IDDMK1.2-22 is ubiquitous in the human
CC   genome but is only expressed in diabetic individuals. The invention
CC   provides IDDMK1.2-22 nucleic acids (see AAX07186-91) and encoded
CC   polypeptides (see AAW97745-48). These can be used in methods for the
CC   diagnosis, treatment and prevention of IDDM
XX
SQ   Sequence 25 BP; 4 A; 4 C; 3 G; 14 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1951 TTTTTGTGTCCGCTAAATATTTA 1973
              |||||| |||| || | |||||||
Db          1 TTTTTGAGTCCCCTTAGTATTTA 23


RESULT 2326
AAX07220
ID   AAX07220 standard; DNA; 25 BP.
XX
AC   AAX07220;
XX
DT   27-AUG-2003  (revised)
DT   21-MAY-1999  (first entry)
XX
DE   Retroviral R-poly(A) primer.
```

```
XX
KW   Human endogenous retrovirus; HERV; IDDKK1.2-22; superantigen; SAg;
KW   antigen; IDDM; insulin-dependent diabetes mellitus; autoimmune disease;
KW   diagnosis; therapy; vaccine; PCR; primer; ss.
XX
OS   Synthetic.
OS   Retroviridae.
XX
PN   WO9905527-A2.
XX
PD   04-FEB-1999.
XX
PF   22-JUL-1998;   98WO-EP004926.
XX
PR   22-JUL-1997;   97EP-00112482.
PR   23-JUL-1997;   97EP-00401773.
XX
PA   (MEDI-) MEDIGEN SA.
XX
PI   Conrad B,  Mach B;
XX
DR   WPI; 1999-143118/12.
XX
PT   New isolated human endogenous retrovirus - used to develop products for
PT   the diagnosis, prevention and treatment of autoimmune disease,
PT   particularly insulin dependent diabetes mellitus.
XX
PS   Disclosure; Page 75; 165pp; English.
XX
CC   This is the nucleotide sequence of primer R-poly(A), which was used with
CC   a U3 primer (see AAX07221) in epidemiological studies of IDDMK1.2-22, a
CC   newly identified human endogenous retrovirus that is the source of
CC   superantigen activity in insulin-dependent diabetes mellitus (IDDM)
CC   patients. IDDMK1.2-22 is found in the plasma of IDDM patients at disease
CC   onset but not in the plasma of healthy controls. The invention provides
CC   nucleic acids (see AAX07186-91) and encoded polypeptides (see AAW97745-
CC   48) of IDDMK1.2-22. These can be used in methods for the diagnosis,
CC   treatment and prevention of IDDM. (Updated on 27-AUG-2003 to correct OS
CC   field.)
XX
SQ   Sequence 25 BP; 4 A; 4 C; 3 G; 14 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1951 TTTTTGTGTCCGCTAAATATTTA 1973
             |||||| |||| || | ||||||
Db          1 TTTTTGAGTCCCCTTAGTATTTA 23


RESULT 2327
AAZ49618
ID   AAZ49618 standard; DNA; 25 BP.
XX
AC   AAZ49618;
XX
DT   07-APR-2000  (first entry)
XX
DE   PCR primer-2 for synthesis of carrot CR16.1 fragment for plant promoter.
XX
KW   PCR primer; synthetic DNA; plant promoter; CR16 fragment; carrot;
KW   transgenic plant; soybean glycinin; stearoyl-ACP-desaturase gene;
KW   male sterility-related gene; ss.
XX
OS   Daucus carota.
XX
PN   EP976832-A2.
XX
PD   02-FEB-2000.
XX
PF   13-JUL-1999;   99EP-00113732.
XX
PR   15-JUL-1998;   98JP-00200372.
XX
PA   (SUMO ) SUMITOMO CHEM CO LTD.
XX
PI   Ishige F,  Nishikawa S,  Oeda K;
XX
DR   WPI; 2000-128374/12.
XX
PT   Novel promoter used to produce transgenic plants with higher expression
PT   of a desired gene.
XX
PS   Example 1; Page 14; 24pp; English.
XX
CC   The present sequence is a PCR primer used to synthesise carrot CR16.1
CC   fragment. This fragment along with a 10 bp synthetic DNA is used in the
CC   construction of a plant promoter. The promoter is used for controlling
CC   the expression of a desired gene e.g. soybean glycinin, stearoyl-ACP-
CC   desaturase and S-locus type specific RNase gene (male sterility-related
CC   gene) in a host cell especially a microorganism or a plant cell. The
CC   transformed plant cells can be used to produce transgenic plants. The
CC   promoter is compact and therefore suitable for higher expression of a
CC   desired gene in a particular tissue compared to other host tissues
XX
SQ   Sequence 25 BP; 8 A; 9 C; 1 G; 7 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1896 CCCTAGATCAACAGATCAACAAT 1918
              | |||||||||||  |||||| |
Db          2 CTCTAGATCAACACCTCAACATT 24


RESULT 2328
AAC96779/c
ID   AAC96779 standard; DNA; 25 BP.
XX
AC   AAC96779;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA HLA-A gene PCR primer #156.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 57; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
```

```
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 0 A; 6 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAA 2801
              |||   | ||||||||||||||||
Db         23 AGACAGGGAAAAAAAAAAAAAAAA 1


RESULT 2329
AAC96092/c
ID   AAC96092 standard; DNA; 25 BP.
XX
AC   AAC96092;
XX
DT   26-FEB-2001  (first entry)
XX
DE   16s rRNA gene PCR primer #59.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 45; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 3 A; 3 C; 4 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAAAAAAAA 2800
              | ||||| | ||||||||||||
Db         23 TGGAATTCCACAAAAAAAAAAAA 1


RESULT 2330
AAC96449
ID   AAC96449 standard; DNA; 25 BP.
XX
AC   AAC96449;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DQB1 gene PCR primer #1.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 51; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 4 A; 2 C; 4 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2175 TTTTTTTTTTTTAACTTTGAAAG 2197
              |||||||||||||| |||  | ||
Db          1 TTTTTTTTTTTTATCTTGCAGAG 23


RESULT 2331
AAC95730
ID   AAC95730 standard; DNA; 25 BP.
XX
AC   AAC95730;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DQB1 gene PCR primer #1.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
```

```
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 39; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 4 A; 2 C; 4 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2175 TTTTTTTTTTTTAACTTTGAAAG 2197
                ||||||||||||| |||  | ||
Db          1 TTTTTTTTTTTTATCTTGCAGAG 23


RESULT 2332
AAC96753
ID   AAC96753 standard; DNA; 25 BP.
XX
AC   AAC96753;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA HLA-A gene PCR primer #130.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 56; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 3 A; 5 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1771 TTTTTTTTTTTGAACCCCATTCT 1793
                ||||||||||||  ||| || ||
Db          2 TTTTTTTTTTGGTCCCAATACT 24


RESULT 2333
AAC96394
ID   AAC96394 standard; DNA; 25 BP.
XX
AC   AAC96394;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DPB1 gene PCR primer #126.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 50; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 4 A; 3 C; 4 G; 14 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;
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```
Qy       1771 TTTTTTTTTTTTGAACCCCATTCT 1793
              |||||||||||||||   ||| ||
Db          2 TTTTTTTTTTTTGAAGGACATCCT 24
```

RESULT 2334
AAC96353/c
ID AAC96353 standard; DNA; 25 BP.
XX
AC AAC96353;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA DPB1 gene PCR primer #85.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 49; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 2 A; 5 C; 2 G; 16 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 2.6e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy       2779 AGAATTGAAAAAAAAAAAAAAAA 2801
              || | || || ||||||||||||
Db         23 AGTACTGGAACAAAAAAAAAAA 1
```

RESULT 2335
AAC96041
ID AAC96041 standard; DNA; 25 BP.
XX
AC AAC96041;
XX
DT 26-FEB-2001 (first entry)
XX
DE 16s rRNA gene PCR primer #8.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 44; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 2 A; 6 C; 1 G; 16 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 2.6e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy       1771 TTTTTTTTTTTGAACCCCATTCT 1793
              ||||||||||   ||||||| |
Db          3 TTTTTTTTTTACCCCCCATTGT 25
```

RESULT 2336
AAC96099
ID AAC96099 standard; DNA; 25 BP.
XX
AC AAC96099;
XX
DT 26-FEB-2001 (first entry)
XX
DE 16s rRNA gene PCR primer #66.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.

```
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 45; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 2 A; 3 C; 3 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTTAACTTTGAAAGT 2198
             ||||||||||  |||||| | |
Db          1 TTTTTTTTTTTTCCTTTGATACT 23


RESULT 2337
AAC96245/c
ID   AAC96245 standard; DNA; 25 BP.
XX
AC   AAC96245;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DPA1 gene PCR primer #2.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 48; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 1 A; 2 C; 3 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAAAAA 2804
              || ||| || | ||||||||||||
Db         24 ATAGAACAACAGAAAAAAAAAAA 2


RESULT 2338
AAC96396/c
ID   AAC96396 standard; DNA; 25 BP.
XX
AC   AAC96396;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DPB1 gene PCR primer #128.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 50; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 3 A; 4 C; 2 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAA 2802
              | | || || ||||||||||||||
Db         23 GTACTGGAACAAAAAAAAAAAAA 1


RESULT 2339
AAC96089/c
ID   AAC96089 standard; DNA; 25 BP.
XX
AC   AAC96089;
XX
DT   26-FEB-2001  (first entry)
```

```
XX
DE   16s rRNA gene PCR primer #56.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 45; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 5 A; 5 C; 2 G; 13 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2777 TTAGAATTGAAAAAAAAAAAAAA 2799
              ||  |  |||  ||||||||||||||
Db         23 TTCGGGTTGTAAAAAAAAAAAAA 1


RESULT 2340
AAC96423
ID   AAC96423 standard; DNA; 25 BP.
XX
AC   AAC96423;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DQA1 gene PCR primer #25.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 51; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 5 A; 4 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTAACTTTGAA 2195
              ||||||||||||||  || | |||
Db          1 TTTTTTTTTTTTTCCACATAGAA 23


RESULT 2341
AAD03602
ID   AAD03602 standard; DNA; 25 BP.
XX
AC   AAD03602;
XX
DT   19-JUN-2001  (first entry)
XX
DE   Human IAP-like protein-2 DNA cloning PCR primer #1.
XX
KW   Human; inhibitor of apoptosis; IAP-like protein-2; ILP-2;
KW   transforming growth factor beta receptor; TGFbetaR; cytostatic;
KW   c-Jun N-terminal kinase; JNK; gene therapy; glutaricaciduria;
KW   cone-rod retinal dystrophy-2; retinitis pigmentosa; colorectal cancer;
KW   T-cell acute lymphoblastic leukaemia; neurodegenerative disease;
KW   retinal degeneration; hyperferritinaemia-cataract syndrome; cancer;
KW   autoimmune disease; diabetes; multiple sclerosis; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200123568-A2.
XX
PD   05-APR-2001.
XX
PF   29-SEP-2000; 2000WO-US026735.
XX
PR   30-SEP-1999;   99US-0157169P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Duckett C,  Mir SS;
XX
DR   WPI; 2001-258135/26.
XX
PT   Inhibitors of apoptosis proteins designated ILP-2 and ILP-3 with
PT   transforming growth factor beta receptor modulating activity, and the
PT   nucleic acids that encode them, useful for treating, e.g. diabetes and
PT   multiple sclerosis.
XX
PS   Example 1; Page 21; 108pp; English.
XX
```

CC The present sequence is a PCR primer used for cloning the human inhibitor
CC of apoptosis (IAP)-like protein-2 (ILP-2) DNA. The ILP-2 interacts with
CC transforming growth factor beta receptor (TGFbetaR) and modulates
CC TGFbetaR activity. It also potently inhibits apoptosis induced by
CC overexpression of Bax or by Caspase-9 and Apaf-1. It also activates c-Jun
CC N-terminal kinase (JNK) activity. ILP-2 is used in the area of genetic
CC testing for predisposition to diseases, such as cone-rod retinal
CC dystrophy-2, retinitis pigmentosa, glutaricaciduria, T-cell acute
CC lymphoblastic leukaemia, colorectal cancer and hyperferritinaemia-
CC cataract syndrome owing to an ILP-2 deletion or mutation. The ILP is also
CC used in the treatment of diseases associated with abnormal apoptosis such
CC as cancer, autoimmune diseases, e.g., diabetes and multiple sclerosis and
CC neurodegenerative diseases including retinal degeneration. The ILP-2 gene
CC is also used in gene therapy for treating patients suffering from ILP-2
CC gene deletions or mutations
XX
SQ Sequence 25 BP; 7 A; 6 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 2.6e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 996 CCTTGCGGGAGAAGTTGGACAAG 1018
||| ||| || ||| ||||||||
Db 1 CCTGGCGCGAAAAGGTGGACAAG 23

RESULT 2342
AAH28308
ID AAH28308 standard; RNA; 25 BP.
XX
AC AAH28308;
XX
DT 05-SEP-2001 (first entry)
XX
DE 3' untranslated region sequence from CTCF gene.
XX
KW mRNA protein complex; tumour development; cell aging; death;
KW ribonomic profile; RNA-binding protein; ss.
XX
OS Unidentified.
XX
PN WO200148480-A1.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US035583.
XX
PR 28-DEC-1999; 99US-0173338P.
XX
PA (KEEN/) KEENE J D.
XX
PI Keene JD, Tenenbaum SA, Carson C;
XX
DR WPI; 2001-425706/45.
XX
PT Partitioning endogenous mRNA-protein complexes in vivo, by contacting
PT sample comprising the complex with ligand that binds to a component of
PT the complex and separating complex by binding ligand with a binding
PT molecule.
XX
PS Example 6; Page 31; 49pp; English.
XX
CC The specification describes a method for partitioning endogenous cellular
CC mRNA-protein (mRNP) complexes. The method comprises contacting a
CC biological sample comprising mRNP complex with ligand that specifically
CC binds a component of mRNP complex, separating mRNP complex by binding the
CC ligand with a molecule specific for ligand, which is attached to the
CC solid support and then collecting the mRNP complex by removing the
CC complex from the support. The method is useful for in vivo partitioning
CC of cellular mRNA protein complexes in a biological sample. The method is
CC useful for determining the ribonomic profile of a cell which has numerous
CC uses including monitoring of tumour development, state of growth or state
CC of development, perturbations of a biological system such as disease,
CC drug or toxin treatment and the state of cell aging or death,
CC distinguishing ribonomic profiles among organisms, to discriminate
CC between transcriptional and post-transcriptional contributions to gene
CC expression and to track the movement of RNAs through RNP complexes,
CC including the interactions of combinations of proteins with RNAs in RNP
CC complexes. AAH28281-AAH28316 represent sequences derived from the 3'
CC untranslated region (UTR) of mRNA of various genes. The sequences contain
CC target sequences for RNA-binding proteins
XX
SQ Sequence 25 BP; 2 A; 4 C; 0 G; 0 T; 19 U; 0 Other;

Query Match 0.6%; Score 16.6; DB 1; Length 25;
Best Local Similarity 13.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 16; Mismatches 4; Indels 0; Gaps 0;

Qy 2152 TGATTTTTTTCTCCTTTTTTTT 2174
: | ::::::|:| ::::::: :
Db 3 UUAAUUUUUUCUCUUUUUUUCU 25

RESULT 2343
AAS20313
ID AAS20313 standard; DNA; 25 BP.
XX
AC AAS20313;
XX
DT 23-APR-2002 (first entry)
XX
DE Human Cgamma gene Cgamma1-hinge intron PCR primer 25657.
XX
KW Human; ss; Cgamma; intron Cgamma-hinge; RCA; SP; LEX; RCB; 25657;
KW antibody; phage display; scFv; T-cell receptor; TCR; PCR primer.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200192291-A2.
XX
PD 06-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-IL000496.
XX
PR 30-MAY-2000; 2000IL-00136459.
XX
PA (GALI-) GALIM-GALIL IMMUNOLOGY LTD.
XX
PI Gross G, Schlesinger Y;
XX
DR WPI; 2002-114322/15.
XX
PT Novel DNA construct for creating immune antibody and T-cell receptor
PT libraries, consists of transcription unit comprising promoter/enhancer
PT elements and template encoding RNA transcript.
XX
PS Example 3d; Page 48; 94pp; English.
XX
CC The invention relates to a DNA construct consisting of a transcription
CC unit useful for covalent intracellular joining of selected exons from
CC transcripts of two different genes A and B in a cell in which the genes A
CC and B are expressible, where the transcription unit comprises promoter/
CC enhancer elements and a template for RNA synthesis which encodes an RNA
CC transcript. The RNA transcript has the formula : RCA-SP-RCB. RCA =
CC nucleotide segment having one or more sequences, each reverse-
CC complementary to one or more sequences of pre-mRNA of gene A and genes
CC related to it, where the sequences of pre-mRNA of gene A and genes
CC related to it are situated downstream to an exon selected to be spliced
CC to pre-mRNA of gene B or genes related to it; SP = either a spacer
CC sequence or SP1-LEX-SP2; SP1 and SP2 = spacer sequences; LEX = an exon
CC encoding a flexible peptide linker or its part preceded by branch point
CC and acceptor splice sequences and followed by a donor splice sequence;
CC and RCB = nucleotide segment having one or more sequences, each reverse-
CC complementary to one or more sequences of pre- mRNA of gene B and genes

```
CC   related to it, where the sequences of pre-mRNA of gene B and genes
CC   related to it are situated upstream to an exon in pre-mRNA of gene B or
CC   genes related to it selected to be spliced to the selected exon of gene
CC   A. The DNA construct is useful for constructing a mouse or human antibody
CC   library. A transgenic non-human animal harbouring the construct is useful
CC   for generating a variegated population of cDNA and double-stranded DNA
CC   molecules suitable for preparation of gene libraries encoding scFv
CC   molecules of antibodies or human T-cell receptors (TCRs) of interest. The
CC   construct is useful for generating a human TCR library, preferably a
CC   phage-display library, comprising a variegated population of scFv
CC   molecules of human TCRs of interest expressed and displayed on the
CC   surface of a cell or viral particle. The transgenic animal is useful for
CC   generating an antibody library comprising a variegated population of scFv
CC   molecules of antibodies of interest expressed and displayed on the
CC   surface of a cell or viral particle. The construct is useful for
CC   intracellular functional joining of antibody heavy and light chain genes
CC   in antibody-producing cells, and for the production of invaluable
CC   reagents in medicine, diagnostic research and industry. The construct
CC   allows the faithful reconstitution of entire antibody immune repertoires
CC   in-vitro as libraries of scFvs displayed on phage or other display units,
CC   and such a capacity combines the extraordinary ability of the immune
CC   system to produce specific, high affinity antibodies in response to
CC   antigen, with the fast and easy protocols of in-vitro display
CC   technologies. The present sequence amplifies a fragment from the human
CC   Cgamma gene being a region of the Cgamal-hinge intron predicted to
CC   contain the branch point and peptide linker sequence
XX
SQ   Sequence 25 BP; 5 A; 7 C; 13 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        478 CGGCCGCCAGAGCCAGGAGGGAG 500
              ||||||||||  |  ||||||||
Db          2 CGGCCGCCAGCACAGGGAGGGAG 24


RESULT 2344
ABN15565
ID   ABN15565 standard; DNA; 25 BP.
XX
AC   ABN15565;
XX
DT   29-MAY-2002  (first entry)
XX
DE   Human GDMLP-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:15557.
XX
KW   Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KW   muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW   skeletal muscle disorder; amplicon; screening; ss.
XX
OS   Homo sapiens.
XX
PN   WO200192524-A2.
XX
PD   06-DEC-2001.
XX
PF   25-MAY-2001; 2001WO-US016981.
XX
PR   26-MAY-2000; 2000US-0207456P.
PR   21-SEP-2000; 2000US-0234687P.
PR   27-SEP-2000; 2000US-0236359P.
PR   04-OCT-2000; 2000GB-00024263.
PR   30-JAN-2001; 2001WO-US000661.
PR   30-JAN-2001; 2001WO-US000662.
PR   30-JAN-2001; 2001WO-US000663.
PR   30-JAN-2001; 2001WO-US000664.
PR   30-JAN-2001; 2001WO-US000665.
PR   30-JAN-2001; 2001WO-US000666.
PR   30-JAN-2001; 2001WO-US000667.
PR   30-JAN-2001; 2001WO-US000668.
PR   30-JAN-2001; 2001WO-US000669.
PR   30-JAN-2001; 2001WO-US000670.
PR   05-FEB-2001; 2001US-0266860P.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Gu Y,  Ji Y,  Penn SG,  Hanzel DK,  Rank DR,  Chen W,  Shannon ME;
XX
DR   WPI; 2002-179446/23.
XX
PT   New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT   or as specific biomolecule capture probes for surface-enhanced laser
PT   desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
PS   Disclosure; SEQ ID NO 15557; 214pp; English.
XX
CC   The present invention describes a human genome-derived myosin-like
CC   protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
CC   1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC   nucleic acids can be used as probes to detect, characterise and quantify
CC   hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC   provide initial substrates for the recombinant engineering of hGDMLP-1
CC   protein variants having desired phenotypic improvements, and for
CC   expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC   used as immunogens to raise antibodies that specifically recognise hGDMLP
CC   -1 proteins, as standards in assays used to determine the concentration
CC   and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC   capture probes for surface-enhanced laser desorption ionisation, as
CC   therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC   production, and in vaccines or for replacement therapy. The
CC   polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC   disorder associated with the expression of hGDMLP-1, in particular heart
CC   and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC   The present sequence represents an oligomer used in the screening of the
CC   hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequence
XX
SQ   Sequence 25 BP; 5 A; 11 C; 8 G; 1 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        443 CCGGCGCCCACAGGCAGCCAGCA 465
              ||||  |  |||  ||  |||||||||
Db          3 CCGGTGGCCAGAGCCAGCCAGCA 25


RESULT 2345
ABN15567
ID   ABN15567 standard; DNA; 25 BP.
XX
AC   ABN15567;
XX
DT   29-MAY-2002  (first entry)
XX
DE   Human GDMLP-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:15559.
XX
KW   Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KW   muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW   skeletal muscle disorder; amplicon; screening; ss.
XX
OS   Homo sapiens.
XX
PN   WO200192524-A2.
XX
PD   06-DEC-2001.
XX
PF   25-MAY-2001; 2001WO-US016981.
XX
PR   26-MAY-2000; 2000US-0207456P.
PR   21-SEP-2000; 2000US-0234687P.
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PR   27-SEP-2000; 2000US-0236359P.
PR   04-OCT-2000; 2000GB-00024263.
PR   30-JAN-2001; 2001WO-US000661.
PR   30-JAN-2001; 2001WO-US000662.
PR   30-JAN-2001; 2001WO-US000663.
PR   30-JAN-2001; 2001WO-US000664.
PR   30-JAN-2001; 2001WO-US000665.
PR   30-JAN-2001; 2001WO-US000666.
PR   30-JAN-2001; 2001WO-US000667.
PR   30-JAN-2001; 2001WO-US000668.
PR   30-JAN-2001; 2001WO-US000669.
PR   30-JAN-2001; 2001WO-US000670.
PR   05-FEB-2001; 2001US-0266860P.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Gu Y,  Ji Y,  Penn SG,  Hanzel DK,  Rank DR,  Chen W,  Shannon ME;
XX
DR   WPI; 2002-179446/23.
XX
PT   New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT   or as specific biomolecule capture probes for surface-enhanced laser
PT   desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
PS   Disclosure; SEQ ID NO 15559; 214pp; English.
XX
CC   The present invention describes a human genome-derived myosin-like
CC   protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
CC   1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC   nucleic acids can be used as probes to detect, characterise and quantify
CC   hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC   provide initial substrates for the recombinant engineering of hGDMLP-1
CC   protein variants having desired phenotypic improvements, and for
CC   expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC   used as immunogens to raise antibodies that specifically recognise hGDMLP
CC   -1 proteins, as standards in assays used to determine the concentration
CC   and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC   capture probes for surface-enhanced laser desorption ionisation, as
CC   therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC   production, and in vaccines or for replacement therapy. The
CC   polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC   disorder associated with the expression of hGDMLP-1, in particular heart
CC   and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC   The present sequence represents an oligomer used in the screening of the
CC   hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequence
XX
SQ   Sequence 25 BP; 5 A; 9 C; 9 G; 2 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        443 CCGGCGCCCACAGGCAGCCAGCA 465
              |||| | ||| || |||||||||
Db          1 CCGGTGGCCAGAGCCAGCCAGCA 23


RESULT 2346
ABN15566
ID   ABN15566 standard; DNA; 25 BP.
XX
AC   ABN15566;
XX
DT   29-MAY-2002  (first entry)
XX
DE   Human GDMLP-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:15558.
XX
KW   Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KW   muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW   skeletal muscle disorder; amplicon; screening; ss.
XX
OS   Homo sapiens.
XX
PN   WO200192524-A2.
XX
PD   06-DEC-2001.
XX
PF   25-MAY-2001; 2001WO-US016981.
XX
PR   26-MAY-2000; 2000US-0207456P.
PR   21-SEP-2000; 2000US-0234687P.
PR   27-SEP-2000; 2000US-0236359P.
PR   04-OCT-2000; 2000GB-00024263.
PR   30-JAN-2001; 2001WO-US000661.
PR   30-JAN-2001; 2001WO-US000662.
PR   30-JAN-2001; 2001WO-US000663.
PR   30-JAN-2001; 2001WO-US000664.
PR   30-JAN-2001; 2001WO-US000665.
PR   30-JAN-2001; 2001WO-US000666.
PR   30-JAN-2001; 2001WO-US000667.
PR   30-JAN-2001; 2001WO-US000668.
PR   30-JAN-2001; 2001WO-US000669.
PR   30-JAN-2001; 2001WO-US000670.
PR   05-FEB-2001; 2001US-0266860P.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Gu Y,  Ji Y,  Penn SG,  Hanzel DK,  Rank DR,  Chen W,  Shannon ME;
XX
DR   WPI; 2002-179446/23.
XX
PT   New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT   or as specific biomolecule capture probes for surface-enhanced laser
PT   desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
PS   Disclosure; SEQ ID NO 15558; 214pp; English.
XX
CC   The present invention describes a human genome-derived myosin-like
CC   protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
CC   1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC   nucleic acids can be used as probes to detect, characterise and quantify
CC   hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC   provide initial substrates for the recombinant engineering of hGDMLP-1
CC   protein variants having desired phenotypic improvements, and for
CC   expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC   used as immunogens to raise antibodies that specifically recognise hGDMLP
CC   -1 proteins, as standards in assays used to determine the concentration
CC   and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC   capture probes for surface-enhanced laser desorption ionisation, as
CC   therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC   production, and in vaccines or for replacement therapy. The
CC   polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC   disorder associated with the expression of hGDMLP-1, in particular heart
CC   and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC   The present sequence represents an oligomer used in the screening of the
CC   hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequence
XX
SQ   Sequence 25 BP; 5 A; 10 C; 8 G; 2 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        443 CCGGCGCCCACAGGCAGCCAGCA 465
              |||| | ||| || |||||||||
Db          2 CCGGTGGCCAGAGCCAGCCAGCA 24


RESULT 2347
ABL43221/c
```

```
ID   ABL43221 standard; DNA; 25 BP.
XX
AC   ABL43221;
XX
DT   11-APR-2002  (first entry)
XX
DE   Human chromosome 1p36-35 PCR primer SEQ ID NO:265.
XX
KW   Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2001321190-A.
XX
PD   20-NOV-2001.
XX
PF   12-MAR-2001; 2001JP-00068285.
XX
PR   10-MAR-2000; 2000JP-00066716.
XX
PA   (RIKA ) RIKAGAKU KENKYUSHO.
PA   (GENO-) GENOTEX YG.
XX
DR   WPI; 2002-144136/19.
XX
PT   Arraying genome clones.
XX
PS   Claim 4; Page 10; 528pp; Japanese.
XX
CC   The present invention describes a method of arraying genome clones. The
CC   method comprises: (a) clones of the genomic libraries contained in
CC   multiwell plates numbered for discrimination are mixed in each of the
CC   multiwell plates; (b) a primer designed based on the chromosome marker
CC   sequence is added to the mixture to carry out an amplification reaction;
CC   (c) a signal corresponding to the marker is detected from the resultant
CC   amplified product to specify the discrimination Nos. of the multiwell
CC   plates containing the clones having said marker sequence; (d) the order
CC   of the markers is changed so that the same discrimination Nos. succeed to
CC   the maximum in the specified discrimination Nos. to array the multiwell
CC   plates; (e) the clones in the multiwell plates of the specified
CC   discrimination Nos. are mixed respectively in each wells of longitudinal
CC   and lateral directions; (f) the mixed clones are cultured and the
CC   resultant cultures are amplified by using the above primer; (g) signals
CC   are detected from the amplified products; (h) the clones in the multiwell
CC   plates are specified from the detected result; and (i) the clones are
CC   reconstituted as the positions on the chromosome and arrayed. The
CC   microarray is useful for gene analysis. ABL42957 to ABL45322 represent
CC   PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
CC   represent PCR primers for human chromosome 21q22.1, which are
CC   specifically claimed for use in the present invention
XX
SQ   Sequence 25 BP; 13 A; 3 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2589 CTATTTAATTGAAACTCTCTGTT 2611
              | |||| ||||||||  ||||||
Db         25 CGATTTTATTGAAACCTTCTGTT 3


RESULT 2348
ABS75946
ID   ABS75946 standard; DNA; 25 BP.
XX
AC   ABS75946;
XX
DT   27-DEC-2002  (first entry)
XX
DE   Human PAPP-Ea associated 25-mer SEQ ID 1472.
XX
KW   PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW   contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW   dysgenetic pregnancy; primer; ss.
XX
OS   Homo sapiens.
XX
PN   US2002102252-A1.
XX
PD   01-AUG-2002.
XX
PF   06-APR-2001; 2001US-00827998.
XX
PR   26-MAY-2000; 2000US-0207456P.
XX
PA   (GUYY/) GU Y.
PA   (SHAN/) SHANNON M E.
XX
PI   Gu Y,  Shannon ME;
XX
DR   WPI; 2002-697817/75.
XX
PT   New isolated nucleic acid encoding an isoform of human pregnancy
PT   associated plasma protein E, for preventing or aborting pregnancy.
XX
PS   Example 2; Page 268; 353pp; English.
XX
CC   This invention describes a novel isolated nucleic acid that encodes one
CC   of three new isoforms of human pregnancy associated plasma protein E,
CC   hPAPP-E. The products of the invention have abortive and contraceptive
CC   activity and can be used for gene therapy or in a vaccine. The nucleic
CC   acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC   used in pharmaceutical compositions or vaccines for preventing or
CC   aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC   dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC   the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC   antibodies can be used to assess the expression levels of PAPP-E isoform
CC   proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC   antenatally. This sequence represents an oligomer used in scanning the
CC   human PAPP-E genes described in the disclosure of the invention
XX
SQ   Sequence 25 BP; 7 A; 8 C; 9 G; 1 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        444 CGGCGCCCACAGGCAGCCAGCAG 466
              ||||   |||||| |||||||||
Db          1 CGGCCAGCACAGGTAGCCAGCAG 23


RESULT 2349
ABS75944
ID   ABS75944 standard; DNA; 25 BP.
XX
AC   ABS75944;
XX
DT   27-DEC-2002  (first entry)
XX
DE   Human PAPP-Ea associated 25-mer SEQ ID 1470.
XX
KW   PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW   contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW   dysgenetic pregnancy; primer; ss.
XX
OS   Homo sapiens.
XX
PN   US2002102252-A1.
XX
PD   01-AUG-2002.
XX
PF   06-APR-2001; 2001US-00827998.
XX
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```
PR   26-MAY-2000; 2000US-0207456P.
XX
PA   (GUYY/) GU Y.
PA   (SHAN/) SHANNON M E.
XX
PI   Gu Y,  Shannon ME;
XX
DR   WPI; 2002-697817/75.
XX
PT   New isolated nucleic acid encoding an isoform of human pregnancy
PT   associated plasma protein E, for preventing or aborting pregnancy.
XX
PS   Example 2; Page 268; 353pp; English.
XX
CC   This invention describes a novel isolated nucleic acid that encodes one
CC   of three new isoforms of human pregnancy associated plasma protein E,
CC   hPAPP-E. The products of the invention have abortive and contraceptive
CC   activity and can be used for gene therapy or in a vaccine. The nucleic
CC   acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC   used in pharmaceutical compositions or vaccines for preventing or
CC   aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC   dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC   the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC   antibodies can be used to assess the expression levels of PAPP-E isoform
CC   proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC   antenatally. This sequence represents an oligomer used in scanning the
CC   human PAPP-E genes described in the disclosure of the invention
XX
SQ   Sequence 25 BP; 7 A; 8 C; 9 G; 1 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        444 CGGCGCCCACAGGCAGCCAGCAG 466
              ||||   |||||| |||||||||
Db          3 CGGCCAGCACAGGTAGCCAGCAG 25


RESULT 2350
ABS75945
ID   ABS75945 standard; DNA; 25 BP.
XX
AC   ABS75945;
XX
DT   27-DEC-2002  (first entry)
XX
DE   Human PAPP-Ea associated 25-mer SEQ ID 1471.
XX
KW   PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW   contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW   dysgenetic pregnancy; primer; ss.
XX
OS   Homo sapiens.
XX
PN   US2002102252-A1.
XX
PD   01-AUG-2002.
XX
PF   06-APR-2001; 2001US-00827998.
XX
PR   26-MAY-2000; 2000US-0207456P.
XX
PA   (GUYY/) GU Y.
PA   (SHAN/) SHANNON M E.
XX
PI   Gu Y,  Shannon ME;
XX
DR   WPI; 2002-697817/75.
XX
PT   New isolated nucleic acid encoding an isoform of human pregnancy
PT   associated plasma protein E, for preventing or aborting pregnancy.
XX
PS   Example 2; Page 268; 353pp; English.
XX
CC   This invention describes a novel isolated nucleic acid that encodes one
CC   of three new isoforms of human pregnancy associated plasma protein E,
CC   hPAPP-E. The products of the invention have abortive and contraceptive
CC   activity and can be used for gene therapy or in a vaccine. The nucleic
CC   acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC   used in pharmaceutical compositions or vaccines for preventing or
CC   aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC   dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC   the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC   antibodies can be used to assess the expression levels of PAPP-E isoform
CC   proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC   antenatally. This sequence represents an oligomer used in scanning the
CC   human PAPP-E genes described in the disclosure of the invention
XX
SQ   Sequence 25 BP; 7 A; 8 C; 9 G; 1 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        444 CGGCGCCCACAGGCAGCCAGCAG 466
              ||||   |||||| |||||||||
Db          2 CGGCCAGCACAGGTAGCCAGCAG 24


RESULT 2351
ABK90953
ID   ABK90953 standard; DNA; 25 BP.
XX
AC   ABK90953;
XX
DT   05-NOV-2002  (first entry)
XX
DE   PCR primer, 25657, used to amplify human C gamma CH1-hinge intron.
XX
KW   Human; PCR; primer; ss; antiHIV; chimeric protein; HIV-1;
KW   human immunodeficiency virus-1; envelope glycoprotein; env; gp120; CD4;
KW   cellular receptor; immunoglobulin; Ig; V1; V2; variable region;
KW   variable region-like membrane distal domain; antibody; heavy chain; VH;
KW   VH3; gene therapy; HIV infection; virus replication; constant gamma;
KW   C gamma; CH1-hinge; CH1.
XX
OS   Homo sapiens.
XX
PN   WO200259258-A2.
XX
PD   01-AUG-2002.
XX
PF   22-JAN-2002; 2002WO-IL000060.
XX
PR   22-JAN-2001; 2001IL-00141023.
XX
PA   (GAVI-) GAVISH-GALILEE BIO APPL LTD.
XX
PI   Gross G,  Meyuhas R;
XX
DR   WPI; 2002-608450/65.
XX
PT   New nucleic acid molecule encoding chimeric proteins with binding
PT   specificity for a site on HIV envelope glycoprotein gp120 and a site on
PT   gp120 protein or on the extracellular portion of human CD4, for
PT   preventing or treating HIV infection.
XX
PS   Example 1; Page 23; 48pp; English.
XX
CC   The invention discloses a nucleic acid molecule encoding a functional
CC   chimeric protein with binding specificity for at least two different
CC   sites. At least one site is on the human immunodeficiency virus-1 (HIV-1)
CC   envelope glycoprotein (env), gp120, and the other site is either on the
CC   gp120 protein or on the extracellular portion of human CD4, the major
CC   cellular receptor for HIV. The chimeric protein essentially comprises a
```

CC first binding region of a soluble extracellular portion of human CD4,
CC consisting of the immunoglobulin (Ig) variable region-like membrane
CC distal domains (V1 and V2) and a second binding region of a variable
CC region of an antibody heavy chain (VH), encoded by the VH3 gene, which is
CC capable of being attached to an adjacent and non-overlapping site on the
CC gp120 protein, or to a site on the extracellular portion of human CD4,
CC and is capable of increasing the capacity of the extracellular portion of
CC human CD4 to interact with gp120 and to block the interaction of HIV with
CC membranal CD4. These two binding regions are physically connected by a
CC linker region. The chimeric protein of the invention is useful for gene
CC therapy and for preventing and treating an HIV infection and for
CC neutralising and inhibiting virus replication and infectivity in a
CC subject, preferably a mammal. The sequence presented is the PCR primer,
CC 25657, which was used to amplify the human constant (C) gamma heavy chain
CC domain, CH1, gene of the Ig chain used in the construction of the
CC chimeric protein
XX
SQ Sequence 25 BP; 5 A; 7 C; 13 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 2.6e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 478 CGGCCGCCAGAGCCAGGAGGGAG 500
||||||||||| | ||||||||
Db 2 CGGCCGCCAGCACAGGGAGGGAG 24

RESULT 2352
ABZ83992/c
ID ABZ83992 standard; DNA; 25 BP.
XX
AC ABZ83992;
XX
DT 14-MAY-2003 (first entry)
XX
DE Toxicologically relevant human PCR primer #1151.
XX
KW Toxicologically relevant gene; toxicological response; PCR primer; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2003016500-A2.
XX
PD 27-FEB-2003.
XX
PF 16-AUG-2002; 2002WO-US026514.
XX
PR 16-AUG-2001; 2001US-0313080P.
XX
PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
XX
PI Neft RE, Dunn RT, Adkins K, Pickett GG, Kier LD, Schmeiser K;
PI Alen P;
XX
DR WPI; 2003-268322/26.
XX
PT Determining a toxicological response to an agent, useful for screening of
PT drugs, comprises comparing the expression profile of one or more human
PT toxic response genes to a reference gene expression profile indicative of
PT toxicity.
XX
PS Claim 1; Page 326; 455pp; English.
XX
CC The present invention describes a method (M1) for determining a
CC toxicological response to an agent, which comprises comparing the
CC expression profile of one or more human toxic response genes to a
CC reference gene expression profile indicative of toxicity, and so
CC determining the presence of a toxic response to the agent. Also
CC described: (1) an array comprising one or more polynucleotides selected
CC from the genes corresponding to the partial sequences given in ABZ82842
CC to ABZ84764, or their fragments of at least 20 nucleotides, or homologues
CC ; and (2) determining if a gene putatively identified to be a toxic
CC response gene plays a role on toxic response pathways by determining the
CC expression profile of the gene after exposure of cells or a human subject
CC to a known toxic pharmaceutical or industrial agent, comprising: (a)
CC exposing cells to an agent or isolating cells from a human subject who
CC was exposed to an agent; (b) obtaining the test gene expression profile
CC for a putatively identified toxic response gene after exposure to a known
CC toxic pharmaceutical or industrial agent; and (c) comparing the test
CC profile to the expression profile of a gene with a similar function or
CC comparing the test profile to the expression profile of that gene after
CC exposure to other known toxic compounds. The methods are useful for
CC predicting and determining toxicological responses on a cellular, organ
CC or system level. The arrays comprising the human genes are useful for
CC toxicological screening of drugs, pharmaceutical compounds and chemicals
XX
SQ Sequence 25 BP; 5 A; 2 C; 12 G; 6 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 2.6e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 424 CATCAACCCCCTGCACCAGCCGG 446
||| ||| |||| |||||||| |
Db 23 CATTAACTCCCTCCACCAGCCTG 1

RESULT 2353
AAD53331
ID AAD53331 standard; DNA; 25 BP.
XX
AC AAD53331;
XX
DT 28-MAY-2003 (first entry)
XX
DE Probe used in human mucin (MUC4) gene expression studies.
XX
KW Human; mucin; calcium activated chloride channel; CLCA4; CLCA2; asthma;
KW COPD; chronic obstructive pulmonary disease; cystic fibrosis; therapy;
KW chronic bronchitis; bronchiectasis; MUC; probe; ss.
XX
OS Homo sapiens.
XX
PN WO200294876-A2.
XX
PD 28-NOV-2002.
XX
PF 08-MAY-2002; 2002WO-EP005119.
XX
PR 18-MAY-2001; 2001US-00861038.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Szymkowski DE;
XX
DR WPI; 2003-140363/13.
XX
PT New murine calcium activated chloride channel (mCLCA4) for identifying
PT mCLCA4 expression regulatory factors for treating respiratory mucin
PT production associated disease conditions, e.g. chronic bronchitis, and
PT asthma.
XX
PS Example 5; Col 44; 39pp; English.
XX
CC The invention relates to methods and compositions for modulating mucin
CC secretion by respiratory system cells. The invention also provides murine
CC calcium activated chloride channel, CLCA4 and human CLCA2 polypeptides
CC and polynucleotides. CLCA2 sequences are used to diagnose the presence of
CC mucin secretion respiratory system associated disease conditions in host.
CC CLCA2 modulators are useful for preparing a composition for the treatment
CC of respiratory mucin production associated disease conditions such as
CC asthma, chronic bronchitis, chronic obstructive pulmonary disease (COPD),
CC cystic fibrosis or bronchiectasis. Sequences of the invention are used in
CC the identification of mCLCA4 homologues, as a source of new promoter

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CC   elements, in the identification of mCLCA4 expression regulatory factors,
CC   as probes and primers in hybridisation applications, in identification of
CC   expression patterns in biological specimens and in the preparation of in
CC   vitro models for mCLCA4 function. The present sequence is a probe used in
CC   human mucin gene expression studies
XX
SQ   Sequence 25 BP; 5 A; 10 C; 6 G; 4 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        293 GCGCCACCCCTCTCCCACACTGG 315
              | || |  ||||||||||||||||
Db          2 GGGCGATACCTCTCCCACACTGG 24


RESULT 2354
AAL61680/c
ID   AAL61680 standard; DNA; 25 BP.
XX
AC   AAL61680;
XX
DT   22-SEP-2003  (first entry)
XX
DE   Oligonucleotide #37 used in the nucleic acid detection method.
XX
KW   Nucleic acid detection; fabrication; ss.
XX
OS   Unidentified.
XX
PN   WO2003035829-A2.
XX
PD   01-MAY-2003.
XX
PF   08-OCT-2002; 2002WO-US032088.
XX
PR   09-OCT-2001; 2001US-0327864P.
PR   07-DEC-2001; 2001US-00008978.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Park S,  Taton TA,  Mirkin CA;
XX
DR   WPI; 2003-430409/40.
XX
PT   Detecting nucleic acid having two portions, by providing nanoparticles
PT   having oligonucleotides attached to it, contacting nucleic acid and
PT   nanoparticles to allow hybridization, and observing detectable change.
XX
PS   Disclosure; Fig 68; 467pp; English.
XX
CC   The invention relates to a method of detecting a nucleic acid having two
CC   portions. The method involves providing nanoparticles having
CC   oligonucleotides attached to it which has a sequence complementary to
CC   sequence of two portions of nucleic acid, contacting nucleic acid and
CC   nanoparticles to allow hybridisation of oligonucleotides with two or more
CC   portions of nucleic acid and observing a detectable change brought about
CC   by hybridisation. The method and aggregate probes are useful for
CC   detecting two or more nucleic acids (from a biological source) having at
CC   least two portions such as viral RNA, bacterial or fungal DNA, a gene
CC   associated with a disease, synthetic or structurally modified natural or
CC   synthetic RNA or DNA, or a product of a polymerase chain reaction
CC   amplification. The invention is useful for preparing a nanoprobe
CC   conjugate for detecting an analyte and for detecting a nucleic acid bound
CC   to an electrode surface. It is also useful for fabrication and for
CC   separating a selected nucleic acid having two portions from other nucleic
CC   acids. The present sequence is an oligo used to illustrate the method of
CC   the invention
XX
SQ   Sequence 25 BP; 15 A; 3 C; 0 G; 7 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1759 TATTCATTAAGCTTTTTTTTTT 1781
              |||| || | | ||||||||||
Db         23 TATTGATAAGGATTTTTTTTTT 1

RESULT 2355
ACI99045/c
ID   ACI99045 standard; DNA; 25 BP.
XX
AC   ACI99045;
XX
DT   14-OCT-2003  (first entry)
XX
DE   Human microarray DNA oligonucleotide SEQ ID NO 99036.
XX
KW   EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW   genetic variation; biallelic marker; polymorphism; human;
KW   cross-species comparison.
XX
OS   Homo sapiens.
XX
PN   US2003104410-A1.
XX
PD   05-JUN-2003.
XX
PF   15-MAR-2002; 2002US-00098263.
XX
PR   16-MAR-2001; 2001US-0276759P.
XX
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Mittmann MP;
XX
DR   WPI; 2003-567953/53.
XX
PT   New array of nucleic acid probes, useful for in situ hybridization, in
PT   Southern, Northern or dot-blot hybridization to identify or detect the
PT   sequence or specific mutations of any gene.
XX
PS   Claim 1; SEQ ID NO 99036; 9pp; English.
XX
CC   The invention discloses a microarray comprising a plurality of nucleic
CC   acid probes including one of 2,018,500 fully defined sequences, or its
CC   perfect match, perfect mismatch, antisense match or antisense mismatch.
CC   Also disclosed is a method of gene expression analysis. The array is used
CC   in monitoring gene expression levels by hybridisation to a DNA library,
CC   in analysis of genetic variation or in hybridisation of tag-labelled
CC   compounds. The nucleic acid probes are specifically designed for analysis
CC   of at least one target sequence. The method of analysis comprises
CC   hybridising at least one or more nucleic acids to at least two or more
CC   nucleic acid probes and detecting the hybridisation. The nucleic acid
CC   probes are attached to a solid support. The analysis comprises monitoring
CC   gene expression levels, identifying biallelic markers or polymorphisms,
CC   or family members of a gene and a cross-species comparison. Each of the
CC   nucleic acids further comprises a tag sequence. The array of nucleic acid
CC   probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC   blot hybridisation to identify or detect the sequence or specific
CC   mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC   primer extensions or in screening cDNA or genomic libraries or subclones
CC   for additional subclones containing segments of DNA that have been
CC   isolated and previously sequenced. The sequence presented is one of the
CC   nucleic acid probes incorporated in the microarray. Note: The sequence
CC   data for this patent can also be obtained in electronic format directly
CC   from USPTO at seqdata.uspto.goc/sequence.html
XX
SQ   Sequence 25 BP; 14 A; 3 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;
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Qy       1774 TTTTTTTTGAACCCCATTCTTTC 1796
              || |||||| || | ||||||||
Db         24 TTCTTTTTGTACACGATTCTTTC 2


RESULT 2356
ACI22395/c
ID   ACI22395 standard; DNA; 25 BP.
XX
AC   ACI22395;
XX
DT   13-OCT-2003  (first entry)
XX
DE   Human microarray DNA oligonucleotide SEQ ID NO 22386.
XX
KW   EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW   genetic variation; biallelic marker; polymorphism; human;
KW   cross-species comparison.
XX
OS   Homo sapiens.
XX
PN   US2003104410-A1.
XX
PD   05-JUN-2003.
XX
PF   15-MAR-2002; 2002US-00098263.
XX
PR   16-MAR-2001; 2001US-0276759P.
XX
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Mittmann MP;
XX
DR   WPI; 2003-567953/53.
XX
PT   New array of nucleic acid probes, useful for in situ hybridization, in
PT   Southern, Northern or dot-blot hybridization to identify or detect the
PT   sequence or specific mutations of any gene.
XX
PS   Claim 1; SEQ ID NO 22386; 9pp; English.
XX
CC   The invention discloses a microarray comprising a plurality of nucleic
CC   acid probes including one of 2,018,500 fully defined sequences, or its
CC   perfect match, perfect mismatch, antisense match or antisense mismatch.
CC   Also disclosed is a method of gene expression analysis. The array is used
CC   in monitoring gene expression levels by hybridisation to a DNA library,
CC   in analysis of genetic variation or in hybridisation of tag-labelled
CC   compounds. The nucleic acid probes are specifically designed for analysis
CC   of at least one target sequence. The method of analysis comprises
CC   hybridising at least one or more nucleic acids to at least two or more
CC   nucleic acid probes and detecting the hybridisation. The nucleic acid
CC   probes are attached to a solid support. The analysis comprises monitoring
CC   gene expression levels, identifying biallelic markers or polymorphisms,
CC   or family members of a gene and a cross-species comparison. Each of the
CC   nucleic acids further comprises a tag sequence. The array of nucleic acid
CC   probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC   blot hybridisation to identify or detect the sequence or specific
CC   mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC   primer extensions or in screening cDNA or genomic libraries or subclones
CC   for additional subclones containing segments of DNA that have been
CC   isolated and previously sequenced. The sequence presented is one of the
CC   nucleic acid probes incorporated in the microarray. Note: The sequence
CC   data for this patent can also be obtained in electronic format directly
CC   from USPTO at seqdata.uspto.goc/sequence.html
XX
SQ   Sequence 25 BP; 4 A; 9 C; 4 G; 8 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1527 ACGAAGAAAGGTTAGGAGAGTAG 1549
                ||||||| || ||||  ||||||
Db         24 ACGAAGACAGCTTAGCGGAGTAG 2


RESULT 2357
ACK13084/c
ID   ACK13084 standard; DNA; 25 BP.
XX
AC   ACK13084;
XX
DT   14-OCT-2003  (first entry)
XX
DE   Human microarray DNA oligonucleotide SEQ ID NO 113065.
XX
KW   EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW   genetic variation; biallelic marker; polymorphism; human;
KW   cross-species comparison.
XX
OS   Homo sapiens.
XX
PN   US2003104410-A1.
XX
PD   05-JUN-2003.
XX
PF   15-MAR-2002; 2002US-00098263.
XX
PR   16-MAR-2001; 2001US-0276759P.
XX
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Mittmann MP;
XX
DR   WPI; 2003-567953/53.
XX
PT   New array of nucleic acid probes, useful for in situ hybridization, in
PT   Southern, Northern or dot-blot hybridization to identify or detect the
PT   sequence or specific mutations of any gene.
XX
PS   Claim 1; SEQ ID NO 113065; 9pp; English.
XX
CC   The invention discloses a microarray comprising a plurality of nucleic
CC   acid probes including one of 2,018,500 fully defined sequences, or its
CC   perfect match, perfect mismatch, antisense match or antisense mismatch.
CC   Also disclosed is a method of gene expression analysis. The array is used
CC   in monitoring gene expression levels by hybridisation to a DNA library,
CC   in analysis of genetic variation or in hybridisation of tag-labelled
CC   compounds. The nucleic acid probes are specifically designed for analysis
CC   of at least one target sequence. The method of analysis comprises
CC   hybridising at least one or more nucleic acids to at least two or more
CC   nucleic acid probes and detecting the hybridisation. The nucleic acid
CC   probes are attached to a solid support. The analysis comprises monitoring
CC   gene expression levels, identifying biallelic markers or polymorphisms,
CC   or family members of a gene and a cross-species comparison. Each of the
CC   nucleic acids further comprises a tag sequence. The array of nucleic acid
CC   probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC   blot hybridisation to identify or detect the sequence or specific
CC   mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC   primer extensions or in screening cDNA or genomic libraries or subclones
CC   for additional subclones containing segments of DNA that have been
CC   isolated and previously sequenced. The sequence presented is one of the
CC   nucleic acid probes incorporated in the microarray. Note: The sequence
CC   data for this patent can also be obtained in electronic format directly
CC   from USPTO at seqdata.uspto.goc/sequence.html
XX
SQ   Sequence 25 BP; 7 A; 4 C; 9 G; 5 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        706 CGACGACCAGCACCTGTTGCTGC 728
              |||||||  |||||| || ||||
Db         25 CGACGACACGCACCTTTTTCTGC 3
```

```
RESULT 2358
ACI81508/c
ID   ACI81508 standard; DNA; 25 BP.
XX
AC   ACI81508;
XX
DT   14-OCT-2003  (first entry)
XX
DE   Human microarray DNA oligonucleotide SEQ ID NO 81499.
XX
KW   EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW   genetic variation; biallelic marker; polymorphism; human;
KW   cross-species comparison.
XX
OS   Homo sapiens.
XX
PN   US2003104410-A1.
XX
PD   05-JUN-2003.
XX
PF   15-MAR-2002; 2002US-00098263.
XX
PR   16-MAR-2001; 2001US-0276759P.
XX
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Mittmann MP;
XX
DR   WPI; 2003-567953/53.
XX
PT   New array of nucleic acid probes, useful for in situ hybridization, in
PT   Southern, Northern or dot-blot hybridization to identify or detect the
PT   sequence or specific mutations of any gene.
XX
PS   Claim 1; SEQ ID NO 81499; 9pp; English.
XX
CC   The invention discloses a microarray comprising a plurality of nucleic
CC   acid probes including one of 2,018,500 fully defined sequences, or its
CC   perfect match, perfect mismatch, antisense match or antisense mismatch.
CC   Also disclosed is a method of gene expression analysis. The array is used
CC   in monitoring gene expression levels by hybridisation to a DNA library,
CC   in analysis of genetic variation or in hybridisation of tag-labelled
CC   compounds. The nucleic acid probes are specifically designed for analysis
CC   of at least one target sequence. The method of analysis comprises
CC   hybridising at least one or more nucleic acids to at least two or more
CC   nucleic acid probes and detecting the hybridisation. The nucleic acid
CC   probes are attached to a solid support. The analysis comprises monitoring
CC   gene expression levels, identifying biallelic markers or polymorphisms,
CC   or family members of a gene and a cross-species comparison. Each of the
CC   nucleic acids further comprises a tag sequence. The array of nucleic acid
CC   probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC   blot hybridisation to identify or detect the sequence or specific
CC   mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC   primer extensions or in screening cDNA or genomic libraries or subclones
CC   for additional subclones containing segments of DNA that have been
CC   isolated and previously sequenced. The sequence presented is one of the
CC   nucleic acid probes incorporated in the microarray. Note: The sequence
CC   data for this patent can also be obtained in electronic format directly
CC   from USPTO at seqdata.uspto.goc/sequence.html
XX
SQ   Sequence 25 BP; 4 A; 9 C; 4 G; 8 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        685 GATGGACGAGGTGCAGAATGTCG 707
              ||  ||| ||| ||||||||||||
Db         23 GACAGACTAGGAGCAGAATGTCG 1
```

```
RESULT 2359
ACI27529
ID   ACI27529 standard; DNA; 25 BP.
XX
AC   ACI27529;
XX
DT   13-OCT-2003  (first entry)
XX
DE   Human microarray DNA oligonucleotide SEQ ID NO 27520.
XX
KW   EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW   genetic variation; biallelic marker; polymorphism; human;
KW   cross-species comparison.
XX
OS   Homo sapiens.
XX
PN   US2003104410-A1.
XX
PD   05-JUN-2003.
XX
PF   15-MAR-2002; 2002US-00098263.
XX
PR   16-MAR-2001; 2001US-0276759P.
XX
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Mittmann MP;
XX
DR   WPI; 2003-567953/53.
XX
PT   New array of nucleic acid probes, useful for in situ hybridization, in
PT   Southern, Northern or dot-blot hybridization to identify or detect the
PT   sequence or specific mutations of any gene.
XX
PS   Claim 1; SEQ ID NO 27520; 9pp; English.
XX
CC   The invention discloses a microarray comprising a plurality of nucleic
CC   acid probes including one of 2,018,500 fully defined sequences, or its
CC   perfect match, perfect mismatch, antisense match or antisense mismatch.
CC   Also disclosed is a method of gene expression analysis. The array is used
CC   in monitoring gene expression levels by hybridisation to a DNA library,
CC   in analysis of genetic variation or in hybridisation of tag-labelled
CC   compounds. The nucleic acid probes are specifically designed for analysis
CC   of at least one target sequence. The method of analysis comprises
CC   hybridising at least one or more nucleic acids to at least two or more
CC   nucleic acid probes and detecting the hybridisation. The nucleic acid
CC   probes are attached to a solid support. The analysis comprises monitoring
CC   gene expression levels, identifying biallelic markers or polymorphisms,
CC   or family members of a gene and a cross-species comparison. Each of the
CC   nucleic acids further comprises a tag sequence. The array of nucleic acid
CC   probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC   blot hybridisation to identify or detect the sequence or specific
CC   mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC   primer extensions or in screening cDNA or genomic libraries or subclones
CC   for additional subclones containing segments of DNA that have been
CC   isolated and previously sequenced. The sequence presented is one of the
CC   nucleic acid probes incorporated in the microarray. Note: The sequence
CC   data for this patent can also be obtained in electronic format directly
CC   from USPTO at seqdata.uspto.goc/sequence.html
XX
SQ   Sequence 25 BP; 13 A; 4 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2496 GTAATCTATAACACATCATAAGG 2518
              ||||| ||  |||||||| ||||
Db          1 GTAATATAAGACACATCAAAAGG 23


RESULT 2360
ADC75076/c
```

```
ID   ADC75076 standard; DNA; 27 BP.
XX
AC   ADC75076;
XX
DT   01-JAN-2004  (first entry)
XX
DE   Biosensor related oligonucleotide of the invention SEQ ID NO:4.
XX
KW   ss; biosensor; hybridisation.
XX
OS   Synthetic.
XX
PN   JP2003172737-A.
XX
PD   20-JUN-2003.
XX
PF   07-DEC-2001; 2001JP-00374764.
XX
PR   07-DEC-2001; 2001JP-00374764.
XX
PA   (TOJO ) TOYO KOHAN CO LTD.
XX
DR   WPI; 2003-819164/77.
XX
PT   Solid support body comprising crystal resonator on which a surface
PT   treatment layer is formed, and a substrate whose surface treatment layer
PT   is chemically modified, useful as biosensor.
XX
PS   Disclosure; SEQ ID NO 4; 7pp; Japanese.
XX
CC   The invention relates to a novel solid support body comprising a crystal
CC   resonator on which a surface treatment layer is formed. The biosensor is
CC   useful for analysing biological samples e.g., gene, a protein, and a
CC   peptide, and for analysing bioactive substances. Preferably, the
CC   biosensor is useful for analysing base sequences by carrying out
CC   hybridisation. The present sequence is used in the exemplification of the
CC   invention.
XX
SQ   Sequence 27 BP; 18 A; 3 C; 0 G; 6 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 27;
  Best Local Similarity   82.6%;  Pred. No. 3e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTAACT 2190
              ||||| ||| |||||||| || |
Db         23 TTTTTATTTATTTTTTTTGAATT 1


RESULT 2361
AAX18372/c
ID   AAX18372 standard; DNA; 18 BP.
XX
AC   AAX18372;
XX
DT   11-MAY-1999  (first entry)
XX
DE   RT-PCR primer of the invention SEQ ID 13.
XX
KW   RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS   Synthetic.
XX
PN   JP11032765-A.
XX
PD   09-FEB-1999.
XX
PF   18-JUL-1997;   97JP-00208312.
XX
PR   18-JUL-1997;   97JP-00208312.
XX
PA   (TAKI ) TAKARA SHUZO CO LTD.
XX
DR   WPI; 1999-183822/16.
XX
PT   Peptides having at least two new nucleotides - useful as primers in RT-
PT   PCR.
XX
PS   Disclosure; Page 11; 19pp; Japanese.
XX
CC   This sequence represents a primer of the invention. The invention relates
CC   to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC   -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC   a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC   natural number indicating the repetition of alpha; beta, delta = V or N;
CC   V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC   thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC   repetition of gamma, in which thymine expressed by gamma is composed of
CC   1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC   useful as primers for RT-PCR and determination of base sequences. The new
CC   sequences allow for reproductive and highly efficient analysis of gene
CC   sequences
XX
SQ   Sequence 18 BP; 2 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAA 2800
              || ||||||||||||||||
Db         18 TTAAAAAAAAAAAAAAAA 1


RESULT 2362
AAF75598
ID   AAF75598 standard; DNA; 18 BP.
XX
AC   AAF75598;
XX
DT   10-MAY-2001  (first entry)
XX
DE   Binary encoded sequence tag method anchored primer #3.
XX
KW   Binary encoded sequence tag; BEST; nucleic acid analysis;
KW   gene expression; adaptor; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO200112855-A2.
XX
PD   22-FEB-2001.
XX
PF   11-AUG-2000; 2000WO-US022164.
XX
PR   13-AUG-1999;   99US-0148870P.
PR   06-APR-2000; 2000US-00544713.
XX
PA   (UYYA ) UNIV YALE.
XX
PI   Kaufman JC,  Roth ME,  Lizardi PM,  Feng L,  Latimer DR;
XX
DR   WPI; 2001-202878/20.
XX
PT   Producing binary sequence tags, useful for analyzing nucleic acid
PT   sequence tags, gene expression or gene-expression patterns, involves
PT   generating nucleic acid fragments, which are mixed with offset adaptors
PT   and adaptor-indexers.
XX
PS   Disclosure; Page 101; 101pp; English.
XX
CC   The present invention describes a method of producing binary sequence
CC   tags from nucleic acid fragments in a sample, involving incubating the
CC   sample with cleaving reagents, mixing offset adaptors with the sample,
CC   incubating with more cleaving reagents and mixing the sample with adaptor
CC   -indexers where the adaptors are coupled to binary sequence tags. The
```

```
CC   method is useful in sequence analysis, including analysis and comparison
CC   of gene expression, nucleic acid samples and genomes
XX
SQ   Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTCA 18


RESULT 2363
AAX18373/c
ID   AAX18373 standard; DNA; 18 BP.
XX
AC   AAX18373;
XX
DT   11-MAY-1999  (first entry)
XX
DE   RT-PCR primer of the invention SEQ ID 14.
XX
KW   RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS   Synthetic.
XX
PN   JP11032765-A.
XX
PD   09-FEB-1999.
XX
PF   18-JUL-1997;   97JP-00208312.
XX
PR   18-JUL-1997;   97JP-00208312.
XX
PA   (TAKI ) TAKARA SHUZO CO LTD.
XX
DR   WPI; 1999-183822/16.
XX
PT   Peptides having at least two new nucleotides - useful as primers in RT-
PT   PCR.
XX
PS   Disclosure; Page 11; 19pp; Japanese.
XX
CC   This sequence represents a primer of the invention. The invention relates
CC   to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC   -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC   a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC   natural number indicating the repetition of alpha; beta, delta = V or N;
CC   V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC   thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC   repetition of gamma, in which thymine expressed by gamma is composed of
CC   1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC   useful as primers for RT-PCR and determination of base sequences. The new
CC   sequences allow for reproductive and highly efficient analysis of gene
CC   sequences
XX
SQ   Sequence 18 BP; 1 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2803
              | |||||||||||||||||
Db         18 ATAAAAAAAAAAAAAAAA 1


RESULT 2364
AAN30173
ID   AAN30173 standard; DNA; 18 BP.
XX
AC   AAN30173;
XX
DT   05-APR-1992  (first entry)
XX
DE   Sequence derived from the L1 region of the bovine papillomavirus (bPV)
DE   type 1a genome.
XX
KW   Diagnostioc reagent; vaccine; medicine; wart; tumour; ss.
XX
OS   Bovine papillomavirus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .18
FT                   /*tag=  a
XX
PN   EP92456-A.
XX
PD   26-OCT-1983.
XX
PF   01-APR-1983;   83EP-00901081.
XX
PR   05-APR-1982;   82FR-00005887.
XX
PA   (INSP ) INST PASTEUR.
PA   (DANO/) DANOS O.
XX
PI   Danos O,  Katinka M,  Yaniv M;
XX
DR   WPI; 1983-802979/44.
DR   P-PSDB; AAP30313.
XX
PT   DNA fragment coding for Papillomavirus antigenic proteins - and derived
PT   immunogen, vaccine and antibody.
XX
PS   Claim 6; Page 16; 25pp; French.
XX
CC   The inventors claim DNA fragments capable of expressing, in a host, a
CC   prod. contg. at least one antigenic determinant of papillomavirus (PV),
CC   (see AAN30170-N30173). Also claimed are immunogens consisting of at least
CC   one peptide sequence coded for by the DNA fragments (see AAP30310-
CC   P30313), vaccines contg. the immunogens and antibodies raised from them.
CC   The vaccines are useful in human and veterinary medicine and the
CC   antibodies are useful as diagnostic reagents. The DNA fragments are most
CC   esp. derived from the L1 region of human PV type 1a
XX
SQ   Sequence 18 BP; 16 A; 1 C; 1 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2802
              | |||||||||||||||||
Db          1 GCAAAAAAAAAAAAAAAA 18


RESULT 2365
AAN92257
ID   AAN92257 standard; DNA; 18 BP.
XX
AC   AAN92257;
XX
DT   25-MAR-2003  (revised)
DT   31-OCT-2002  (revised)
DT   25-APR-1990  (first entry)
XX
DE   SS probe #300.
XX
KW   Probe #300; ribonuclease.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
```

```
FT   misc_feature    1. .7
FT                   /*tag=  a
FT                   /note= "deoxyribonucleotides."
FT   misc_feature    8. .11
FT                   /*tag=  b
FT                   /note= "ribonucleotides."
FT   misc_feature    12. .18
FT                   /*tag=  c
FT                   /note= "deoxyribonucleotides."
XX
PN   WO8910415-A.
XX
PD   02-NOV-1989.
XX
PF   29-APR-1988;    88US-00187814.
XX
PR   29-APR-1988;    88US-00187814.
XX
PA   (MEIO-) MEIOGENICS INC.
XX
PI   Duck P,  Bender R;
XX
DR   WPI; 1989-339977/46.
XX
PT   Detecting target nucleic acid molecules - using excess complementary
PT   nucleic acid probes and nicking to complete a cycling sequence.
XX
PS   Disclosure; Page 25; 34pp; English.
XX
CC   Probe #300 is used by reacting it in excess with a target nucleic acid;
CC   nicking hybridised probe at least once within a predetermined sequence to
CC   form 2 or more probe fragments hybridised to the target sequence, which
CC   results in the probe fragments becoming hybridised to another probe; and
CC   identifying probe fragments, so detecting the target sequence. The probe
CC   can react with target sequence to complete a cycling sequence. Using this
CC   system, sensitivity of 10 exp. -19 to 10 exp. -20 molecules of target can
CC   be obtd. The probe is cleavable at the ribonucleotides by a ds RNase, eg
CC   RNase H or ExoIII. (Updated on 31-OCT-2002 to add missing OS field.)
CC   (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ   Sequence 18 BP; 0 A; 4 C; 0 G; 14 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTT 2172
              ||||||||| |||||||||
Db          1 TTTTTTTCCCCTTTTTTT 18


RESULT 2366
AAQ20109/c
ID   AAQ20109 standard; DNA; 18 BP.
XX
AC   AAQ20109;
XX
DT   01-APR-1992  (first entry)
XX
DE   Cross-linking oligomer 943 to target human TNF Receptor mRNA.
XX
KW   deoxyribonucleic acid; major groove; ethanoamino group;
KW   tumour necrosis factor; receptor; messenger RNA; aziridinylcytosine;
KW   cross-linking group; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   5
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "N-methyl-8-oxo-2'-deoxyadenine"
FT   modified_base   18
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "N4N4-ethanocytosine"
XX
PN   WO9118997-A.
XX
PD   12-DEC-1991.
XX
PF   25-MAY-1990;    90US-00529346.
XX
PR   25-MAY-1990;    90US-00529346.
PR   14-JAN-1991;    91US-00640654.
XX
PA   (GILE-) GILEAD SCIE INC.
XX
PI   Matteucci MD,  Krawczyk S;
XX
DR   WPI; 1992-007480/01.
XX
PT   New sequence-specific non-photo-activated crosslinking agents - bind to
PT   the major groove of duplex DNA and are esp. useful for treating latent
PT   infections e.g. HIV.
XX
PS   Example 4; Page 27; 42pp; English.
XX
CC   The oligomer was designed to target human TNF receptor mRNA beginning at
CC   nucleotide 2354 and to covalently cross-link to the target via the N4N4-
CC   ethanocytosine group. See also AAQ20108
XX
SQ   Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              |||||||||||| ||||
Db         18 GAAAAAAAAAAAATAAAA 1


RESULT 2367
AAQ20108/c
ID   AAQ20108 standard; DNA; 18 BP.
XX
AC   AAQ20108;
XX
DT   01-APR-1992  (first entry)
XX
DE   Cross-linking oligomer 942 to target human TNF Receptor mRNA.
XX
KW   deoxyribonucleic acid; major groove; ethanoamino group;
KW   tumour necrosis factor; receptor; messenger RNA; aziridinylcytosine;
KW   cross-linking group; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   5
FT                   /*tag=  a
FT                   /mod_base= m5c
FT   modified_base   18
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "N4N4-ethanocytosine"
XX
PN   WO9118997-A.
XX
PD   12-DEC-1991.
XX
PF   25-MAY-1990;    90US-00529346.
XX
PR   25-MAY-1990;    90US-00529346.
PR   14-JAN-1991;    91US-00640654.
```

```
XX
PA   (GILE-) GILEAD SCIE INC.
XX
PI   Matteucci MD,  Krawczyk S;
XX
DR   WPI; 1992-007480/01.
XX
PT   New sequence-specific non-photo-activated crosslinking agents - bind to
PT   the major groove of duplex DNA and are esp. useful for treating latent
PT   infections e.g. HIV.
XX
PS   Example 4; Page 27; 42pp; English.
XX
CC   The oligomer was designed to target human TNF receptor mRNA beginning at
CC   nucleotide 2354 and to covalently cross-link to the target via the N4N4-
CC   ethanocytosine group. See also AAQ20109
XX
SQ   Sequence 18 BP; 0 A; 2 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||||||||||| ||||
Db         18 GAAAAAAAAAAAAGAAAA 1


RESULT 2368
AAQ30446
ID   AAQ30446 standard; DNA; 18 BP.
XX
AC   AAQ30446;
XX
DT   25-MAR-2003  (revised)
DT   07-DEC-1992  (first entry)
XX
DE   Oligomer TNFR941 for forming triplex with HUMNFR target duplex.
XX
KW   Human tumour necrosis factor receptor mRNA; AIDS; modified; HIV; RSV;
KW   HPV; malignancy; hepatitis; inflammation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   5
FT                   /*tag=  a
FT                   /mod_base= m5c
FT   modified_base   18
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
XX
PN   WO9209705-A1.
XX
PD   11-JUN-1992.
XX
PF   25-NOV-1991;   91WO-US008811.
XX
PR   23-NOV-1990;   90US-00617907.
PR   18-JAN-1991;   91US-00643382.
PR   08-APR-1991;   91US-00683420.
PR   17-APR-1991;   91US-00686544.
PR   17-APR-1991;   91US-00686546.
PR   17-APR-1991;   91US-00686547.
PR   27-SEP-1991;   91US-00766733.
XX
PA   (GILE-) GILEAD SCI INC.
XX
PI   Froehler B,  Krawczyk S,  Matteucci MD,  Milligan J;
XX
DR   WPI; 1992-217083/26.
XX
PT   New oligomers contg. modified bases - which form a triplex with G-C
PT   doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
PT   herpes malignancy and inflammation.
XX
PS   Claim 12; Page 72; 77pp; English.
XX
CC   The synthetic oligomer is capable of forming a triplex at physiological
CC   pH with a purine rich target sequence by coupling into the major groove
CC   of the duplex. The specific target sequence of this oligomer is the human
CC   tumour necrosis factor receptor mRNA beginning at nucleotide 2354 contg.
CC   a purine rich sequence concd. on one strand of the duplex. The oligomer,
CC   and others like it are useful in diagnosis and therapy of diseases
CC   characterised by specific DNA duplex targets, e.g. HPV, HER, HIV,
CC   hepatitis B, herpes, malignant tumours and inflammation. The triple
CC   helices form under mild conditions thus assays may be carried out without
CC   subjecting the test specimen to harsh conditions. See also AAQ25452-25501
CC   and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN field.) (Updated
CC   on 25-MAR-2003 to correct PD field.)
XX
SQ   Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTA 2187
              |||| ||||||||||||||
Db          1 TTTTCTTTTTTTTTTTA 18


RESULT 2369
AAQ25501/c
ID   AAQ25501 standard; DNA; 18 BP.
XX
AC   AAQ25501;
XX
DT   25-MAR-2003  (revised)
DT   07-DEC-1992  (first entry)
XX
DE   Purine rich HUMNFR target duplex sequence.
XX
KW   Target; human tumour necrosis factor receptor mRNA; AIDS; triplex; HIV;
KW   hepatitis; malignancy; inflammation; ds.
XX
OS   Synthetic.
XX
PN   WO9209705-A1.
XX
PD   11-JUN-1992.
XX
PF   25-NOV-1991;   91WO-US008811.
XX
PR   23-NOV-1990;   90US-00617907.
PR   18-JAN-1991;   91US-00643382.
PR   08-APR-1991;   91US-00683420.
PR   17-APR-1991;   91US-00686544.
PR   17-APR-1991;   91US-00686546.
PR   17-APR-1991;   91US-00686547.
PR   27-SEP-1991;   91US-00766733.
XX
PA   (GILE-) GILEAD SCI INC.
XX
PI   Froehler B,  Krawczyk S,  Matteucci MD,  Milligan J;
XX
DR   WPI; 1992-217083/26.
XX
PT   New oligomers contg. modified bases - which form a triplex with G-C
PT   doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
PT   herpes malignancy and inflammation.
XX
PS   Claim 11; Page 64; 77pp; English.
XX
CC   The sequence depicts a HUMNFR (tumour necrosis factor receptor) mRNA
```

```
CC   sequence beginning at nucleotide 2354. The sequence is a viral duplex
CC   sequence contg. a purine-rich region concentrated on one chain of the
CC   duplex. The sequence may be prepd. by standard DNA synthesis. The HUMNFR
CC   duplex sequence is used as a target for novel oligomers which are capable
CC   of forming a triplex at physiological pH by coupling into the major
CC   groove of the DNA duplex. Three such oligomers TNFR 941-32 are capable of
CC   forming a triplex with this sequence. The oligomers are used in the
CC   treatment of inflammation. Similar oligomers may be used to target viral
CC   DNA duplexes specific for HIV, herpes and other viruses. The triple
CC   helices form under mild conditions thus assays may be carried out without
CC   subjecting the test specimen to harsh conditions. The oligomer is able to
CC   inhibit gene expression, as verified by in vitro systems. See also
CC   AAQ25452-25500 and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN
CC   field.)
XX
SQ   Sequence 18 BP; 16 A; 0 C; 2 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTT 2182
              ||||||||||||| ||||
Db         18 CTTTTTTTTTTTTCTTTT 1
```

```
RESULT 2370
AAQ30448/c
ID   AAQ30448 standard; DNA; 18 BP.
XX
AC   AAQ30448;
XX
DT   25-MAR-2003  (revised)
DT   07-DEC-1992  (first entry)
XX
DE   Oligomer TNFR943 for forming triplex with HUMNFR target duplex.
XX
KW   Human tumour necrosis factor receptor mRNA; AIDS; modified; HIV; RSV;
KW   HPV; malignancy; hepatitis; inflammation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    5
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "N6 methyl-8-oxo-2' deoxyadenine"
FT   modified_base    18
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "OTHER= N4 N4 ethanocytosine"
XX
PN   WO9209705-A1.
XX
PD   11-JUN-1992.
XX
PF   25-NOV-1991;   91WO-US008811.
XX
PR   23-NOV-1990;   90US-00617907.
PR   18-JAN-1991;   91US-00643382.
PR   08-APR-1991;   91US-00683420.
PR   17-APR-1991;   91US-00686544.
PR   17-APR-1991;   91US-00686546.
PR   17-APR-1991;   91US-00686547.
PR   27-SEP-1991;   91US-00766733.
XX
PA   (GILE-) GILEAD SCI INC.
XX
PI   Froehler B,  Krawczyk S,  Matteucci MD,  Milligan J;
XX
DR   WPI; 1992-217083/26.
XX
PT   New oligomers contg. modified bases - which form a triplex with G-C
PT   doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
PT   herpes malignancy and inflammation.
XX
PS   Claim 12; Page 72; 77pp; English.
XX
CC   The synthetic oligomer is capable of forming a triplex at physiological
CC   pH with a purine rich target sequence by coupling into the major groove
CC   of the duplex. The specific target sequence of this oligomer is the human
CC   tumour necrosis factor receptor mRNA beginning at nucleotide 2354 contg.
CC   a purine rich sequence concd. on one strand of the duplex. The oligomer,
CC   and others like it are useful in diagnosis and therapy of diseases
CC   characterised by specific DNA duplex targets, e.g. HPV, HER, HIV,
CC   hepatitis B, herpes, malignant tumours and inflammation. The triple
CC   helices form under mild conditions thus assays may be carried out without
CC   subjecting the test specimen to harsh conditions. See also AAQ25452-25501
CC   and AAQ30226-447. (Updated on 25-MAR-2003 to correct PN field.) (Updated
CC   on 25-MAR-2003 to correct PD field.)
XX
SQ   Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2802
              ||||||||||||| ||||
Db         18 GAAAAAAAAAAAATAAAA 1
```

```
RESULT 2371
AAQ30447/c
ID   AAQ30447 standard; DNA; 18 BP.
XX
AC   AAQ30447;
XX
DT   25-MAR-2003  (revised)
DT   07-DEC-1992  (first entry)
XX
DE   Oligomer TNFR942 for forming triplex with HUMNFR target duplex.
XX
KW   Human tumour necrosis factor receptor mRNA; AIDS; modified; HIV; RSV;
KW   HPV; malignancy; hepatitis; inflammation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    5
FT                    /*tag=  a
FT                    /mod_base= m5c
FT   modified_base    18
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "OTHER= N4 N4 ethanocytosine"
XX
PN   WO9209705-A1.
XX
PD   11-JUN-1992.
XX
PF   25-NOV-1991;   91WO-US008811.
XX
PR   23-NOV-1990;   90US-00617907.
PR   18-JAN-1991;   91US-00643382.
PR   08-APR-1991;   91US-00683420.
PR   17-APR-1991;   91US-00686544.
PR   17-APR-1991;   91US-00686546.
PR   17-APR-1991;   91US-00686547.
PR   27-SEP-1991;   91US-00766733.
XX
PA   (GILE-) GILEAD SCI INC.
XX
PI   Froehler B,  Krawczyk S,  Matteucci MD,  Milligan J;
XX
DR   WPI; 1992-217083/26.
```

```
XX
PT   New oligomers contg. modified bases - which form a triplex with G-C
PT   doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
PT   herpes malignancy and inflammation.
XX
PS   Claim 12; Page 72; 77pp; English.
XX
CC   The synthetic oligomer is capable of forming a triplex at physiological
CC   pH with a purine rich target sequence by coupling into the major groove
CC   of the duplex. The specific target sequence of this oligomer is the human
CC   tumour necrosis factor receptor mRNA beginning at nucleotide 2354 contg.
CC   a purine rich sequence concd. on one strand of the duplex. The oligomer,
CC   and others like it are useful in diagnosis and therapy of diseases
CC   characterised by specific DNA duplex targets, e.g. HPV, HER, HIV,
CC   hepatitis B, herpes, malignant tumours and inflammation. The triple
CC   helices form under mild conditions thus assays may be carried out without
CC   subjecting the test specimen to harsh conditions. See also AAQ25452-25501
CC   and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN field.) (Updated
CC   on 25-MAR-2003 to correct PD field.)
XX
SQ   Sequence 18 BP; 0 A; 2 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2802
              ||||||||||||| ||||
Db         18 GAAAAAAAAAAAAGAAAA 1


RESULT 2372
AAF75596/c
ID   AAF75596 standard; DNA; 18 BP.
XX
AC   AAF75596;
XX
DT   10-MAY-2001  (first entry)
XX
DE   Binary encoded sequence tag method anchored primer #1.
XX
KW   Binary encoded sequence tag; BEST; nucleic acid analysis;
KW   gene expression; adaptor; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO200112855-A2.
XX
PD   22-FEB-2001.
XX
PF   11-AUG-2000; 2000WO-US022164.
XX
PR   13-AUG-1999;   99US-0148870P.
PR   06-APR-2000; 2000US-00544713.
XX
PA   (UYYA ) UNIV YALE.
XX
PI   Kaufman JC,  Roth ME,  Lizardi PM,  Feng L,  Latimer DR;
XX
DR   WPI; 2001-202878/20.
XX
PT   Producing binary sequence tags, useful for analyzing nucleic acid
PT   sequence tags, gene expression or gene-expression patterns, involves
PT   generating nucleic acid fragments, which are mixed with offset adaptors
PT   and adaptor-indexers.
XX
PS   Disclosure; Page 100; 101pp; English.
XX
CC   The present invention describes a method of producing binary sequence
CC   tags from nucleic acid fragments in a sample, involving incubating the
CC   sample with cleaving reagents, mixing offset adaptors with the sample,
CC   incubating with more cleaving reagents and mixing the sample with adaptor
CC   -indexers where the adaptors are coupled to binary sequence tags. The
CC   method is useful in sequence analysis, including analysis and comparison
CC   of gene expression, nucleic acid samples and genomes
XX
SQ   Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2802
              | |||||||||||||||
Db         18 GCAAAAAAAAAAAAAAA 1


RESULT 2373
AAF75597
ID   AAF75597 standard; DNA; 18 BP.
XX
AC   AAF75597;
XX
DT   10-MAY-2001  (first entry)
XX
DE   Binary encoded sequence tag method anchored primer #2.
XX
KW   Binary encoded sequence tag; BEST; nucleic acid analysis;
KW   gene expression; adaptor; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO200112855-A2.
XX
PD   22-FEB-2001.
XX
PF   11-AUG-2000; 2000WO-US022164.
XX
PR   13-AUG-1999;   99US-0148870P.
PR   06-APR-2000; 2000US-00544713.
XX
PA   (UYYA ) UNIV YALE.
XX
PI   Kaufman JC,  Roth ME,  Lizardi PM,  Feng L,  Latimer DR;
XX
DR   WPI; 2001-202878/20.
XX
PT   Producing binary sequence tags, useful for analyzing nucleic acid
PT   sequence tags, gene expression or gene-expression patterns, involves
PT   generating nucleic acid fragments, which are mixed with offset adaptors
PT   and adaptor-indexers.
XX
PS   Disclosure; Page 100; 101pp; English.
XX
CC   The present invention describes a method of producing binary sequence
CC   tags from nucleic acid fragments in a sample, involving incubating the
CC   sample with cleaving reagents, mixing offset adaptors with the sample,
CC   incubating with more cleaving reagents and mixing the sample with adaptor
CC   -indexers where the adaptors are coupled to binary sequence tags. The
CC   method is useful in sequence analysis, including analysis and comparison
CC   of gene expression, nucleic acid samples and genomes
XX
SQ   Sequence 18 BP; 0 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTGT 18


RESULT 2374
AAF75597/c
ID   AAF75597 standard; DNA; 18 BP.
```

XX
AC AAF75597;
XX
DT 10-MAY-2001 (first entry)
XX
DE Binary encoded sequence tag method anchored primer #2.
XX
KW Binary encoded sequence tag; BEST; nucleic acid analysis;
KW gene expression; adaptor; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200112855-A2.
XX
PD 22-FEB-2001.
XX
PF 11-AUG-2000; 2000WO-US022164.
XX
PR 13-AUG-1999; 99US-0148870P.
PR 06-APR-2000; 2000US-00544713.
XX
PA (UYYA) UNIV YALE.
XX
PI Kaufman JC, Roth ME, Lizardi PM, Feng L, Latimer DR;
XX
DR WPI; 2001-202878/20.
XX
PT Producing binary sequence tags, useful for analyzing nucleic acid
PT sequence tags, gene expression or gene-expression patterns, involves
PT generating nucleic acid fragments, which are mixed with offset adaptors
PT and adaptor-indexers.
XX
PS Disclosure; Page 100; 101pp; English.
XX
CC The present invention describes a method of producing binary sequence
CC tags from nucleic acid fragments in a sample, involving incubating the
CC sample with cleaving reagents, mixing offset adaptors with the sample,
CC incubating with more cleaving reagents and mixing the sample with adaptor
CC -indexers where the adaptors are coupled to binary sequence tags. The
CC method is useful in sequence analysis, including analysis and comparison
CC of gene expression, nucleic acid samples and genomes
XX
SQ Sequence 18 BP; 0 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAA 2803
| ||||||||||||||||
Db 18 ACAAAAAAAAAAAAAAAA 1

RESULT 2375
AAF99943
ID AAF99943 standard; DNA; 20 BP.
XX
AC AAF99943;
XX
DT 12-JUL-2001 (first entry)
XX
DE Synthetic oligonucleotide #9.
XX
KW Oligonucleotide purification; liquid chromatography;
KW hydrophobic protective group; deprotection; ds.
XX
OS Synthetic.
XX
PN JP2000342265-A.
XX
PD 12-DEC-2000.
XX
PF 02-JUN-1999; 99JP-00154974.
XX
PR 02-JUN-1999; 99JP-00154974.
XX
PA (TOAG) TOA GOSEI CHEM IND LTD.
XX
DR WPI; 2001-268251/28.
XX
PT A process for purification of oligonucleotides using liquid
PT chromatography.
XX
PS Example 1; Page 4; 13pp; Japanese.
XX
CC The present sequence is an oligonucleotide provided in a specification
CC relating to the simplified purification of oligonucleotides by liquid
CC chromatography. The process comprises: (a) pouring oligonucleotides
CC protected with a hydrophobic group and oligonucleotide with no protective
CC group into a liquid chromatography column packed with an acid and alkali
CC resistant packing agent, such as polystyrene resin; (b) pouring a mixed
CC developing solvent composed of a buffer made from a volatile salt and a
CC water soluble organic solvent at a suitable concentration gradient into
CC the column; (c) pouring an acid, particularly 6-16 v/v% acetic acid, into
CC the column to deprotect the oligonucleotides protected with the
CC hydrophobic group; (d) pouring a mixed developing solvent composed of a
CC buffer made from a volatile salt, particularly 0.05-0.5 N aqueous
CC ammonium hydrogencarbonate solution adjusted at pH 8-10, and a water
CC soluble organic solvent at a suitable concentration gradient to elute the
CC deprotected oligonucleotides; and (e) removal of the solvent and the salt
CC from the eluted oligonucleotides
XX
SQ Sequence 20 BP; 17 A; 1 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAA 2803
||||||||| ||||||||
Db 2 AAAAAAAAAGAAAAAAAA 19

RESULT 2376
ABZ91658
ID ABZ91658 standard; DNA; 20 BP.
XX
AC ABZ91658;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.

XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 6900; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 15 A; 1 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2783 TTGAAAAAAAAAAAAAAA 2800
|| ||||||||||||||||
Db 3 TTTAAAAAAAAAAAAAAA 20

RESULT 2377
ABZ89872
ID ABZ89872 standard; DNA; 20 BP.
XX
AC ABZ89872;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.

XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 5114; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 16 A; 2 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2784 TGAAAAAAAAAAAAAAAA 2801
| ||||||||||||||||
Db 2 TCAAAAAAAAAAAAAAAA 19

RESULT 2378
AAV12302
ID AAV12302 standard; DNA; 20 BP.
XX
AC AAV12302;
XX
DT 17-JUN-1998 (first entry)
XX
DE Ribonucleotide reductase R1 3'UTR fragment SEQ ID NO:46.
XX
KW Ribonucleotide reductase R1; 3'-untranslated region; 3'UTR; tumour;
KW housekeeping gene; identification; modulator; metastasis; neoplastic;
KW papilloma; atherosclerosis; angiogenesis; viral infection; ss.
XX
OS Homo sapiens.
XX
PN WO9800532-A2.
XX
PD 08-JAN-1998.
XX
PF 30-JUN-1997; 97WO-CA000454.
XX
PR 01-JUL-1996; 96US-0021152P.
XX
PA (WRIG/) WRIGHT J A.
PA (YOUN/) YOUNG A H.
XX
PI Wright JA, Young AH;
XX
DR WPI; 1998-086958/08.
XX
PT New oligo-nucleotide(s) complementary to untranslated regions of
PT housekeeping genes - are useful in, e.g. identifying modulators of tumour

```
PT   growth/metastasis and inhibiting growth of neoplastic cells.
XX
PS   Claim 4; Page 29; 64pp; English.
XX
CC   The present sequence represents a 3'-untranslated region (3'UTR) fragment
CC   of ribonucleotide reductase R1. The present invention describes: (1)
CC   oligonucleotides (ON) comprising at least 7 consecutive nucleotides (nt)
CC   or their analogues of a UTR of a housekeeping gene; (2) antisense ON
CC   (AON) complementary to ON; (3) ribozymes (Rb) complementary or homologous
CC   to ON, and able to cleave it; (4) DNA sequence encoding ON, OAN and Rb;
CC   (5) an antibody (Ab) that binds to ON, OAN and Rb; (6) a nt probe ntP
CC   that hybridise to ON, OAN and Rb. ON, AON, Rb and Ab are used to modulate
CC   (especially inhibit) growth of tumour cells (especially neoplastic cells)
CC   and to reduce their capacity for metastasis. The above may also be used
CC   to treat benign proliferative disorders e.g. papillomas, atherosclerosis,
CC   angiogenesis and viral infections, e.g. human immunodeficiency virus,
CC   hepatitis or herpes. ON may further be used: (i) to identify modulators
CC   of tumour growth/metastasis; (ii) to identify compounds (especially
CC   potential antitumour agents) that inhibit or enhance interaction between
CC   ON and its binding substances; (iii) as probes for detecting related
CC   sequences, and (iv) to generate Ab, used for detection and quantification
CC   of UTR especially for monitoring progress of cancer therapy. SON inhibit
CC   tumorigenicity of neoplastic cells, particularly where these are
CC   resistant to hydroxyurea
XX
SQ   Sequence 20 BP; 17 A; 1 C; 2 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 20;
  Best Local Similarity   94.4%;  Pred. No. 1.8e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2803
              ||||||| ||||||||||
Db          1 AAAAAAAGAAAAAAAAAA 18


RESULT 2379
AAX32010
ID   AAX32010 standard; DNA; 20 BP.
XX
AC   AAX32010;
XX
DT   14-JUN-1999  (first entry)
XX
DE   MSH2 gene specific primer.
XX
KW   Allele profile; diagnosis; treatment; pharmacogenetic; breast cancer;
KW   CFTR; cystic fibrosis; dystrophin; Duchenne muscular dystrophy; p53;
KW   Becker muscular dystrophy; Li-Fraumeni syndrome; neurofibromatosis;
KW   colorectal cancer; MSH2 gene; MLH1 gene; BRCA1 gene; BRCA2 gene;
KW   BAP1 gene; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO9906598-A2.
XX
PD   11-FEB-1999.
XX
PF   04-AUG-1998;   98WO-US016574.
XX
PR   04-AUG-1997;   97US-00905772.
PR   22-MAY-1998;   98US-00084471.
XX
PA   (ONCO-) ONCORMED INC.
XX
PI   Murphy PD;
XX
DR   WPI; 1999-153820/13.
XX
PT   Determining common functional alleles in a population - useful in the
PT   diagnosis of disease associated with allelic heterogeneity.
XX
PS   Example 1; Page 24; 78pp; English.
XX
CC   The invention relates to methods of determining a functional allele
CC   profile of a gene in a population. Functional allele profiles comprise
CC   the commonly occurring alleles in a population, and the relative
CC   frequencies at which such alleles of a given gene occur. The methods are
CC   used to identity and determine the frequency of the functional alleles of
CC   genes which display extensive allelic heterogeneity, particularly those
CC   implicated in disease or conditions, such as the BRCA1 gene associated
CC   with breast cancer, CFTR associated with cystic fibrosis, dystrophin
CC   associated with Duchenne muscular dystrophy and Becker muscular
CC   dystrophy, and p53 associated with Li-Fraumeni syndrome. The methods can
CC   also be employed for diseases where allelic and genetic heterogeneity
CC   exist, such as breast cancer, neurofibromatosis, and hereditary non-
CC   polyposis colorectal cancer. Identification of functional alleles is
CC   necessary for identification of mutations which may be implicated in the
CC   disease. Sequences AAX32001-172 represent primers for determining the
CC   functional allele profiles of various genes. The primers are specific for
CC   genes such as MSH2 gene, MLH1 gene, BRCA1 gene, BRCA2 gene and BAP1 gene
XX
SQ   Sequence 20 BP; 2 A; 2 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 20;
  Best Local Similarity   94.4%;  Pred. No. 1.8e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTAACT 2190
              |||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTACCT 18


RESULT 2380
AAC82913
ID   AAC82913 standard; DNA; 20 BP.
XX
AC   AAC82913;
XX
DT   21-MAR-2001  (first entry)
XX
DE   Human beta-actin derived oligonucleotide #6.
XX
KW   Recognition system; screening; identification; pharmaceutical; toxin;
KW   plant protection agent; toxin; venom; carcinogen; venom; teratogen;
KW   herbicide; fungicide; pesticide; beta-actin; human; ss.
XX
OS   Homo sapiens.
XX
PN   DE19923966-A1.
XX
PD   30-NOV-2000.
XX
PF   25-MAY-1999;   99DE-01023966.
XX
PR   25-MAY-1999;   99DE-01023966.
XX
PA   (AVET ) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
XX
PI   Boekenkamp D,  Hoppe H,  Burgstaller P;
XX
DR   WPI; 2001-050938/07.
XX
PT   Recognition system, e.g. for identifying nucleic acids, comprises at
PT   least one recognition unit comprising a region with a defined structure
PT   adjacent to a region with a randomized structure.
XX
PS   Example; Fig 1; 8pp; German.
XX
CC   This invention describes a novel recognition system comprising at least 1
CC   recognition unit bound to a support, each recognition unit comprising a
CC   region A with a defined structure adjacent to a region B with a
CC   randomized structure. The recognition system is useful for screening,
CC   identifying, or characterizing at least 1 component of a sample,
CC   especially nucleic acids and/or proteins, and for screening for and/or
CC   identifying cellular or synthetic binding partners, preferably proteins,
```

```
CC   peptides, nucleic acids, chemical agents, preferably organic compounds,
CC   pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
CC   teratogens, herbicides, fungicides or pesticides
XX
SQ   Sequence 20 BP; 2 A; 0 C; 2 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 20;
  Best Local Similarity   94.4%;  Pred. No. 1.8e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAACTT 2191
              ||||||||||||||| ||
Db          1 TTTTTTTTTTTTTAAGTT 18


RESULT 2381
ABZ72190
ID   ABZ72190 standard; DNA; 20 BP.
XX
AC   ABZ72190;
XX
DT   03-APR-2003  (first entry)
XX
DE   Gene 216 SSCP sequencing primer SEQ ID NO 162.
XX
KW   Human; Gene 216; chromosome 20p13-p12; antiasthmatic; anorectic;
KW   antiinflammatory; gastrointestinal; gene therapy; vaccine; asthma;
KW   obesity; inflammatory bowel disease; primer; ss.
XX
OS   Synthetic.
XX
PN   WO200178894-A2.
XX
PD   25-OCT-2001.
XX
PF   13-APR-2001; 2001WO-US012245.
XX
PR   13-APR-2000; 2000US-00548797.
XX
PA   (GENO-) GENOME THERAPEUTICS CORP.
XX
PI   Keith T;
XX
DR   WPI; 2001-639428/73.
XX
PT   Isolated genes (Gene 216) from human chromosome 20p13-p12 and the
PT   proteins they encode, useful for the prevention, diagnosis and treatment
PT   of asthma, obesity and inflammatory bowel disease.
XX
PS   Example 10; Page 150; 520pp; English.
XX
CC   The invention relates to isolated genes (Gene 216) from human chromosome
CC   20p13-p12 and the proteins they encode. The nucleic acids and proteins
CC   may be used in the prevention, diagnosis and treatment of diseases
CC   associated with inappropriate Gene 216 expression. For example, the
CC   nucleic acids (or vectors) and proteins may be used to treat disorders
CC   associated with decreased expression by rectifying mutations or deletions
CC   in a patient's genome that affect the activity of gene 216 by expressing
CC   inactive proteins or to supplement the patients own production of Gene
CC   216 proteins. Additionally, the nucleic acids may be used to produce the
CC   secreted Gene 216 protein, by inserting the nucleic acids into a host
CC   cell and culturing the cell to express the protein. The nucleic acids and
CC   complementary sequences may also be used as DNA probes in diagnostic
CC   assays to detect and quantitate the presence of similar nucleic acid
CC   sequences in samples and therefore which patients may be in need of
CC   restorative therapy. The Gene 216 protein may also be used as antigens in
CC   the production of antibodies against Gene 216 and in assays to identify
CC   modulators of Gene 216 expression and activity. The anti-Gene 216
CC   antibodies and antagonists may also be used to down regulate expression
CC   and activity. The anti-Gene 216 antibodies may also be used as diagnostic
CC   agents for detecting the presence of Gene 216 proteins in samples (e.g.
CC   by enzyme linked immunosorbant assay or ELISA). Disorders that may be
CC   prevented, diagnosed and/or treated by the above methods include, for
CC   example asthma, obesity and inflammatory bowel disease. The present
CC   sequence is that of a Gene 216 related primer used in examples of the
CC   invention. The primers are used in the physical mapping of the gene
CC   (ABZ72067-ABZ72088), polymorphism identifiction using single strand
CC   conformational polymorphism (SSCP) analysis (ABZ72091-ABZ72184),
CC   sequencing (ABZ72185-ABZ72268) and genotyping (ABZ72317-ABZ72362)
XX
SQ   Sequence 20 BP; 7 A; 6 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 20;
  Best Local Similarity   94.4%;  Pred. No. 1.8e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1558 CAGGACTGCAAAAATCCT 1575
              |||||||||||| |||||
Db          1 CAGGACTGCAAACATCCT 18


RESULT 2382
ABA05916
ID   ABA05916 standard; DNA; 20 BP.
XX
AC   ABA05916;
XX
DT   05-MAR-2002  (first entry)
XX
DE   Hepatitis B virus diagnostic PCR primer SEQ ID NO 6.
XX
KW   Hepatitis B virus; HBV; infection; hepatocellular carcinoma; diagnosis;
KW   PCR primer; ss.
XX
OS   Hepatitis B virus.
XX
PN   EP1152063-A1.
XX
PD   07-NOV-2001.
XX
PF   03-MAY-2000; 2000EP-00109436.
XX
PR   03-MAY-2000; 2000EP-00109436.
XX
PA   (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI   Schroeder KH,  Koike K;
XX
DR   WPI; 2002-068256/10.
XX
PT   Diagnosing hepatitis B virus (HBV) infection stages and determining the
PT   risk for hepatocellular carcinoma, comprises identifying full length HBV
PT   transcripts and truncated HBV transcripts in a serum sample.
XX
PS   Example 1; Page 6; 25pp; English.
XX
CC   The invention relates to diagnosis of hepatitis B virus (HBV) infection
CC   stages comprising identification of full length HBV transcripts (I) and
CC   truncated HBV transcripts (II) in a serum sample, where the ratio of I:II
CC   is indicative of a particular infection stage. The method is useful for
CC   diagnosing HBV infection stages and determining the risk for developing
CC   hepatocellular carcinoma. The present sequence is that of a HBV
CC   diagnostic PCR primer, useful for the invention
XX
SQ   Sequence 20 BP; 2 A; 1 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 20;
  Best Local Similarity   94.4%;  Pred. No. 1.8e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTAA 2188
              |||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTGAA 18


RESULT 2383
```

ABA05916/c
ID ABA05916 standard; DNA; 20 BP.
XX
AC ABA05916;
XX
DT 05-MAR-2002 (first entry)
XX
DE Hepatitis B virus diagnostic PCR primer SEQ ID NO 6.
XX
KW Hepatitis B virus; HBV; infection; hepatocellular carcinoma; diagnosis;
KW PCR primer; ss.
XX
OS Hepatitis B virus.
XX
PN EP1152063-A1.
XX
PD 07-NOV-2001.
XX
PF 03-MAY-2000; 2000EP-00109436.
XX
PR 03-MAY-2000; 2000EP-00109436.
XX
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI Schroeder KH, Koike K;
XX
DR WPI; 2002-068256/10.
XX
PT Diagnosing hepatitis B virus (HBV) infection stages and determining the
PT risk for hepatocellular carcinoma, comprises identifying full length HBV
PT transcripts and truncated HBV transcripts in a serum sample.
XX
PS Example 1; Page 6; 25pp; English.
XX
CC The invention relates to diagnosis of hepatitis B virus (HBV) infection
CC stages comprising identification of full length HBV transcripts (I) and
CC truncated HBV transcripts (II) in a serum sample, where the ratio of I:II
CC is indicative of a particular infection stage. The method is useful for
CC diagnosing HBV infection stages and determining the risk for developing
CC hepatocellular carcinoma. The present sequence is that of a HBV
CC diagnostic PCR primer, useful for the invention
XX
SQ Sequence 20 BP; 2 A; 1 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2783 TTGAAAAAAAAAAAAAAA 2800
|| ||||||||||||||||
Db 18 TTCAAAAAAAAAAAAAAA 1

RESULT 2384
ABZ87902
ID ABZ87902 standard; DNA; 20 BP.
XX
AC ABZ87902;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 3144; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 3 A; 5 C; 10 G; 2 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 551 TCCGGGCTGGAGGCGGGC 568
|||||||||||||| ||||
Db 3 TCCGGGCTGGAGGAGGGC 20

RESULT 2385
ABX75043
ID ABX75043 standard; DNA; 20 BP.
XX
AC ABX75043;
XX
DT 25-MAR-2003 (first entry)
XX
DE Human gene 216 polymorphism detection PCR primer #100.
XX
KW Human; mouse; ss; primer; gene 216; antiasthmatic; antiinflammatory;
KW anorectic; chromosome 20p13-p12; single nucleotide polymorphism; SNP;
KW gene therapy; respiratory disease; asthma; obesity; PCR;
KW bronchial hyper-responsiveness; chronic obstructive pulmonary disease;
KW adult respiratory distress syndrome; inflammatory bowel syndrome.
XX
OS Homo sapiens.
XX
PN WO200283077-A2.
XX

```
PD   24-OCT-2002.
XX
PF   15-APR-2002; 2002WO-US012063.
XX
PR   13-APR-2001; 2001US-00834597.
PR   13-APR-2001; 2001WO-US012245.
XX
PA   (SCHE ) SCHERING CORP.
PA   (GENO-) GENOME THERAPEUTICS CORP.
XX
PI   Keith T,  Little RD,  Van Eerdewegh P,  Dupuis J,  Del Mastro RG;
PI   Simon J,  Allen K,  Pandit S;
XX
DR   WPI; 2003-092960/08.
XX
PT   New isolated gene 216 nucleic acids, useful for diagnosing, preventing or
PT   treating a disorder, such as asthma, bronchial hyper-responsiveness,
PT   chronic obstructive pulmonary disease, obesity or inflammatory bowel
PT   syndrome.
XX
PS   Example 10; Page 156; 650pp; English.
XX
CC   This invention relates to a novel isolated nucleic acid, gene 216,
CC   identified from human chromosome 20p13-p12. The invention also discloses
CC   regions of the 216 gene that contain single nucleotide polymorphisms
CC   (SNP's) which may be used as markers for disease susceptibility or
CC   severity. The nucleotides of the invention may have antiasthmatic,
CC   antiinflammatory or anorectic activities and may be used in gene therapy.
CC   The nucleic acids, antibodies or its fragments are useful for diagnosing,
CC   preventing or treating a disorder, such as respiratory diseases (e.g.
CC   asthma, bronchial hyper-responsiveness, chronic obstructive pulmonary
CC   disease or adult respiratory distress syndrome), obesity, or inflammatory
CC   bowel syndrome. The nucleic acids are also useful for identifying
CC   increased susceptibility of a subject to the disorders mentioned. The
CC   nucleic acids can also be used as primers and templates for the
CC   recombinant production of disorder-associated peptides or polypeptides,
CC   for chromosome and gene mapping, or for tissue distribution studies. The
CC   present sequence represents a gene 216 specific PCR primer used in the
CC   scope of the invention
XX
SQ   Sequence 20 BP; 7 A; 6 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 20;
  Best Local Similarity   94.4%;  Pred. No. 1.8e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1558 CAGGACTGCAAAAATCCT 1575
              ||||||||||| |||||
Db          1 CAGGACTGCAAACATCCT 18


RESULT 2386
ADA45251
ID   ADA45251 standard; DNA; 20 BP.
XX
AC   ADA45251;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MSH2 gene PCR primer #10.
XX
KW   Functional allele profile; genetic inheritance; haplotype; population;
KW   disease; pharmacogenetic application; selective pressure; human; MSH2;
KW   MLH1; BRCA1; BRCA2; PTEN; BAP1; BARD1; p53; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   US2003096236-A1.
XX
PD   22-MAY-2003.
XX
PF   08-AUG-2001; 2001US-00923327.
XX
PR   12-FEB-1996;   96US-00598591.
PR   12-FEB-1997;   97US-00798691.
PR   04-AUG-1997;   97US-00905772.
PR   22-MAY-1998;   98US-00084471.
PR   04-AUG-1998;   98US-00129134.
PR   14-MAR-2000; 2000US-00524794.
XX
PA   (ONCO-) ONCORMED INC.
XX
PI   Murphy PD;
XX
DR   WPI; 2003-576875/54.
XX
PT   Determining a functional allele profile of a gene in a population by
PT   identifying the nucleotide sequence of a gene of genomic DNA from each of
PT   the individuals with a family history of functional alleles of the gene
PT   of interest.
XX
PS   Example 1; Page 9; 28pp; English.
XX
CC   The present invention relates to a method for determining a functional
CC   allele profile of a gene in a population. The method comprises
CC   identifying the nucleotide sequence of a gene of interest out of genomic
CC   DNA from each of a population of individuals identified as having a
CC   family history which indicates inheritance of functional alleles of the
CC   gene of interest, and rank ordering the frequency of occurrence of each
CC   haplotype, where the identity of the alleles containing each haplotype
CC   and the determination of their relative frequencies constitutes the
CC   functional allele profile of the gene of interest in the population. The
CC   method is useful for determining functional allele profiles which are
CC   useful in the treatment and diagnosis of diseases, for genetic and
CC   pharmacogenetic applications, and for evaluating the degree to which the
CC   gene(s) are under selective pressure. The present sequence represents a
CC   PCR primer used in the method of the invention.
XX
SQ   Sequence 20 BP; 2 A; 2 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 20;
  Best Local Similarity   94.4%;  Pred. No. 1.8e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTAACT 2190
              |||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTACCT 18


RESULT 2387
AAZ26563
ID   AAZ26563 standard; DNA; 21 BP.
XX
AC   AAZ26563;
XX
DT   30-NOV-1999  (first entry)
XX
DE   Human polymorphic region 752.
XX
KW   Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW   cell viability; loss of heterozygosity; precancerous condition; ASI;
KW   allele specific inhibitor; somatic cell; diagnosis; prevention;
KW   atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW   dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW   graft versus host disease; malignant cell removal; bone marrow; ss.
XX
OS   Homo sapiens.
XX
PN   WO9841648-A2.
XX
PD   24-SEP-1998.
XX
PF   19-MAR-1998;   98WO-US005419.
XX
PR   20-MAR-1997;   97US-0041057P.
XX
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```
PA   (VARI-) VARIAGENICS INC.
XX
PI   Housman D,  Ledley FD,  Stanton VP;
XX
DR   WPI; 1998-521232/44.
XX
PT   Identifying target genes for allele-specific drugs - used for diagnosis,
PT   prevention and treatment of, e.g. cancers, atherosclerotic plaque,
PT   dysplastic lesions, endometriosis or graft versus host disease.
XX
PS   Disclosure; Fig 7; 605pp; English.
XX
CC   This invention describes a novel method for identifying an inhibitor
CC   potentially useful for treatment of cancer, where the inhibitor is active
CC   on a gene vital for cell growth or viability, and where the gene is
CC   subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC   used for preventing the development of cancer in a patient having a
CC   precancerous condition, by administering to the patient a first allele
CC   specific inhibitor (ASI) targeted to an allele of a first essential gene
CC   present in cells of the precancerous condition, where the normal somatic
CC   cells of the patient are heterozygous for the first gene, the inhibitor
CC   is active on at least one but less than all allelic forms of the gene
CC   present in a population and targets only one allelic form present in the
CC   normal somatic cells, and the first gene. The products and methods can be
CC   used in the diagnosis, prevention and treatment of LOH disorders, e.g.
CC   cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
CC   lesions, benign tumours, endometriosis, polycystic kidney disease, and
CC   graft versus host disease. The method can also be used to remove
CC   malignant cells from bone marrow transplants. AAZ25812-Z26825 represent
CC   human polymorphic sites described in the method of the invention
XX
SQ   Sequence 21 BP; 19 A; 1 C; 1 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 21;
  Best Local Similarity   94.4%;  Pred. No. 2e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2803
              ||| |||||||||||||
Db          4 AAAGAAAAAAAAAAAAA 21


RESULT 2388
AAZ26584
ID   AAZ26584 standard; DNA; 21 BP.
XX
AC   AAZ26584;
XX
DT   30-NOV-1999  (first entry)
XX
DE   Human polymorphic region 773.
XX
KW   Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW   cell viability; loss of heterozygosity; precancerous condition; ASI;
KW   allele specific inhibitor; somatic cell; diagnosis; prevention;
KW   atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW   dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW   graft versus host disease; malignant cell removal; bone marrow; ss.
XX
OS   Homo sapiens.
XX
PN   WO9841648-A2.
XX
PD   24-SEP-1998.
XX
PF   19-MAR-1998;   98WO-US005419.
XX
PR   20-MAR-1997;   97US-0041057P.
XX
PA   (VARI-) VARIAGENICS INC.
XX
PI   Housman D,  Ledley FD,  Stanton VP;
XX
DR   WPI; 1998-521232/44.
XX
PT   Identifying target genes for allele-specific drugs - used for diagnosis,
PT   prevention and treatment of, e.g. cancers, atherosclerotic plaque,
PT   dysplastic lesions, endometriosis or graft versus host disease.
XX
PS   Disclosure; Fig 7; 605pp; English.
XX
CC   This invention describes a novel method for identifying an inhibitor
CC   potentially useful for treatment of cancer, where the inhibitor is active
CC   on a gene vital for cell growth or viability, and where the gene is
CC   subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC   used for preventing the development of cancer in a patient having a
CC   precancerous condition, by administering to the patient a first allele
CC   specific inhibitor (ASI) targeted to an allele of a first essential gene
CC   present in cells of the precancerous condition, where the normal somatic
CC   cells of the patient are heterozygous for the first gene, the inhibitor
CC   is active on at least one but less than all allelic forms of the gene
CC   present in a population and targets only one allelic form present in the
CC   normal somatic cells, and the first gene. The products and methods can be
CC   used in the diagnosis, prevention and treatment of LOH disorders, e.g.
CC   cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
CC   lesions, benign tumours, endometriosis, polycystic kidney disease, and
CC   graft versus host disease. The method can also be used to remove
CC   malignant cells from bone marrow transplants. AAZ25812-Z26825 represent
CC   human polymorphic sites described in the method of the invention
XX
SQ   Sequence 21 BP; 15 A; 0 C; 1 G; 5 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 21;
  Best Local Similarity   94.4%;  Pred. No. 2e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAA 2800
              || ||||||||||||||||
Db          4 TTTAAAAAAAAAAAAAAA 21


RESULT 2389
AAZ26142
ID   AAZ26142 standard; DNA; 21 BP.
XX
AC   AAZ26142;
XX
DT   30-NOV-1999  (first entry)
XX
DE   Human polymorphic region 331.
XX
KW   Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW   cell viability; loss of heterozygosity; precancerous condition; ASI;
KW   allele specific inhibitor; somatic cell; diagnosis; prevention;
KW   atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW   dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW   graft versus host disease; malignant cell removal; bone marrow; ss.
XX
OS   Homo sapiens.
XX
PN   WO9841648-A2.
XX
PD   24-SEP-1998.
XX
PF   19-MAR-1998;   98WO-US005419.
XX
PR   20-MAR-1997;   97US-0041057P.
XX
PA   (VARI-) VARIAGENICS INC.
XX
PI   Housman D,  Ledley FD,  Stanton VP;
XX
DR   WPI; 1998-521232/44.
XX
PT   Identifying target genes for allele-specific drugs - used for diagnosis,
PT   prevention and treatment of, e.g. cancers, atherosclerotic plaque,
```

```
PT   dysplastic lesions, endometriosis or graft versus host disease.
XX
PS   Disclosure; Fig 7; 605pp; English.
XX
CC   This invention describes a novel method for identifying an inhibitor
CC   potentially useful for treatment of cancer, where the inhibitor is active
CC   on a gene vital for cell growth or viability, and where the gene is
CC   subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC   used for preventing the development of cancer in a patient having a
CC   precancerous condition, by administering to the patient a first allele
CC   specific inhibitor (ASI) targeted to an allele of a first essential gene
CC   present in cells of the precancerous condition, where the normal somatic
CC   cells of the patient are heterozygous for the first gene, the inhibitor
CC   is active on at least one but less than all allelic forms of the gene
CC   present in a population and targets only one allelic form present in the
CC   normal somatic cells, and the first gene. The products and methods can be
CC   used in the diagnosis, prevention and treatment of LOH disorders, e.g.
CC   cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
CC   lesions, benign tumours, endometriosis, polycystic kidney disease, and
CC   graft versus host disease. The method can also be used to remove
CC   malignant cells from bone marrow transplants. AAZ25812-Z26825 represent
CC   human polymorphic sites described in the method of the invention
XX
SQ   Sequence 21 BP; 17 A; 3 C; 0 G; 1 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 21;
  Best Local Similarity   94.4%;  Pred. No. 2e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2803
              ||| |||||||||||||||
Db          1 AAATAAAAAAAAAAAAA 18


RESULT 2390
AAZ26142/c
ID   AAZ26142 standard; DNA; 21 BP.
XX
AC   AAZ26142;
XX
DT   30-NOV-1999  (first entry)
XX
DE   Human polymorphic region 331.
XX
KW   Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW   cell viability; loss of heterozygosity; precancerous condition; ASI;
KW   allele specific inhibitor; somatic cell; diagnosis; prevention;
KW   atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW   dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW   graft versus host disease; malignant cell removal; bone marrow; ss.
XX
OS   Homo sapiens.
XX
PN   WO9841648-A2.
XX
PD   24-SEP-1998.
XX
PF   19-MAR-1998;   98WO-US005419.
XX
PR   20-MAR-1997;   97US-0041057P.
XX
PA   (VARI-) VARIAGENICS INC.
XX
PI   Housman D,  Ledley FD,  Stanton VP;
XX
DR   WPI; 1998-521232/44.
XX
PT   Identifying target genes for allele-specific drugs - used for diagnosis,
PT   prevention and treatment of, e.g. cancers, atherosclerotic plaque,
PT   dysplastic lesions, endometriosis or graft versus host disease.
XX
PS   Disclosure; Fig 7; 605pp; English.
XX
CC   This invention describes a novel method for identifying an inhibitor
CC   potentially useful for treatment of cancer, where the inhibitor is active
CC   on a gene vital for cell growth or viability, and where the gene is
CC   subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC   used for preventing the development of cancer in a patient having a
CC   precancerous condition, by administering to the patient a first allele
CC   specific inhibitor (ASI) targeted to an allele of a first essential gene
CC   present in cells of the precancerous condition, where the normal somatic
CC   cells of the patient are heterozygous for the first gene, the inhibitor
CC   is active on at least one but less than all allelic forms of the gene
CC   present in a population and targets only one allelic form present in the
CC   normal somatic cells, and the first gene. The products and methods can be
CC   used in the diagnosis, prevention and treatment of LOH disorders, e.g.
CC   cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
CC   lesions, benign tumours, endometriosis, polycystic kidney disease, and
CC   graft versus host disease. The method can also be used to remove
CC   malignant cells from bone marrow transplants. AAZ25812-Z26825 represent
CC   human polymorphic sites described in the method of the invention
XX
SQ   Sequence 21 BP; 17 A; 3 C; 0 G; 1 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 21;
  Best Local Similarity   94.4%;  Pred. No. 2e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2183
              ||||||||||||||| |||
Db         18 TTTTTTTTTTTTTTATTT 1


RESULT 2391
AAZ26268
ID   AAZ26268 standard; DNA; 21 BP.
XX
AC   AAZ26268;
XX
DT   30-NOV-1999  (first entry)
XX
DE   Human polymorphic region 457.
XX
KW   Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW   cell viability; loss of heterozygosity; precancerous condition; ASI;
KW   allele specific inhibitor; somatic cell; diagnosis; prevention;
KW   atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW   dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW   graft versus host disease; malignant cell removal; bone marrow; ss.
XX
OS   Homo sapiens.
XX
PN   WO9841648-A2.
XX
PD   24-SEP-1998.
XX
PF   19-MAR-1998;   98WO-US005419.
XX
PR   20-MAR-1997;   97US-0041057P.
XX
PA   (VARI-) VARIAGENICS INC.
XX
PI   Housman D,  Ledley FD,  Stanton VP;
XX
DR   WPI; 1998-521232/44.
XX
PT   Identifying target genes for allele-specific drugs - used for diagnosis,
PT   prevention and treatment of, e.g. cancers, atherosclerotic plaque,
PT   dysplastic lesions, endometriosis or graft versus host disease.
XX
PS   Disclosure; Fig 7; 605pp; English.
XX
CC   This invention describes a novel method for identifying an inhibitor
CC   potentially useful for treatment of cancer, where the inhibitor is active
CC   on a gene vital for cell growth or viability, and where the gene is
CC   subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
```

```
CC   used for preventing the development of cancer in a patient having a
CC   precancerous condition, by administering to the patient a first allele
CC   specific inhibitor (ASI) targeted to an allele of a first essential gene
CC   present in cells of the precancerous condition, where the normal somatic
CC   cells of the patient are heterozygous for the first gene, the inhibitor
CC   is active on at least one but less than all allelic forms of the gene
CC   present in a population and targets only one allelic form present in the
CC   normal somatic cells, and the first gene. The products and methods can be
CC   used in the diagnosis, prevention and treatment of LOH disorders, e.g.
CC   cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
CC   lesions, benign tumours, endometriosis, polycystic kidney disease, and
CC   graft versus host disease. The method can also be used to remove
CC   malignant cells from bone marrow transplants. AAZ25812-Z26825 represent
CC   human polymorphic sites described in the method of the invention
XX
SQ   Sequence 21 BP; 5 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 21;
  Best Local Similarity   94.4%;  Pred. No. 2e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTAACT 2190
              ||||||||||||||||| |
Db          3 TTTTTTTTTTTTTTAATT 20


RESULT 2392
AAZ26268/c
ID   AAZ26268 standard; DNA; 21 BP.
XX
AC   AAZ26268;
XX
DT   30-NOV-1999  (first entry)
XX
DE   Human polymorphic region 457.
XX
KW   Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW   cell viability; loss of heterozygosity; precancerous condition; ASI;
KW   allele specific inhibitor; somatic cell; diagnosis; prevention;
KW   atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW   dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW   graft versus host disease; malignant cell removal; bone marrow; ss.
XX
OS   Homo sapiens.
XX
PN   WO9841648-A2.
XX
PD   24-SEP-1998.
XX
PF   19-MAR-1998;   98WO-US005419.
XX
PR   20-MAR-1997;   97US-0041057P.
XX
PA   (VARI-) VARIAGENICS INC.
XX
PI   Housman D,  Ledley FD,  Stanton VP;
XX
DR   WPI; 1998-521232/44.
XX
PT   Identifying target genes for allele-specific drugs - used for diagnosis,
PT   prevention and treatment of, e.g. cancers, atherosclerotic plaque,
PT   dysplastic lesions, endometriosis or graft versus host disease.
XX
PS   Disclosure; Fig 7; 605pp; English.
XX
CC   This invention describes a novel method for identifying an inhibitor
CC   potentially useful for treatment of cancer, where the inhibitor is active
CC   on a gene vital for cell growth or viability, and where the gene is
CC   subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC   used for preventing the development of cancer in a patient having a
CC   precancerous condition, by administering to the patient a first allele
CC   specific inhibitor (ASI) targeted to an allele of a first essential gene
CC   present in cells of the precancerous condition, where the normal somatic
CC   cells of the patient are heterozygous for the first gene, the inhibitor
CC   is active on at least one but less than all allelic forms of the gene
CC   present in a population and targets only one allelic form present in the
CC   normal somatic cells, and the first gene. The products and methods can be
CC   used in the diagnosis, prevention and treatment of LOH disorders, e.g.
CC   cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
CC   lesions, benign tumours, endometriosis, polycystic kidney disease, and
CC   graft versus host disease. The method can also be used to remove
CC   malignant cells from bone marrow transplants. AAZ25812-Z26825 represent
CC   human polymorphic sites described in the method of the invention
XX
SQ   Sequence 21 BP; 5 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 21;
  Best Local Similarity   94.4%;  Pred. No. 2e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAA 2798
              |||| ||||||||||||||
Db         20 AATTAAAAAAAAAAAAAA 3


RESULT 2393
AAZ26141
ID   AAZ26141 standard; DNA; 21 BP.
XX
AC   AAZ26141;
XX
DT   30-NOV-1999  (first entry)
XX
DE   Human polymorphic region 330.
XX
KW   Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW   cell viability; loss of heterozygosity; precancerous condition; ASI;
KW   allele specific inhibitor; somatic cell; diagnosis; prevention;
KW   atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW   dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW   graft versus host disease; malignant cell removal; bone marrow; ss.
XX
OS   Homo sapiens.
XX
PN   WO9841648-A2.
XX
PD   24-SEP-1998.
XX
PF   19-MAR-1998;   98WO-US005419.
XX
PR   20-MAR-1997;   97US-0041057P.
XX
PA   (VARI-) VARIAGENICS INC.
XX
PI   Housman D,  Ledley FD,  Stanton VP;
XX
DR   WPI; 1998-521232/44.
XX
PT   Identifying target genes for allele-specific drugs - used for diagnosis,
PT   prevention and treatment of, e.g. cancers, atherosclerotic plaque,
PT   dysplastic lesions, endometriosis or graft versus host disease.
XX
PS   Disclosure; Fig 7; 605pp; English.
XX
CC   This invention describes a novel method for identifying an inhibitor
CC   potentially useful for treatment of cancer, where the inhibitor is active
CC   on a gene vital for cell growth or viability, and where the gene is
CC   subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC   used for preventing the development of cancer in a patient having a
CC   precancerous condition, by administering to the patient a first allele
CC   specific inhibitor (ASI) targeted to an allele of a first essential gene
CC   present in cells of the precancerous condition, where the normal somatic
CC   cells of the patient are heterozygous for the first gene, the inhibitor
CC   is active on at least one but less than all allelic forms of the gene
CC   present in a population and targets only one allelic form present in the
CC   normal somatic cells, and the first gene. The products and methods can be
```

```
CC   used in the diagnosis, prevention and treatment of LOH disorders, e.g.
CC   cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
CC   lesions, benign tumours, endometriosis, polycystic kidney disease, and
CC   graft versus host disease. The method can also be used to remove
CC   malignant cells from bone marrow transplants. AAZ25812-Z26825 represent
CC   human polymorphic sites described in the method of the invention
XX
SQ   Sequence 21 BP; 17 A; 3 C; 0 G; 1 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 21;
  Best Local Similarity   94.4%;  Pred. No. 2e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2803
              ||| |||||||||||||||
Db          1 AAATAAAAAAAAAAAAA 18


RESULT 2394
AAZ26141/c
ID   AAZ26141 standard; DNA; 21 BP.
XX
AC   AAZ26141;
XX
DT   30-NOV-1999  (first entry)
XX
DE   Human polymorphic region 330.
XX
KW   Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW   cell viability; loss of heterozygosity; precancerous condition; ASI;
KW   allele specific inhibitor; somatic cell; diagnosis; prevention;
KW   atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW   dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW   graft versus host disease; malignant cell removal; bone marrow; ss.
XX
OS   Homo sapiens.
XX
PN   WO9841648-A2.
XX
PD   24-SEP-1998.
XX
PF   19-MAR-1998;   98WO-US005419.
XX
PR   20-MAR-1997;   97US-0041057P.
XX
PA   (VARI-) VARIAGENICS INC.
XX
PI   Housman D,  Ledley FD,  Stanton VP;
XX
DR   WPI; 1998-521232/44.
XX
PT   Identifying target genes for allele-specific drugs - used for diagnosis,
PT   prevention and treatment of, e.g. cancers, atherosclerotic plaque,
PT   dysplastic lesions, endometriosis or graft versus host disease.
XX
PS   Disclosure; Fig 7; 605pp; English.
XX
CC   This invention describes a novel method for identifying an inhibitor
CC   potentially useful for treatment of cancer, where the inhibitor is active
CC   on a gene vital for cell growth or viability, and where the gene is
CC   subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC   used for preventing the development of cancer in a patient having a
CC   precancerous condition, by administering to the patient a first allele
CC   specific inhibitor (ASI) targeted to an allele of a first essential gene
CC   present in cells of the precancerous condition, where the normal somatic
CC   cells of the patient are heterozygous for the first gene, the inhibitor
CC   is active on at least one but less than all allelic forms of the gene
CC   present in a population and targets only one allelic form present in the
CC   normal somatic cells, and the first gene. The products and methods can be
CC   used in the diagnosis, prevention and treatment of LOH disorders, e.g.
CC   cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
CC   lesions, benign tumours, endometriosis, polycystic kidney disease, and
CC   graft versus host disease. The method can also be used to remove
CC   malignant cells from bone marrow transplants. AAZ25812-Z26825 represent
CC   human polymorphic sites described in the method of the invention
XX
SQ   Sequence 21 BP; 17 A; 3 C; 0 G; 1 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 21;
  Best Local Similarity   94.4%;  Pred. No. 2e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2183
              ||||||||||||||| |||
Db         18 TTTTTTTTTTTTTTATTT 1


RESULT 2395
ABK15655
ID   ABK15655 standard; DNA; 21 BP.
XX
AC   ABK15655;
XX
DT   21-MAY-2002  (first entry)
XX
DE   Anchored oligo-dt reverse primer.
XX
KW   ss; lipoxygenase; RCI-1; transgenic; plant; plant antifungal;
KW   rice chemically induced cDNA; promoter; transit peptide; plastid;
KW   fungal mycotoxin inhibitor; plant breeding; PCR; primer.
XX
OS   Synthetic.
XX
PN   WO200206490-A1.
XX
PD   24-JAN-2002.
XX
PF   12-JUL-2001; 2001WO-EP008085.
XX
PR   13-JUL-2000; 2000GB-00017275.
PR   15-SEP-2000; 2000GB-00022739.
XX
PA   (SYGN ) SYNGENTA PARTICIPATIONS AG.
PA   (UYZU-) UNIV ZUERICH.
XX
PI   Dudler R,  Schaffrath U,  Lawton KA;
XX
DR   WPI; 2002-188550/24.
XX
PT   Novel isolated nucleic acid encoding a promoter which is capable of
PT   driving chemically inducible but not wound- or pathogen-inducible
PT   expression of an associated nucleotide sequence.
XX
PS   Example 3; Page 30; 88pp; English.
XX
CC   The invention relates to an isolated nucleic acid molecule (a promoter of
CC   rice chemically induced cDNA (RCI-1), which encodes a lipoxygenase)
CC   capable of driving chemically-inducible but not wound- or pathogen-
CC   inducible expression of an associated nucleotide sequence. Also included
CC   are the RCI-1 cDNA, its encoded protein, a 4.5kb genomic clone for the
CC   lipoxygenase gene, promoter fragments, the lipoxygenase transit peptide
CC   which directs expressed proteins to the plastid, a vector comprising the
CC   promoter or fragments and a transgenic plant comprising the vector. The
CC   promoter or fragments are useful for expressing a nucleotide sequence of
CC   interest. The transit peptide is useful for targeting an associated
CC   protein of interest to plastids. A nucleic acid which expresses
CC   polypeptide having lipoxygenase activity is useful for inhibiting fungal
CC   mycotoxins when transformed into a plant. The lipoxygenase is useful for
CC   inhibiting fungal mycotoxins. The promoter is useful for regulating
CC   transcription of a chemically inducible but not wound or pathogen
CC   inducible gene, which involves applying a chemical regulator to a plant
CC   or seed containing a chemically regulatable nucleotide sequence.
CC   Transgenic plants as described above are useful for breeding improved
CC   plant lines that for example increase the effectiveness of conventional
CC   methods such as herbicide or pesticide treatment or allow to dispense
CC   with the methods due to their modified genetic properties. New crops with
```

```
CC   improved stress tolerance can be obtained that, due to their optimised
CC   genetic equipment yield harvested product of better quality than products
CC   that were not able to tolerate comparable adverse developmental
CC   conditions. The present sequence is an anchored oligo-dt reverse RT-PCR
CC   primer (reverse transcriptase PCR) used to isolate the cDNA encoding rice
CC   lipoxygenase
XX
SQ   Sequence 21 BP; 2 A; 1 C; 1 G; 16 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 21;
  Best Local Similarity   94.4%;  Pred. No. 2e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTT 2180
              | ||||||||||||||||
Db          3 TGCTTTTTTTTTTTTTT 20


RESULT 2396
ABK99283/c
ID   ABK99283 standard; RNA; 21 BP.
XX
AC   ABK99283;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Hepatitis C virus (HCV) NS5B replicase RNA synthesis template #13.
XX
KW   Hepatitis C virus; HCV; NS5B replicase; ss; RNA polymerase.
XX
OS   Synthetic.
XX
PN   US2002064771-A1.
XX
PD   30-MAY-2002.
XX
PF   06-APR-2001; 2001US-00828034.
XX
PR   07-APR-2000; 2000US-0195852P.
XX
PA   (ZHON/) ZHONG W.
PA   (HONG/) HONG Z.
PA   (FERR/) FERRARI E.
XX
PI   Zhong W,  Hong Z,  Ferrari E;
XX
DR   WPI; 2002-582330/62.
XX
PT   Novel replicase complex comprising hepatitis C virus NS5B replicase, a 3
PT   nucleotide-long template to which a 2 nucleotide-long primer is annealed,
PT   and template and primer which do not form a stable duplex in the absence
PT   of HCV NS5B.
XX
PS   Example; Page 6; 17pp; English.
XX
CC   The invention relates to a replicase complex comprising a hepatitis C
CC   virus (HCV) NS5B replicase protein, a linear nucleic acid template and a
CC   complementary nucleic acid primer which is annealed to the 3' terminus of
CC   the template, where the template is at least three nucleotides and the
CC   primer is two or three nucleotides, and the template and primer do not
CC   form a stable duplex in solution in the absence of the HCV NS5B protein.
CC   The complex is useful for detecting HCV replicase activity and permits
CC   establishment of sensitive RNA-dependent RNA polymerase assays to screen
CC   and evaluate antiviral inhibitors and to improve the specificity and
CC   efficacy of the inhibitors. The complex is also useful in the development
CC   of a reliable system for determining kinetic and thermodynamic constants
CC   of HCV NS5B-catalysed nucleotide incorporation and investigation of
CC   mechanistic inhibitors for mis-incorporation or chain termination.
CC   Specifically, the short RNA template and primer pairs are useful in
CC   screening assays which are used for determining kinetic, thermodynamic
CC   and mechanistic properties of NS5B replication and ultimately in the
CC   development of inhibitors of NS5B. Newly identified inhibitors of
CC   replicase activity may be used for developing anti-HCV pharmaceuticals.
CC   Sequences ABK99271-ABK99296 represent HCV NS5B replicase RNA synthesis
CC   templates
XX
SQ   Sequence 21 BP; 16 A; 3 C; 1 G; 0 T; 1 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 21;
  Best Local Similarity   94.4%;  Pred. No. 2e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTT 2182
              || ||||||||||||||||
Db         18 CTGTTTTTTTTTTTTTT 1


RESULT 2397
ADE80960
ID   ADE80960 standard; DNA; 21 BP.
XX
AC   ADE80960;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human papillomavirus L1 gene type-specific PCR primer SEQ ID NO:10.
XX
KW   detection; human papillomavirus; HPV; genotype;
KW   HPV genus-specific primer; HPV genus-specific probe; amplification;
KW   hybridisation; genotyping; L1 gene; PCR primer; ss.
XX
OS   Synthetic.
OS   Human papillomavirus.
XX
PN   WO2003076667-A1.
XX
PD   18-SEP-2003.
XX
PF   10-MAR-2003; 2003WO-HU000020.
XX
PR   14-MAR-2002; 2002HU-00000981.
XX
PA   (JENE/) JENEY C.
PA   (TAKA/) TAKACS T.
XX
PI   Jeney C,  Takacs T;
XX
DR   WPI; 2003-902774/82.
XX
PT   Use of amplification primer-mixture and human papillomavirus genus-
PT   specific hybridization probes, for detecting and genotyping human
PT   papillomavirus in biological samples.
XX
PS   Claim 2; SEQ ID NO 10; 61pp; English.
XX
CC   The present invention describes a method for detecting many human
CC   papillomavirus (HPV) genotypes from biological samples. The method
CC   comprises amplifying and hybridising the extracted nucleic acid molecules
CC   with HPV genus-specific primers and probes designed from HPV genomic
CC   regions. Amplification primer-mixtures, consensus primers, type-specific
CC   primers, hybridisation probes, and reagent kits of the present invention
CC   can be used for detecting and genotyping HPV. The primer mixture is
CC   useful for the amplification of the 3, 4, 6, 7, 9, 10, 11, 12, 13, 14,
CC   16, 18, 20, 24, 26, 28, 29, 30, 31, 32, 33, 34, 35, 36, 39, 39, 40, 41,
CC   42, 44, 45, 51, 52, 53, 54, 55, 56, 58, 49, 60, 61, 66, 67, 68, 72, 74 or
CC   77 genotypes of HPV. The HPV genomic regions are useful for designing HPV
CC   genus-specific and HPV genotype-specific hybridisation probes. The
CC   present sequence is used in the exemplification of the present invention.
XX
SQ   Sequence 21 BP; 9 A; 2 C; 4 G; 6 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 21;
  Best Local Similarity   94.4%;  Pred. No. 2e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2533 ATACAGGGTATTAAGAAT 2550
```

```
                     |||||||||||| |||||
Db          3 ATACAGGGTATTTAGAAT 20
```

RESULT 2398
AAT28053
ID AAT28053 standard; DNA; 22 BP.
XX
AC AAT28053;
XX
DT 31-DEC-1996 (first entry)
XX
DE 3'-primer K for human fibroblasts.
XX
KW Polymerase chain reaction; PCR; primer; amplify; human; fibroblast; AIDS;
KW enhanced differential display; EDD; mRNA preparation; senescent cell;
KW quiescent cell; dividing cell; senescence-related gene; gene expression;
KW non-senescent cell; age-related lipofuscin; retina; therapy; liver spot;
KW donor tissue; senescent melanocyte; melanin; hypopigmentation; ss.
XX
OS Synthetic.
XX
PN WO9613610-A2.
XX
PD 09-MAY-1996.
XX
PF 24-AUG-1995; 95WO-US011230.
XX
PR 31-OCT-1994; 94US-00332420.
XX
PA (GERO-) GERON CORP.
XX
PI Linskens MHK, Hirsch KS, Villeponteau B, Feng J, Funk W, West MD;
XX
DR WPI; 1996-251464/25.
XX
PT Identifying, isolating and regulating senescence-related genes - useful
PT to ameliorate problems associated with accumulation of senescent cells,
PT e.g. age-related lipofuscin accumulation in the retina and AIDS.
XX
PS Claim 6; Page 25; 135pp; English.
XX
CC AAT28044-T28075 represent primers for human fibroblasts in enhanced
CC differential display (EDD), which is used in conjuncture with the method
CC of the invention. EDD is an mRNA preparation method. AAT28044-T28055
CC represent T-rich 3'-primers, while AAT28056-T28075 are randomly selected
CC 5'-primers used in EDD of human fibroblasts. The 3'-primers used are
CC complementary to the poly-A tail of the mRNA. In the method of the
CC invention, mRNA is isolated from a senescent cell, and a young quiescent
CC cell, and the mRNAs are amplified in separate reaction mixtures. The
CC amplified sequences are then separated by size or charge, and the
CC products are analysed to identify a gene from young quiescent cells and
CC dividing cells, that is present at a different level from senescent
CC cells. The method can be used for the rapid and efficient identification
CC and isolation of senescence-related genes and gene products, and to
CC detect and distinguish between senescent and non-senescent cells. It can
CC also be used to destroy cells expressing senescence specific (or related)
CC gene products, and to screen for compounds capable of altering gene
CC expression in senescent cells. The method can also be used to ameliorate
CC problems associated with the accumulation of senescent cells such as age-
CC related lipofuscin accumulation in the retina, and in the treatment of
CC AIDS. Also, the method can be used to distinguish young cells from
CC senescent cells in donor tissue, which is useful in removing senescent
CC melanocytes overexpressing melanin which cause hypopigmentation, or liver
CC spots
XX
SQ Sequence 22 BP; 4 A; 3 C; 3 G; 12 T; 0 U; 0 Other;

```
  Query Match             0.6%;  Score 16.4;  DB 1;  Length 22;
  Best Local Similarity   94.4%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTGAA 1784
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                     |||||||||||||| ||
Db          5 AAGCTTTTTTTTTTTTAA 22
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RESULT 2399
AAT58493
ID AAT58493 standard; DNA; 22 BP.
XX
AC AAT58493;
XX
DT 24-MAR-1997 (first entry)
XX
DE First primer #10 for use in enhanced differential display method.
XX
KW Differential Display; Enhanced Differential Display; EDD; screening;
KW gene expression; cell type; different; cell development; gene typing;
KW identification; differentiation; aging; and disease; primer; PCR; ss.
XX
OS Synthetic.
XX
PN US5580726-A.
XX
PD 03-DEC-1996.
XX
PF 29-APR-1994; 94US-00235180.
XX
PR 29-APR-1994; 94US-00235180.
XX
PA (GERO-) GERON CORP.
XX
PI Linskens MHK, Feng J, Villeponteau B, Funk W;
XX
DR WPI; 1997-033564/03.
XX
PT Detection of differentially expressed mRNA mols. - using two-step
PT polymerase chain reaction amplification method.
XX
PS Claim 9; Col 17; 15pp; English.
XX
CC An improved method of Differential Display, named Enhanced Differential
CC Display (EDD) has been designed as a technique for screening differences
CC in gene expression between various cell types or between different stages
CC of cell development. The technique is highly reproducible, leading to
CC precise typing of the expressed genes in any given cell. EDD analysis
CC permits the identification of novel genes involved in differentiation,
CC aging and disease, and enables direct comparisons of different cell types
CC and disease states. By using longer primers, and/or an alteration in the
CC annealing temperatures, the number of false positives can be reduced.
CC First, cDNA is prepared from total cellular RNA using 12 different 22-
CC base oligonucleotides (AAT58484-95) that are targeted to the poly A tail
CC of pol II mRNA transcripts. The last two bases of each primer varies so
CC as to anchor the primer to the 3' end of different sets of mRNAs. A
CC second set of 12 22-base oligo primers (AAT58472-83) is designed to
CC randomly select a subset of cDNAs from each of the twelve 3' primers. PCR
CC amplification of a subset of cDNAs is carried out in a two step process
CC using particular 5' and 3' primers. The amplified gene products can then
CC be directly sequenced or rapidly subcloned for DNA sequencing
XX
SQ Sequence 22 BP; 4 A; 3 C; 3 G; 12 T; 0 U; 0 Other;

```
  Query Match             0.6%;  Score 16.4;  DB 1;  Length 22;
  Best Local Similarity   94.4%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTGAA 1784
                ||||||||||||||| ||
Db          5 AAGCTTTTTTTTTTTTAA 22
```

RESULT 2400
AAZ47351
ID AAZ47351 standard; DNA; 22 BP.
XX

AC AAZ47351;
XX
DT 06-MAR-2000 (first entry)
XX
DE PCR primer K used in differential display analysis of Aspergillus oryzae.
XX
KW Dopa decarboxylase; DDC2; DDC3; increased yield; hormone; receptor;
KW antibody; reporter; enzyme; polypeptide production; primer; ss.
XX
OS Synthetic.
OS Aspergillus oryzae.
XX
PN WO9960136-A1.
XX
PD 25-NOV-1999.
XX
PF 14-MAY-1999; 99WO-US010689.
XX
PR 15-MAY-1998; 98US-00079344.
PR 15-MAY-1998; 98US-00079601.
XX
PA (NOVO) NOVO NORDISK BIOTECH INC.
PA (NOVO) NOVO-NORDISK AS.
XX
PI Wahleithner J, Christensen T;
XX
DR WPI; 2000-062459/05.
XX
PT New isolated Aspergillus oryzae signaling sequences, used to increase the
PT production of polypeptides by recombinant host filamentous fungal cells.
XX
PS Example 2; Page 35; 78pp; English.
XX
CC Sequences AAZ47342-Z47353 are oligo(dT12N2) primers used in the
CC differential display analysis of the Aspergillus oryzae strains HC4.01
CC and 27. The strains were analysed to find the genetic basis for phenotype
CC differences in the strains which are used in a method for producing a
CC polypeptide in an enhanced amount. The method involves cultivating a
CC mutant of a parent filamentous fungal cell in suitable nutrient medium.
CC The mutant cell contains the nucleotide sequence encoding the polypeptide
CC to be synthesised and one or more second nucleotide sequences encoding a
CC DDC polypeptide (see AAZ47338-Z47339). The mutant cell produces more of
CC the polypeptide than the parent cell and the polypeptide can be recovered
CC from the nutrient medium of the mutant cell. The method can be used for
CC the production of polypeptides such as hormones, receptors, antibodies,
CC reporters or enzymes, e.g. an aminopeptidase, amylase, carbohydrase,
CC carboxypeptidase, catalase, cellulase, chitinase, cutinase, cyclodextrin
CC glycosyltransferase, deoxyribonuclease, esterase, alpha-galactosidase,
CC beta-galactosidase, glucoamylase, alpha-glucosidase, beta-glucosidase,
CC invertase, laccase, lipase, mannosidase, mutanase, oxidase, pectinolytic
CC enzyme, peroxidase, phytase, polyphenoloxidase, proteolytic enzyme,
CC ribonuclease, transglutaminase or xylanase
XX
SQ Sequence 22 BP; 4 A; 3 C; 3 G; 12 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.4; DB 1; Length 22;
Best Local Similarity 94.4%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       1767 AAGCTTTTTTTTTTTGAA 1784
              ||||||||||||||| ||
Db          5 AAGCTTTTTTTTTTTTAA 22
```

RESULT 2401
AAH22194
ID AAH22194 standard; DNA; 22 BP.
XX
AC AAH22194;
XX
DT 20-AUG-2001 (first entry)
XX
DE Human hepatocyte auxin related 3'-(T-rich) primer J.
XX
KW Human; hepatocyte; auxin; liver; hepatitis; chronic hepatitis;
KW liver fibrosis; cirrhosis; liver damage; primer; ss.
XX
OS Homo sapiens.
XX
PN CN1280985-A.
XX
PD 24-JAN-2001.
XX
PF 20-JUL-1999; 99CN-00110801.
XX
PR 20-JUL-1999; 99CN-00110801.
XX
PA (HOSP-) HOSPITAL NO 458 CHINESE PLA.
XX
PI Kong X, Yi X, Zeng P;
XX
DR WPI; 2001-291394/31.
XX
PT Novel recombinant human hepatocyte auxin, its preparation and clinical
PT application.
XX
PS Example 1; Page 2 (disclosure); 13pp; Chinese.
XX
CC The present invention describes a differential indication PCR (polymerase
CC chain reaction) technique which is used to obtain a new complete gene
CC able to promote the repair of damaged liver cells and with substance
CC total length of 0.7 kb by screening the cDNA library of human foetal
CC liver. The induction expression of engineering bacteria, the separation
CC and cracking of inclusion body and the process for restoring and
CC decontaminating proteins are built up to obtain high purity recombinant
CC human hepatocyte auxin. It can externally promote the reproduction of
CC primary culture liver cells and liver cancer cells BEL-7402 and
CC internally promote the synthesis of mouse liver cell DNA after CCL4 is
CC damaged and the repair of liver cells. The method may be used to treat
CC serious hepatitis, chronic hepatitis, liver fibrosis and cirrhosis. The
CC present sequence represents a primer which is used in the exemplification
CC of the present invention
XX
SQ Sequence 22 BP; 4 A; 3 C; 3 G; 12 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.4; DB 1; Length 22;
Best Local Similarity 94.4%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       1767 AAGCTTTTTTTTTTTGAA 1784
              ||||||||||||||| ||
Db          5 AAGCTTTTTTTTTTTTAA 22
```

RESULT 2402
AAV61555/c
ID AAV61555 standard; DNA; 23 BP.
XX
AC AAV61555;
XX
DT 08-DEC-1998 (first entry)
XX
DE Double-anchored oligo-dT primer, used to synthesise apolipoprotein cDNA.
XX
KW Primer; PCR; amplification; RT-PCR; quantitate; amount ratio; liver;
KW kidney; apolipoprotein; ATAC-PCR; Adaptor-tagged Competitive PCR;
KW gene expression; internal standard; calibration curve; ss.
XX
OS Synthetic.
OS Mus sp.
XX
PN EP870842-A2.
XX
PD 14-OCT-1998.
XX
PF 07-APR-1998; 98EP-00302726.

```
XX
PR   07-APR-1997;   97JP-00088495.
XX
PA   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI   Kato K;
XX
DR   WPI; 1998-523164/45.
XX
PT   Determination of gene expression levels - using combinations of different
PT   cDNA samples tagged with different PCR adaptors.
XX
PS   Example 2; Page 9; 22pp; English.
XX
CC   The present sequence represents a primer which was used to synthesise
CC   Apolipoprotein cDNA in a RT-PCR reaction. This primer as well as primers
CC   AAV61554 and AAV61556 were added to both mouse liver-derived and mouse
CC   kidney-derived total RNA to generate single-stranded cDNA. These primers
CC   were used in the method of the invention to determine the amount ratio
CC   between a cDNA coding for mouse liver-derived Apolipoprotein and a cDNA
CC   that codes for the mouse kidney-derived Apolipoprotein by using Adaptor-
CC   tagged Competitive PCR (ATAC-PCR). This method allows gene expression to
CC   be quantitatively determined, and because internal standards are not
CC   required to prepare a calibration curve, it is a quicker and less
CC   laborious process
XX
SQ   Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 23;
  Best Local Similarity   94.4%;  Pred. No. 2.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||| |
Db         22 AAAAAAAAAAAAAAAACA 5


RESULT 2403
AAX23577
ID   AAX23577 standard; DNA; 23 BP.
XX
AC   AAX23577;
XX
DT   18-JUN-1999  (first entry)
XX
DE   Deletion sequence oligonucleotide 30.
XX
KW   Deletion sequence oligonucleotide; sensor array; eukaryotic pathogen;
KW   probe; cellular adhesion modulator; cellular proliferation modulator;
KW   human retrovirus; human immunodeficiency virus; non-human retrovirus;
KW   HIV; primer; ss.
XX
OS   Synthetic.
XX
PN   WO9911820-A1.
XX
PD   11-MAR-1999.
XX
PF   01-SEP-1998;   98WO-US018084.
XX
PR   02-SEP-1997;   97US-00923771.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Chen D,  Srivatsa GS;
XX
DR   WPI; 1999-205198/17.
XX
PT   New compositions comprising sensor arrays made up of unique probe
PT   oligonucleotides - useful for characterizing a sample of target deletion
PT   oligonucleotides.
XX
PS   Example 9; Page 99; 163pp; English.
XX
CC   This invention describes a novel composition comprising a number of
CC   sensor arrays, where each array comprises a unique probe oligonucleotide,
CC   which is the reverse complement of part of a unique target
CC   oligonucleotide present in a mixture of target deletion sequence
CC   oligonucleotides. The compositions form a method for characterizing a
CC   sample of target deletion oligonucleotides which are labelled and
CC   hybridize with the probe oligonucleotides of the sensor arrays. Such
CC   oligonucleotides and their targets are represented in AAX23548-X23709.
CC   Oligonucleotides characterized by the method form pharmaceutical
CC   compositions that are useful for modulating cellular adhesion or
CC   proliferation, and being active against a eukaryotic pathogen, a human
CC   retrovirus, a human immunodeficiency virus (HIV), or a non-human
CC   retrovirus, including influenza virus, Epstein-Barr virus, Respiratory
CC   Syncytial Virus or cytomegalovirus (CMV). The compositions enable
CC   characterization of deletion sequence oligonucleotides having related,
CC   but different nucleobase sequences, and quantification of different
CC   species of deletion sequence ("target") oligonucleotides in a mixture.
CC   Also, if the specificity of the oligonucleotide's nucleobase sequence for
CC   its reverse complement is not modified, the method may be performed using
CC   oligodeoxynucleotides
XX
SQ   Sequence 23 BP; 4 A; 1 C; 3 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 23;
  Best Local Similarity   94.4%;  Pred. No. 2.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTAA 2188
              ||||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTGAA 18


RESULT 2404
AAV35580
ID   AAV35580 standard; DNA; 23 BP.
XX
AC   AAV35580;
XX
DT   04-SEP-1998  (first entry)
XX
DE   STS probe GV10 generating upper primer.
XX
KW   Hydronephrosis gene; HNG gene; USF2 gene; renal disease; renal aplasia;
KW   vesical-ureteral reflux; pelvi-ureteral junction obstruction;
KW   multicystic renal dysplasia; renal agenesis; hydronephrosis; MRD;
KW   Von Mayer-Rokitansky-Kuester disorder; bifid ureter; STS probe;
KW   sequence tagged site; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9815650-A2.
XX
PD   16-APR-1998.
XX
PF   09-OCT-1997;   97WO-EP005583.
XX
PR   09-OCT-1996;   96EP-00202820.
XX
PA   (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
XX
PI   Van De Ven WJM,  Fryns JPGJ,  Groenen PMA;
XX
DR   WPI; 1998-240833/21.
XX
PT   Hydronephrosis gene - useful to treat or diagnose renal diseases and
PT   disorders, e.g. vesical-ureteral reflux, pelvi-ureteral junction
PT   obstruction, multicystic renal dysplasia or renal agenesis.
XX
PS   Example 3; Page 46; 73pp; English.
XX
CC   This primer is used for the generation of sequence tagged sites (STS)
```

```
CC   probes used for pinpointing chromosome 6 breakpoint. This was used for
CC   isolating the human hydronephrosis (HNG) gene of the invention. A
CC   translocation partner to this HNG gene on chromosome 6 is the chromosome
CC   19 USF2 gene. The HNG gene can be used as a starting point to design
CC   suitable compounds or techniques for the treatment of renal diseases or
CC   disorders, or nucleotide probes for diagnosing cells involved in renal
CC   diseases or disorders. A protein or a fragment encoded by HNG gene can be
CC   used as a starting point for preparing suitable antibodies for diagnosing
CC   cells involved in renal diseases and disorders. The products and method
CC   can be used to treat or diagnose renal diseases and disorders selected
CC   from vesical-ureteral reflux, uni or bilateral pelvi-ureteral junction
CC   obstruction, multicystic renal dysplasia (MRD), renal agenesis, renal
CC   aplasia, hydronephrosis, Von Mayer-Rokitansky-Kuester disorder and bifid
CC   ureter
XX
SQ   Sequence 23 BP; 4 A; 6 C; 9 G; 4 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 23;
  Best Local Similarity   94.4%;  Pred. No. 2.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1367 GGCAGCCAGGCCATCTGT 1384
              |||||||||| |||||||
Db          5 GGCAGCCAGGTCATCTGT 22


RESULT 2405
AAZ87324
ID   AAZ87324 standard; DNA; 23 BP.
XX
AC   AAZ87324;
XX
DT   22-MAY-2000  (first entry)
XX
DE   Maize cytochrome P450 monooxygenase CYP71C3v2 RT-PCR primer 5' PC-1.
XX
KW   Cytochrome P450 monooxygenase; CYP71C3v2; herbicide detoxification;
KW   triasulfuron; transgenic plant; herbicide identification;
KW   reverse transcription-PCR; RT-PCR primer; ss.
XX
OS   Zea mays.
XX
PN   WO200000585-A2.
XX
PD   06-JAN-2000.
XX
PF   28-JUN-1999;   99WO-US014689.
XX
PR   26-JUN-1998;   98US-0090759P.
XX
PA   (UNII ) UNIV ILLINOIS FOUND.
XX
PI   Schuler MA,  Persans MW;
XX
DR   WPI; 2000-170909/15.
XX
PT   Novel maize cytochrome P450 monooxygenase cDNA used to confer herbicide
PT   resistance to plants.
XX
PS   Example 1c; Fig 5; 85pp; English.
XX
CC   The invention relates to maize cytochrome P450 monooxygenase CYP71C3v2
CC   (AAY77232) and nucleotides which encode it. CYP71C3v2 cDNA was generated
CC   via reverse transcriptase-PCR (RT-PCR) from poly (A)+ mRNA isolated from
CC   naphthalic anhydride and herbicide (triasulfuron)-treated maize
CC   seedlings. This was used to construct a cDNA library, which was screened
CC   using previously generated cDNA as hybridisation probes. The CYP71C3v2
CC   cDNA clone was extended via 5' RACE (rapid amplification of cDNA ends)
CC   and cloned into pBluescript. Genomic DNA was also screened for clones
CC   encoding CYP71C3v2 - this was found to contain 2 introns (AAZ87321-
CC   Z87322). Cytochrome P450 monooxygenase CYP71C3v2 reductively cleaves
CC   molecular dioxygen to produce functionalised organic substrates.
CC   Nucleotides encoding cytochrome P450 monooxygenase CYP71C3v2 are used to
CC   produce transgenic plants with increased resistance to herbicides, such
CC   as triasulfuron. When such transgenic plants are grown, undesired
CC   vegetation such as pigweed, velvet leaf, lambs quarters, Chenopodium
CC   album and quack grass, can easily be controlled. The methods may also be
CC   used to identify those compounds with herbicidal activity. Sequences
CC   AAZ87323-Z87335 represent PCR primers used to isolate, clone and study
CC   maize CYP71C3v2 nucleotide sequences in the exemplifications and the
CC   disclosure of the present invention
XX
SQ   Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 23;
  Best Local Similarity   94.4%;  Pred. No. 2.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTT 2180
              | ||||||||||||||||
Db          6 TTCTTTTTTTTTTTTTTT 23


RESULT 2406
AAZ87324/c
ID   AAZ87324 standard; DNA; 23 BP.
XX
AC   AAZ87324;
XX
DT   22-MAY-2000  (first entry)
XX
DE   Maize cytochrome P450 monooxygenase CYP71C3v2 RT-PCR primer 5' PC-1.
XX
KW   Cytochrome P450 monooxygenase; CYP71C3v2; herbicide detoxification;
KW   triasulfuron; transgenic plant; herbicide identification;
KW   reverse transcription-PCR; RT-PCR primer; ss.
XX
OS   Zea mays.
XX
PN   WO200000585-A2.
XX
PD   06-JAN-2000.
XX
PF   28-JUN-1999;   99WO-US014689.
XX
PR   26-JUN-1998;   98US-0090759P.
XX
PA   (UNII ) UNIV ILLINOIS FOUND.
XX
PI   Schuler MA,  Persans MW;
XX
DR   WPI; 2000-170909/15.
XX
PT   Novel maize cytochrome P450 monooxygenase cDNA used to confer herbicide
PT   resistance to plants.
XX
PS   Example 1c; Fig 5; 85pp; English.
XX
CC   The invention relates to maize cytochrome P450 monooxygenase CYP71C3v2
CC   (AAY77232) and nucleotides which encode it. CYP71C3v2 cDNA was generated
CC   via reverse transcriptase-PCR (RT-PCR) from poly (A)+ mRNA isolated from
CC   naphthalic anhydride and herbicide (triasulfuron)-treated maize
CC   seedlings. This was used to construct a cDNA library, which was screened
CC   using previously generated cDNA as hybridisation probes. The CYP71C3v2
CC   cDNA clone was extended via 5' RACE (rapid amplification of cDNA ends)
CC   and cloned into pBluescript. Genomic DNA was also screened for clones
CC   encoding CYP71C3v2 - this was found to contain 2 introns (AAZ87321-
CC   Z87322). Cytochrome P450 monooxygenase CYP71C3v2 reductively cleaves
CC   molecular dioxygen to produce functionalised organic substrates.
CC   Nucleotides encoding cytochrome P450 monooxygenase CYP71C3v2 are used to
CC   produce transgenic plants with increased resistance to herbicides, such
CC   as triasulfuron. When such transgenic plants are grown, undesired
CC   vegetation such as pigweed, velvet leaf, lambs quarters, Chenopodium
CC   album and quack grass, can easily be controlled. The methods may also be
CC   used to identify those compounds with herbicidal activity. Sequences
CC   AAZ87323-Z87335 represent PCR primers used to isolate, clone and study
```

```
CC   maize CYP71C3v2 nucleotide sequences in the exemplifications and the
CC   disclosure of the present invention
XX
SQ   Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 23;
  Best Local Similarity   94.4%;  Pred. No. 2.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2803
              ||||||||||||||| ||
Db         23 AAAAAAAAAAAAAAAGAA 6


RESULT 2407
AAA10767/c
ID   AAA10767 standard; DNA; 23 BP.
XX
AC   AAA10767;
XX
DT   04-JUL-2000  (first entry)
XX
DE   Primer CaYOR110D used in the amplification of the CaOR110 gene.
XX
KW   CaOR110; essential gene; inhibitor; dihydropteroate synthase; DHPS;
KW   7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase; HPPK; treatment;
KW   antimycete substance; infection; fungal infection; mycosis; probe;
KW   PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO200015838-A2.
XX
PD   23-MAR-2000.
XX
PF   13-SEP-1999;   99WO-EP007376.
XX
PR   11-SEP-1998;   98EP-00402255.
XX
PA   (HMRI ) HOECHST MARION ROUSSEL.
XX
PI   Lalanne J,  Rocher C,  Chalwatzis N,  Leeuw T,  Margerie D;
PI   Nitsche A,  Reinhard-Rupp J;
XX
DR   WPI; 2000-271469/23.
XX
PT   Novel genes from Candida albicans, useful for screening for antifungal
PT   drugs for treatment or prevention of fungal infection.
XX
PS   Example 5; Page 36; 139pp; English.
XX
CC   This sequence represents a primer used in the amplification of the
CC   Candida albicans gene CaOR110 nucleotide sequence. The invention relates
CC   to eight nucleotide sequences representing essential C. albicans genes,
CC   and the polynucleotides that they encode. An antibody against the
CC   polypeptides, and a method for screening for antimycotic substances using
CC   one of the essential genes or the peptides encoded by them as a target is
CC   also included in the invention. The method may be used to screen for
CC   substances that inhibit the expression of the target essential Candida
CC   albicans or Aspergillus fumigatus genes or inhibit the activity of
CC   essential proteins from these species. This method is particularly useful
CC   for screening for inhibitors of dihydropteroate synthase (DHPS) and/or
CC   7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase (HPPK). The method
CC   may also be used to identify antimycete substances acting on other mycete
CC   species. These inhibitors may be used to treat infections caused by these
CC   organisms or may be used prophylactically to prevent infection in
CC   immunosuppressed individuals. The nucleotide sequences may be used to
CC   identify functionally similar genes in other mycete species, and may also
CC   be used as a probe to screen a C. albicans genomic library. The genes and
CC   polypeptides may also be used to identify fungal infections. The new
CC   method of screening for antimycotic substances using essential genes or
CC   protein allows the identification of drugs which will only inhibit growth
CC   of specific mycete species
XX
SQ   Sequence 23 BP; 6 A; 3 C; 7 G; 7 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 23;
  Best Local Similarity   94.4%;  Pred. No. 2.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1238 CTGTGTAAAGAATTCACA 1255
              |||||| ||||||||||
Db         18 CTGTGTCAAGAATTCACA 1


RESULT 2408
AAZ50028
ID   AAZ50028 standard; DNA; 23 BP.
XX
AC   AAZ50028;
XX
DT   25-APR-2000  (first entry)
XX
DE   Oligo dT primer 3'PC-1, for RNA extraction from maize seedling.
XX
KW   Cytochrome p450 monooxygenase; CYP71C3v2; maize; chromosome 4p; weed;
KW   p450 gene; molecular dioxygen; herbicidal; pigweed; transgenic organism;
KW   herbicide resistant; triasulfuron; quack grass; velvet leaf; PCR primer;
KW   labs quarter; Chenopodium album; naphthalic anhydride; ss.
XX
OS   Zea mays.
XX
PN   WO200000502-A1.
XX
PD   06-JAN-2000.
XX
PF   23-JUN-1999;   99WO-US014117.
XX
PR   26-JUN-1998;   98US-0090759P.
XX
PA   (UNII ) UNIV ILLINOIS FOUND.
XX
PI   Schuler MA,  Persans MW;
XX
DR   WPI; 2000-170902/15.
XX
PT   Novel maize cytochrome P450 monooxygenase polypeptides and
PT   polynucleotides, used to confer triasulfuron herbicide resistance to
PT   plants.
XX
PS   Example 1c; Page 52; 77pp; English.
XX
CC   The present sequence is the oligo (dT) non-degenerate RT-PCR primer, 3'PC
CC   -1, complementary to the poly(A) tract of the CYP71C3v2 mRNA. It is used
CC   to extract and amplify mRNA isolated from naphthalic anhydride-treated
CC   maize seedlings. The CYP71C3v2 gene is mapped to a single locus on the
CC   short arm of maize chromosome 4 (4p). CYP71C3v2 reductively cleaves
CC   molecular dioxygen to produce functionalised organic substrates. It has
CC   herbicidal activity. CYP71C3v2 polynucleotides are used to produce
CC   transgenic organisms, such as yeast, plants and bacteria that are
CC   resistant to herbicides, such as triasulfurons. Undesired vegetation,
CC   e.g. weed, pigweed, velvet leaf, labs quarters, Chenopodium album and
CC   quack grass, can easily be controlled when such transgenic plants are
CC   grown. Transformed organisms can also be used to identify compounds with
CC   herbicidal activity
XX
SQ   Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 23;
  Best Local Similarity   94.4%;  Pred. No. 2.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTT 2180
              | ||||||||||||||||
Db          6 TTCTTTTTTTTTTTTTTT 23
```

```
RESULT 2409
AAZ50028/c
ID   AAZ50028 standard; DNA; 23 BP.
XX
AC   AAZ50028;
XX
DT   25-APR-2000  (first entry)
XX
DE   Oligo dT primer 3'PC-1, for RNA extraction from maize seedling.
XX
KW   Cytochrome p450 monooxygenase; CYP71C3v2; maize; chromosome 4p; weed;
KW   p450 gene; molecular dioxygen; herbicidal; pigweed; transgenic organism;
KW   herbicide resistant; triasulfuron; quack grass; velvet leaf; PCR primer;
KW   labs quarter; Chenopodium album; naphthalic anhydride; ss.
XX
OS   Zea mays.
XX
PN   WO200000502-A1.
XX
PD   06-JAN-2000.
XX
PF   23-JUN-1999;   99WO-US014117.
XX
PR   26-JUN-1998;   98US-0090759P.
XX
PA   (UNII ) UNIV ILLINOIS FOUND.
XX
PI   Schuler MA,  Persans MW;
XX
DR   WPI; 2000-170902/15.
XX
PT   Novel maize cytochrome P450 monooxygenase polypeptides and
PT   polynucleotides, used to confer triasulfuron herbicide resistance to
PT   plants.
XX
PS   Example 1c; Page 52; 77pp; English.
XX
CC   The present sequence is the oligo (dT) non-degenerate RT-PCR primer, 3'PC
CC   -1, complementary to the poly(A) tract of the CYP71C3v2 mRNA. It is used
CC   to extract and amplify mRNA isolated from naphthalic anhydride-treated
CC   maize seedlings. The CYP71C3v2 gene is mapped to a single locus on the
CC   short arm of maize chromosome 4 (4p). CYP71C3v2 reductively cleaves
CC   molecular dioxygen to produce functionalised organic substrates. It has
CC   herbicidal activity. CYP71C3v2 polynucleotides are used to produce
CC   transgenic organisms, such as yeast, plants and bacteria that are
CC   resistant to herbicides, such as triasulfurons. Undesired vegetation,
CC   e.g. weed, pigweed, velvet leaf, labs quarters, Chenopodium album and
CC   quack grass, can easily be controlled when such transgenic plants are
CC   grown. Transformed organisms can also be used to identify compounds with
CC   herbicidal activity
XX
SQ   Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 23;
  Best Local Similarity   94.4%;  Pred. No. 2.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2803
              ||||||||||||||| ||
Db         23 AAAAAAAAAAAAAAAGAA 6


RESULT 2410
ABA01048/c
ID   ABA01048 standard; DNA; 24 BP.
XX
AC   ABA01048;
XX
DT   24-JAN-2002  (first entry)
XX
DE   Human sodium pump subunit 12 PCR primer 1.
XX
KW   Human; sodium pump; subunit 12; cytostatic; virucide; immunomodulator;
KW   antiinflammatory; haemostatic; gene therapy; cancer; haemopathy;
KW   human immunodeficiency virus; HIV; infection; immunological disease;
KW   inflammatory disorder; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200177162-A1.
XX
PD   18-OCT-2001.
XX
PF   26-MAR-2001; 2001WO-CN000422.
XX
PR   27-MAR-2000; 2000CN-00115156.
XX
PA   (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-017442/02.
XX
PT   Human sodium pump subunit 12 of sodium pump and encoded polynucleotide,
PT   used in diagnosis and treatment of malignant tumors, hemopathy, human
PT   immunodeficiency virus infection, immunological diseases and
PT   inflammation.
XX
PS   Example 2; Page 16; 35pp; Chinese.
XX
CC   The invention relates to an isolated polypeptide of human sodium pump
CC   subunit 12 comprising a 110 residue amino acid sequence, fully defined in
CC   the specification, or its fragment, analogue or derivative. The
CC   polypeptide is used in the diagnosis and treatment of malignant tumours,
CC   haemopathy, human immunodeficiency virus (HIV) infection, immunological
CC   diseases and various inflammatory disorders. The present sequence is a
CC   primer used to isolate a polynucleotide encoding the polypeptide of the
CC   invention
XX
SQ   Sequence 24 BP; 0 A; 0 C; 4 G; 20 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 24;
  Best Local Similarity   94.4%;  Pred. No. 2.6e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2803
              ||||||||| ||||||||
Db         23 AAAAAAAAACAAAAAAA 6


RESULT 2411
AAC96428
ID   AAC96428 standard; DNA; 24 BP.
XX
AC   AAC96428;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DQA1 gene PCR primer #30.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
```

```
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 51; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 24 BP; 3 A; 5 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 24;
  Best Local Similarity   94.4%;  Pred. No. 2.6e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2175 TTTTTTTTTTTTAACTTT 2192
              ||||||||||||||||| |
Db          1 TTTTTTTTTTTTAACTCT 18


RESULT 2412
AAA94317/c
ID   AAA94317 standard; DNA; 24 BP.
XX
AC   AAA94317;
XX
DT   11-JAN-2001  (first entry)
XX
DE   RNA-protein fusion oligonucleotide 25-P.
XX
KW   RNA-protein fusion; protein library; protein isolation; gene cloning; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   24
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "attached to puromycin, a peptide acceptor"
XX
PN   WO200047775-A1.
XX
PD   17-AUG-2000.
XX
PF   01-FEB-2000; 2000WO-US002589.
XX
PR   09-FEB-1999;   99US-00247190.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Szostak JW,  Roberts RW,  Liu R;
XX
DR   WPI; 2000-533022/48.
XX
PT   Producing protein or DNA libraries which are useful for improving
PT   existing proteins, by in vitro translating protein coding sequences to
PT   produce RNA-protein fusions and incubating these protein fusions under
PT   high salt conditions.
XX
PS   Disclosure; Page 43; 121pp; English.
XX
CC   The present sequence is one of a number of oligonucleotides which were
CC   used for the generation of RNA-protein fusions, including fusions having
CC   a myc epitope tag. The RNA-protein fusions comprise a protein covalently
CC   linked to the 3' end of its own mRNA. This is accomplished by synthesis
CC   and in vitro or in situ translation of an mRNA molecule with a peptide
CC   acceptor attached to its 3' end. The RNA-protein fusions are incubated
CC   under high salt conditions to produce a protein library. This method is
CC   useful for improving or altering existing proteins, as well as for
CC   isolating new proteins and nucleic acid or small molecule targets. It may
CC   also be used to improve human or humanised single-chain antibodies for
CC   the treatment of a number of diseases. The method is useful for the
CC   isolation of proteins with specific binding properties, for screening
CC   cDNA libraries and cloning new genes on the basis of protein-protein
CC   interactions. Unlike prior art, the new method does not rely on
CC   maintaining the integrity of an mRNA:ribosome:nascent chain ternary
CC   complex, which is very fragile and is therefore of limited use. The
CC   method does not rely on topological links between the protein and the
CC   nucleic acid so that the information of the protein is retained and can
CC   be recovered in readable, nucleic acid form
XX
SQ   Sequence 24 BP; 1 A; 4 C; 3 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 24;
  Best Local Similarity   94.4%;  Pred. No. 2.6e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              |||||||||||| |||||
Db         23 GAAAAAAAAAAATAAAAA 6


RESULT 2413
ABL57074/c
ID   ABL57074 standard; DNA; 24 BP.
XX
AC   ABL57074;
XX
DT   22-JUL-2002  (first entry)
XX
DE   Molecular beacon oligonucleotide probe.
XX
KW   Molecular beacon; probe; fluorophore; nanoparticle;
KW   nucleic acid detection; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_binding    1. .20
FT                   /*tag=  d
FT                   /bound_moiety= "Target oligonucleotide"
FT                   /note= "Forms double-stranded region with bases 1-20 of
FT                   sequence in ABL57070"
FT   modified_base   1
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "disulfide or primary amine joined via a linker to
FT                   the 5' phosphate"
FT   stem_loop       2. .24
FT                   /*tag=  a
FT   modified_base   24
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "3' linker joined to an amine-reactive
FT                   fluorophore"
XX
PN   WO200218951-A2.
XX
PD   07-MAR-2002.
XX
PF   29-AUG-2001; 2001WO-US041941.
XX
PR   29-AUG-2000; 2000US-0228728P.
PR   30-MAR-2001; 2001US-0280350P.
XX
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```
PA   (UYRQ ) UNIV ROCKEFELLER.
XX
PI   Dubertret B,  Calame M,  Libchaber A;
XX
DR   WPI; 2002-404569/43.
XX
PT   Sensitively detecting proximity changes in a system that utilizes an
PT   interacting fluorophore and quencher, for high sensitivity applications,
PT   involves utilizing a metal surface as quencher.
XX
PS   Example 5; Page 33; 62pp; English.
XX
CC   The present sequence is an oligonucleotide probe that was used in a
CC   molecular beacon in an example from the invention. The probe forms a
CC   hairpin structure in the native state. The 5' end of the probe is
CC   covalently joined via a linker to a disulfide or primary amine. The 3'
CC   end of the probe is covalently joined to an amine-reactive fluorescent
CC   dye such as fluorescein. A gold surface or other metal film surface is
CC   attached to the disulfide or amine group to form the molecular beacon. In
CC   the native state with hybridised termini, the proximity of the
CC   fluorophore and quencher (gold surface) in the molecular beacon is such
CC   that little or no fluorescence is detectable. Upon hybridisation of the
CC   central complementary stretch of the probe to a target sequence (e.g. the
CC   sequence in ABL57070), the hairpin undergoes a conformational change
CC   resulting in an increase in fluorescence, the extent of which is
CC   proportional to the amount of binding partner present. The invention
CC   relates generally to the use of metal surface quenchers such as particles
CC   or films for high sensitivity applications in, for example, detection and
CC   diagnostic systems
XX
SQ   Sequence 24 BP; 1 A; 3 C; 4 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 24;
  Best Local Similarity   94.4%;  Pred. No. 2.6e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2802
              || |||||||||||||||
Db         23 GAGAAAAAAAAAAAAAA 6


RESULT 2414
ABX92831
ID   ABX92831 standard; DNA; 24 BP.
XX
AC   ABX92831;
XX
DT   16-MAY-2003  (first entry)
XX
DE   Borrelia burgdoferi K1L10 ZS7 B31 E61 and PKO primer.
XX
KW   ss; primer; ospC; vaccine; antibacterial; Lyme disease; erythema migrans;
KW   acrodermatitis chronica atrophicans; neuro-borreliosis; arthritis; PCR.
XX
OS   Borrelia burgdoferi.
XX
PN   US6486130-B1.
XX
PD   26-NOV-2002.
XX
PF   27-JUN-1996;   96US-00671548.
XX
PR   11-JUL-1991;   91US-00727245.
PR   22-JAN-1992;   92US-00824161.
PR   25-JUN-1992;   92US-00903580.
PR   29-APR-1993;   93US-00053863.
PR   19-AUG-1994;   94US-00284667.
XX
PA   (BAXT ) BAXTER VACCINE AG.
XX
PI   Livey I,  Crowe R,  Dorner F;
XX
DR   WPI; 2003-287432/28.
XX
PT   Recombinant Borrelia burgdorferi DNA sequence, OspC DNA sequence, useful
PT   for the production of OspC antigen which is useful as a vaccine for
PT   treating Lyme diseases.
XX
PS   Example 8; Col 29-30; 112pp; English.
XX
CC   The invention relates to a recombinant Borrelia burgdorferi DNA sequence,
CC   named ospC that encodes an OspC antigen containing amino acid sequence.
CC   The nucleic acid and an expression vector containing it are useful for
CC   the recombinant production of OspC antigen which is useful as a vaccine
CC   for treating Lyme disease and its related disorders e.g. erythema
CC   migrans, acrodermatitis chronica atrophicans, neuro-borreliosis and
CC   arthritis. The present sequence represents a PCR primer used to amplify
CC   Borrelia ospC genes
XX
SQ   Sequence 24 BP; 6 A; 1 C; 6 G; 11 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 24;
  Best Local Similarity   94.4%;  Pred. No. 2.6e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1760 ATTCATTAAGCTTTTTTT 1777
              ||||||||| |||||||
Db          4 ATTCATTAAGGTTTTTTT 21


RESULT 2415
ADC51227
ID   ADC51227 standard; DNA; 24 BP.
XX
AC   ADC51227;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Brassica defensin gene PCR primer #2.
XX
KW   antimicrobial protein; defensin; transgenic plant;
KW   composite disease resistance; pathogenic bacteria;
KW   rice white leaf blight; brown-stripe disease; glume blight;
KW   seedling damping-off disease; filamentous fungi; rice blight;
KW   sheath blight disease; leaf blight; gene; ss; PCR.
XX
OS   Unidentified.
OS   Brassica sp.
XX
PN   JP2003088379-A.
XX
PD   25-MAR-2003.
XX
PF   18-SEP-2001; 2001JP-00283117.
XX
PR   18-SEP-2001; 2001JP-00283117.
XX
PA   (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
XX
DR   WPI; 2003-621123/59.
XX
PT   Novel protein from Brassica campestris, useful as antimicrobial against
PT   plant pathogenic filamentous fungi or pathogenic bacteria, especially for
PT   treating e.g. rice white leaf blight and sheath blight disease.
XX
PS   Example 1; SEQ ID NO 7; 34pp; Japanese.
XX
CC   The invention comprises the amino acid and coding sequences of
CC   antimicrobial (defensin) proteins from Brassica. The DNA and protein
CC   sequences of the invention are useful for producing transformed plants
CC   with composite disease resistance, especially resistant to diseases
CC   caused by pathogenic bacteria, such as: rice white leaf blight, brown-
CC   stripe disease, glume blight, and seedling damping-off disease. As well
CC   as diseases caused by filamentous fungi, such as: rice blight, sheath
CC   blight disease, and leaf blight. The present DNA sequence represents a
CC   PCR primer that was used in the exemplification of the invention.
```

```
XX
SQ   Sequence 24 BP; 1 A; 5 C; 2 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 24;
  Best Local Similarity   94.4%;  Pred. No. 2.6e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTTT 2179
              ||| ||||||||||||||
Db          7 CTCTTTTTTTTTTTTTTT 24


RESULT 2416
AAC96214
ID   AAC96214 standard; DNA; 25 BP.
XX
AC   AAC96214;
XX
DT   26-FEB-2001  (first entry)
XX
DE   16s rRNA gene PCR primer #181.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 47; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 4 A; 3 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTAACT 2190
              |||||||||||||| |||
Db          1 TTTTTTTTTTTTTTCACT 18


RESULT 2417
AAC96549/c
ID   AAC96549 standard; DNA; 25 BP.
XX
AC   AAC96549;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DRB345 gene PCR primer #20.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 53; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 1 A; 2 C; 4 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2803
              || |||||||||||||||
Db         18 AAGAAAAAAAAAAAAAA 1


RESULT 2418
AAC96718/c
ID   AAC96718 standard; DNA; 25 BP.
XX
AC   AAC96718;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA HLA-A gene PCR primer #95.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
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```
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 56; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 1 A; 5 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAA 2798
                || ||||||||||||||
Db         18 AAGTGAAAAAAAAAAAAA 1


RESULT 2419
AAC96830/c
ID   AAC96830 standard; DNA; 25 BP.
XX
AC   AAC96830;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA HLA-C gene PCR primer #35.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 58; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 2 A; 4 C; 3 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAA 2799
                | ||||||||||||||||
Db         18 AGTGAAAAAAAAAAAAA 1


RESULT 2420
AAC96121/c
ID   AAC96121 standard; DNA; 25 BP.
XX
AC   AAC96121;
XX
DT   26-FEB-2001  (first entry)
XX
DE   16s rRNA gene PCR primer #88.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 45; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 4 A; 1 C; 5 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAA 2799
                | ||||||||||||||||
Db         18 ACTGAAAAAAAAAAAAA 1
```

```
RESULT 2421
ADB04575/c
ID   ADB04575 standard; DNA; 25 BP.
XX
AC   ADB04575;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ7 scanning oligonucleotide SEQ ID 5561.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 5561; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 25 BP; 4 A; 2 C; 3 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAA 2801
              | ||||||||||||||||
Db         19 TCAAAAAAAAAAAAAAAA 2


RESULT 2422
AAC96251
ID   AAC96251 standard; DNA; 25 BP.
XX
AC   AAC96251;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DPA1 gene PCR primer #8.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 48; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 3 A; 3 C; 3 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTA 2187
              |||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTGTA 18


RESULT 2423
AAC95851/c
ID   AAC95851 standard; DNA; 25 BP.
XX
AC   AAC95851;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA HLA-A gene PCR primer #31.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
```

```
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 41; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 3 A; 2 C; 4 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAA 2799
              ||||| ||||||||||||
Db         18 ATTGACAAAAAAAAAAAA 1


RESULT 2424
AAC96884
ID   AAC96884 standard; DNA; 25 BP.
XX
AC   AAC96884;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA HLA-C gene PCR primer #89.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 59; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 4 A; 3 C; 2 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTAAC 2189
              ||||||||||||| ||||
Db          1 TTTTTTTTTTTTTATAAC 18


RESULT 2425
AAC95722/c
ID   AAC95722 standard; DNA; 25 BP.
XX
AC   AAC95722;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DQA1 gene PCR primer #19.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 39; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 4 A; 1 C; 4 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAA 2797
              ||||| ||||||||||||
Db         18 GAATTTAAAAAAAAAAAA 1


RESULT 2426
AAC96511
ID   AAC96511 standard; DNA; 25 BP.
```

XX
AC AAC96511;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA DQB1 gene PCR primer #63.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 52; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 2 A; 2 C; 5 G; 16 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.4; DB 1; Length 25;
Best Local Similarity 94.4%; Pred. No. 2.8e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2171 TTTTTTTTTTTTTTTAA 2188
||||||||||||| |||||
Db 1 TTTTTTTTTTTTGTTTAA 18

RESULT 2427
AAC95684
ID AAC95684 standard; DNA; 25 BP.
XX
AC AAC95684;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA DPB1 gene PCR primer #19.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 38; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 4 A; 3 C; 3 G; 15 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.4; DB 1; Length 25;
Best Local Similarity 94.4%; Pred. No. 2.8e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2173 TTTTTTTTTTTTTTAACT 2190
||||||||||||| |||||
Db 1 TTTTTTTTTTTTGTAACT 18

RESULT 2428
AAC96213/c
ID AAC96213 standard; DNA; 25 BP.
XX
AC AAC96213;
XX
DT 26-FEB-2001 (first entry)
XX
DE 16s rRNA gene PCR primer #180.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 47; 66pp; English.
XX

```
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 5 A; 3 C; 3 G; 14 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAA 2797
              || |||||||||||||||
Db         18 GAGTTGAAAAAAAAAAAA 1


RESULT 2429
AAC96504
ID   AAC96504 standard; DNA; 25 BP.
XX
AC   AAC96504;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DQB1 gene PCR primer #56.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 52; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 5 A; 4 C; 2 G; 14 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTAAC 2189
              ||||||||||||| ||||
Db          1 TTTTTTTTTTTTTGTAAC 18


RESULT 2430
AAC96618
ID   AAC96618 standard; DNA; 25 BP.
XX
AC   AAC96618;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DRB345 gene PCR primer #89.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 54; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 2 A; 5 C; 3 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1771 TTTTTTTTTTTGAACCCC 1788
              |||||||||||||| ||
Db          2 TTTTTTTTTTTGAACTCC 19


RESULT 2431
AAC96321
ID   AAC96321 standard; DNA; 25 BP.
XX
AC   AAC96321;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DPB1 gene PCR primer #53.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
```

XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 49; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 4 A; 3 C; 3 G; 15 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.4; DB 1; Length 25;
Best Local Similarity 94.4%; Pred. No. 2.8e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2173 TTTTTTTTTTTTTTAACT 2190
||||||||||||| |||||
Db 1 TTTTTTTTTTTTGTAACT 18

RESULT 2432
AAC95753
ID AAC95753 standard; DNA; 25 BP.
XX
AC AAC95753;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA DQB1 gene PCR primer #24.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 39; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 5 A; 4 C; 2 G; 14 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.4; DB 1; Length 25;
Best Local Similarity 94.4%; Pred. No. 2.8e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2172 TTTTTTTTTTTTTTAAC 2189
||||||||||||| ||||
Db 1 TTTTTTTTTTTTGTAAC 18

RESULT 2433
AAC95751/c
ID AAC95751 standard; DNA; 25 BP.
XX
AC AAC95751;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA DQB1 gene PCR primer #22.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 39; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 2 A; 3 C; 6 G; 14 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.4; DB 1; Length 25;
Best Local Similarity 94.4%; Pred. No. 2.8e+03;

```
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1973 ACCTTGAAAAAAAGAAAA 1990
              |||||||||||| ||||
Db         18 ACCTTGAAAAAAAAAAAA 1


RESULT 2434
AAC96028
ID   AAC96028 standard; DNA; 25 BP.
XX
AC   AAC96028;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA HLA-C gene PCR primer #40.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 44; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 4 A; 3 C; 2 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTAAC 2189
              |||||||||||| ||||
Db          1 TTTTTTTTTTTTATAAC 18


RESULT 2435
AAC96424/c
ID   AAC96424 standard; DNA; 25 BP.
XX
AC   AAC96424;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DQA1 gene PCR primer #26.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 51; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 4 A; 1 C; 4 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAA 2797
              ||||| ||||||||||||
Db         18 GAATTTAAAAAAAAAAAA 1


RESULT 2436
ABL57069/c
ID   ABL57069 standard; DNA; 25 BP.
XX
AC   ABL57069;
XX
DT   22-JUL-2002  (first entry)
XX
DE   Molecular beacon oligonucleotide probe.
XX
KW   Molecular beacon; probe; fluorophore; nanoparticle;
KW   nucleic acid detection; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   stem_loop       1. .25
FT                   /*tag=  a
FT   misc_binding    1. .21
FT                   /*tag=  e
FT                   /bound_moiety= "Target oligonucleotide"
FT                   /note= "Forms double-stranded region with bases 1-21 of
FT                   sequence in ABL57071"
FT   misc_binding    1. .20
FT                   /*tag=  d
FT                   /bound_moiety= "Target oligonucleotide"
FT                   /note= "Forms double-stranded region with bases 1-20 of
```

```
FT                   sequence in ABL57070"
FT   modified_base   1
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "5' disulfide group"
FT   modified_base   25
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "3' amino group"
XX
PN   WO200218951-A2.
XX
PD   07-MAR-2002.
XX
PF   29-AUG-2001; 2001WO-US041941.
XX
PR   29-AUG-2000; 2000US-0228728P.
PR   30-MAR-2001; 2001US-0280350P.
XX
PA   (UYRQ ) UNIV ROCKEFELLER.
XX
PI   Dubertret B,  Calame M,  Libchaber A;
XX
DR   WPI; 2002-404569/43.
XX
PT   Sensitively detecting proximity changes in a system that utilizes an
PT   interacting fluorophore and quencher, for high sensitivity applications,
PT   involves utilizing a metal surface as quencher.
XX
PS   Example 1; Page 22; 62pp; English.
XX
CC   The present sequence is an oligonucleotide probe that was used in a
CC   molecular beacon in examples from the invention. The probe has a hairpin
CC   structure in the native state. The disulfide group at the 5' end of the
CC   probe was covalently linked to the 5' phosphate via a (CH2)6 spacer, and
CC   the primary amino group at the 3' was attached to the 3' hydroxyl via a
CC   (CH2)7 spacer. An amino-reactive dye, such as fluorescein, rhodamine 6G
CC   or Texas Red, was covalently linked to the 3'-amino group. A
CC   monomaleimido-gold nanoparticle was then covalently linked to the 5'
CC   sulfhydryl group to form the molecular beacon. In the native state with
CC   hybridised termini, the proximity of the fluorophore and quencher (gold
CC   nanoparticle) in the molecular beacon is such that little or no
CC   fluorescence is detectable. Upon hybridisation of the central
CC   complementary stretch of the probe to a target sequence (e.g. the
CC   sequence in ABL57070 or ABL57071), the hairpin undergoes a conformational
CC   change resulting in an increase in fluorescence, the extent of which is
CC   proportional to the amount of binding partner present. Single mismatch
CC   detection was demonstrated. The invention relates generally to the use of
CC   metal surface quenchers such as particles or films for high sensitivity
CC   applications in, for example, detection and diagnostic systems
XX
SQ   Sequence 25 BP; 1 A; 4 C; 4 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2802
              || ||||||||||||||||
Db         23 GAGAAAAAAAAAAAAAA 6


RESULT 2437
ABL57077/c
ID   ABL57077 standard; DNA; 25 BP.
XX
AC   ABL57077;
XX
DT   22-JUL-2002  (first entry)
XX
DE   Molecular beacon oligonucleotide probe.
XX
KW   Molecular beacon; probe; fluorophore; nanoparticle;
KW   nucleic acid detection; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   stem_loop       1. .22
FT                   /*tag=  a
FT   modified_base   1
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "5' amine"
FT   misc_binding    6. .21
FT                   /*tag=  d
FT                   /bound_moiety= "Target oligonucleotide"
FT                   /note= "Forms double-stranded region with bases 1-16 of
FT                   sequence in ABL57075"
FT   modified_base   25
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "3' DABCYL"
XX
PN   WO200218951-A2.
XX
PD   07-MAR-2002.
XX
PF   29-AUG-2001; 2001WO-US041941.
XX
PR   29-AUG-2000; 2000US-0228728P.
PR   30-MAR-2001; 2001US-0280350P.
XX
PA   (UYRQ ) UNIV ROCKEFELLER.
XX
PI   Dubertret B,  Calame M,  Libchaber A;
XX
DR   WPI; 2002-404569/43.
XX
PT   Sensitively detecting proximity changes in a system that utilizes an
PT   interacting fluorophore and quencher, for high sensitivity applications,
PT   involves utilizing a metal surface as quencher.
XX
PS   Example 3; Page 30; 62pp; English.
XX
CC   The present sequence is an oligonucleotide probe that was used in a
CC   molecular beacon in an example from the invention. A rhodamine 6G dye was
CC   attached to the primary amine at the 5' end of the oligonucleotide, which
CC   had DABCYL attached to its 3' end. A rhodamine-DNA-gold conjugate
CC   molecular beacon (see ABL57069) was also used. In the native state with
CC   hybridised termini, the proximity of the fluorophore and quencher (gold
CC   nanoparticle) in the molecular beacon is such that little or no
CC   fluorescence is detectable. Upon hybridisation of the central
CC   complementary stretch of the probe to a target sequence, the hairpin
CC   undergoes a conformational change resulting in an increase in
CC   fluorescence, the extent of which is proportional to the amount of
CC   binding partner present. Single mismatch detection was demonstrated. The
CC   invention relates generally to the use of metal surface quenchers such as
CC   particles or films for high sensitivity applications in, for example,
CC   detection and diagnostic systems
XX
SQ   Sequence 25 BP; 1 A; 4 C; 4 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2802
              || ||||||||||||||||
Db         23 GAGAAAAAAAAAAAAAA 6


RESULT 2438
ADE64628/c
ID   ADE64628 standard; DNA; 25 BP.
XX
```

```
AC   ADE64628;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Recombinant blood coagulation factor VIII protein related oligo #34.
XX
KW   blood coagulation factor VIII; type-A haemophilia; ss.
XX
OS   Unidentified.
XX
PN   CN1361178-A.
XX
PD   31-JUL-2002.
XX
PF   29-DEC-2000; 2000CN-00137779.
XX
PR   29-DEC-2000; 2000CN-00137779.
XX
PA   (SHAN-) SHANGHAI BIO-CHEM INST CHINESE ACAD SCI.
XX
PI   Qi Z,  Wang Q,  Chen C;
XX
DR   WPI; 2002-741852/81.
XX
PT   New recombinant blood coagulation factor VIII and its production process
PT   and medicinal composition.
XX
PS   Example 6; Page 18 (disclosure); 31pp; Chinese.
XX
CC   The invention relates to a novel recombinant blood coagulation factor
CC   VIII, its production process and its medicinal composite for treating
CC   type-A haemophilia. The invention further comprises a medicinal
CC   composition containing the blood coagulation factor which promotes blood
CC   coagulation to the blood plasma of type-A haemophilia patients. This
CC   polynucleotide sequence represents an oligo relating to the recombinant
CC   blood coagulation factor VIII protein of the invention.
XX
SQ   Sequence 25 BP; 1 A; 8 C; 8 G; 8 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        454 AGGCAGCCAGCAGCAGGC 471
              |||||| ||||||||||
Db         24 AGGCAGGCAGCAGCAGGC 7


RESULT 2439
ADB04566
ID   ADB04566 standard; DNA; 25 BP.
XX
AC   ADB04566;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ7 scanning oligonucleotide SEQ ID 5552.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 5552; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 25 BP; 2 A; 2 C; 4 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTT 2180
              | ||||||||||||||||
Db          8 TTCTTTTTTTTTTTTTT 25


RESULT 2440
ADB04566/c
ID   ADB04566 standard; DNA; 25 BP.
XX
AC   ADB04566;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ7 scanning oligonucleotide SEQ ID 5552.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
```

```
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 5552; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 25 BP; 2 A; 2 C; 4 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||| ||
Db         25 AAAAAAAAAAAAAAAGAA 8


RESULT 2441
ADB04576
ID   ADB04576 standard; DNA; 25 BP.
XX
AC   ADB04576;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ7 scanning oligonucleotide SEQ ID 5562.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 5562; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 25 BP; 4 A; 1 C; 4 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTGA 18


RESULT 2442
ADB04576/c
ID   ADB04576 standard; DNA; 25 BP.
XX
AC   ADB04576;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ7 scanning oligonucleotide SEQ ID 5562.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 5562; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
```

```
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 25 BP; 4 A; 1 C; 4 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAA 2801
              | |||||||||||||||
Db         18 TCAAAAAAAAAAAAAAA 1


RESULT 2443
ACI83927/c
ID   ACI83927 standard; DNA; 25 BP.
XX
AC   ACI83927;
XX
DT   14-OCT-2003  (first entry)
XX
DE   Human microarray DNA oligonucleotide SEQ ID NO 83918.
XX
KW   EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW   genetic variation; biallelic marker; polymorphism; human;
KW   cross-species comparison.
XX
OS   Homo sapiens.
XX
PN   US2003104410-A1.
XX
PD   05-JUN-2003.
XX
PF   15-MAR-2002; 2002US-00098263.
XX
PR   16-MAR-2001; 2001US-0276759P.
XX
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Mittmann MP;
XX
DR   WPI; 2003-567953/53.
XX
PT   New array of nucleic acid probes, useful for in situ hybridization, in
PT   Southern, Northern or dot-blot hybridization to identify or detect the
PT   sequence or specific mutations of any gene.
XX
PS   Claim 1; SEQ ID NO 83918; 9pp; English.
XX
CC   The invention discloses a microarray comprising a plurality of nucleic
CC   acid probes including one of 2,018,500 fully defined sequences, or its
CC   perfect match, perfect mismatch, antisense match or antisense mismatch.
CC   Also disclosed is a method of gene expression analysis. The array is used
CC   in monitoring gene expression levels by hybridisation to a DNA library,
CC   in analysis of genetic variation or in hybridisation of tag-labelled
CC   compounds. The nucleic acid probes are specifically designed for analysis
CC   of at least one target sequence. The method of analysis comprises
CC   hybridising at least one or more nucleic acids to at least two or more
CC   nucleic acid probes and detecting the hybridisation. The nucleic acid
CC   probes are attached to a solid support. The analysis comprises monitoring
CC   gene expression levels, identifying biallelic markers or polymorphisms,
CC   or family members of a gene and a cross-species comparison. Each of the
CC   nucleic acids further comprises a tag sequence. The array of nucleic acid
CC   probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC   blot hybridisation to identify or detect the sequence or specific
CC   mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC   primer extensions or in screening cDNA or genomic libraries or subclones
CC   for additional subclones containing segments of DNA that have been
CC   isolated and previously sequenced. The sequence presented is one of the
CC   nucleic acid probes incorporated in the microarray. Note: The sequence
CC   data for this patent can also be obtained in electronic format directly
CC   from USPTO at seqdata.uspto.goc/sequence.html
XX
SQ   Sequence 25 BP; 4 A; 8 C; 5 G; 8 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        954 GAGGTGTTCTCAGAAGAG 971
              ||||| ||||||||||||
Db         23 GAGGTCTTCTCAGAAGAG 6


RESULT 2444
ADA14835/c
ID   ADA14835 standard; DNA; 25 BP.
XX
AC   ADA14835;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Hairpin oligonucleotide, #1, used in an example of the invention.
XX
KW   Hairpin sensor; hairpin loop; complementary probe; inverse repeat arm;
KW   quenchable fluorescing agent; microarray; semiconductor; nanocrystal;
KW   rhodamine B-labelled dye; detection; gold support; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER= thiol group"
FT   misc_binding    6. .20
FT                   /*tag=  b
FT                   /bound_moiety= "Target sequence #1"
FT                   /note= "Forms a doube-stranded region with the target
FT                   sequence shown in example 2"
FT   modified_base   25
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "OTHER= amino group"
XX
PN   US2003013109-A1.
XX
PD   16-JAN-2003.
XX
PF   21-JUN-2002; 2002US-00176055.
XX
PR   21-JUN-2001; 2001US-0299460P.
XX
PA   (BALL/) BALLINGER C T.
PA   (LOCA/) LOCASCIO M.
PA   (LAND/) LANDRY D P.
XX
PI   Ballinger CT,  Locascio M,  Landry DP;
XX
DR   WPI; 2003-596312/56.
XX
PT   Hairpin sensor useful for detecting a target nucleotide sequence in a
PT   sample, comprises a hairpin loop assembly including a complementary probe
PT   and a quenchable fluorescing agent.
XX
PS   Example 2; Page 11; 16pp; English.
XX
CC   The invention discloses a hairpin sensor comprising a hairpin loop
CC   assembly including a complementary probe positioned between a first
CC   inverse repeat arm and a second inverse repeat arm, and a quenchable
CC   fluorescing agent joined, directly or indirectly, to the end of the
CC   second inverse repeat arm of the hairpin loop assembly opposite the
CC   complementary probe. Also claimed is a microarray comprising the hairpin
```

```
CC   sensor, where the end of the first inverse repeat arm opposite the
CC   complementary probe is bound, directly or indirectly, to a support, a kit
CC   for detecting a target nucleotide sequence in a sample comprising the
CC   hairpin sensor, and a support, and a hairpin sensor system, in which the
CC   particle is conductive or semi-conductive, including at least one of the
CC   above hairpin sensor assemblies. The hairpin sensor further comprises a
CC   functional group joined to the end of the first inverse repeat arm
CC   opposite the complementary probe, or first spacer opposite the first
CC   inverse repeat arm, the functional group selected from amino, carboxyl,
CC   thiol and hydroxyl. Further, the sensor comprises a ligand positioned
CC   between the second inverse repeat arm and the quenchable fluorescing
CC   agent, where the ligand is selected from mercapto, hydroxyl, amino,
CC   nitrile and carboxyl, carboxylic acid, organic acid and amino acid. The
CC   second spacer is positioned between the second inverse repeat arm and the
CC   quenchable fluorescing agent which comprises a semiconductor nanocrystal
CC   or rhodamine B-labelled dye. Within the microarray the support is capable
CC   of accepting a charge. At least one hairpin sensor comprises two or more
CC   hairpin sensors. The two or more hairpin sensors include complementary
CC   probes that are the same or different and respective quenchable
CC   fluorescing agents that are the same or different. The two or more
CC   hairpin sensors are arranged in a spatially-defined pattern. The sensor
CC   and system are useful for detecting a target nucleotide sequence in a
CC   sample. Further, the method involves identifying the target nucleotide
CC   sequence by the location of the complementary probe to which the target
CC   nucleotide sequence binds. The two or more hairpin sensors include
CC   complementary probes or quenchable fluorescing agents, that are
CC   different. The sequence presented is the hairpin oligonucleotide, #1,
CC   used in an example of the invention.
XX
SQ   Sequence 25 BP; 1 A; 4 C; 4 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2802
              || |||||||||||||||
Db         23 GAGAAAAAAAAAAAAAA 6


RESULT 2445
AAD57902/c
ID   AAD57902 standard; DNA; 25 BP.
XX
AC   AAD57902;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Oligonucleotide used in nonlinear optical technique.
XX
KW   Nonlinear optical technique; screening; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Linked to Au particle"
FT   modified_base   25
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "Linked to Dye"
XX
PN   WO2003064991-A2.
XX
PD   07-AUG-2003.
XX
PF   17-JUL-2002; 2002WO-US022681.
XX
PR   17-JUL-2001; 2001US-0306040P.
PR   23-OCT-2001; 2001US-0347821P.
PR   06-FEB-2002; 2002US-0354668P.
XX
PA   (SALA/) SALAFSKY J S.
XX
PI   Salafsky JS;
XX
DR   WPI; 2003-646172/61.
XX
PT   Screening candidate binding partner(s) for binding to test molecule by
PT   applying external force field to sample in homogeneous phase,
PT   illuminating sample with light beam(s) at fundamental frequencies, and
PT   measuring physical properties.
XX
PS   Disclosure; Fig 20B; 146pp; English.
XX
CC   The present invention relates to a method for detecting interactions
CC   between biological components using a nonlinear optical technique. The
CC   invention is used for screening candidate binding partner(s) for binding
CC   to test molecule. It can also be used to detect changes in orientation or
CC   conformation of the probe and/or target. The present sequence is an
CC   oligonucleotide used in nonlinear optical technique
XX
SQ   Sequence 25 BP; 1 A; 4 C; 4 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2802
              || |||||||||||||||
Db         23 GAGAAAAAAAAAAAAAA 6


RESULT 2446
AAD57848
ID   AAD57848 standard; DNA; 25 BP.
XX
AC   AAD57848;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Oligonucleotide related to the invention.
XX
KW   Nonlinear optical technique; screening; ss.
XX
OS   Unidentified.
XX
PN   WO2003064991-A2.
XX
PD   07-AUG-2003.
XX
PF   17-JUL-2002; 2002WO-US022681.
XX
PR   17-JUL-2001; 2001US-0306040P.
PR   23-OCT-2001; 2001US-0347821P.
PR   06-FEB-2002; 2002US-0354668P.
XX
PA   (SALA/) SALAFSKY J S.
XX
PI   Salafsky JS;
XX
DR   WPI; 2003-646172/61.
XX
PT   Screening candidate binding partner(s) for binding to test molecule by
PT   applying external force field to sample in homogeneous phase,
PT   illuminating sample with light beam(s) at fundamental frequencies, and
PT   measuring physical properties.
XX
PS   Disclosure; Page 146; 146pp; English.
XX
CC   The present invention relates to a method for detecting interactions
CC   between biological components using a nonlinear optical technique. The
CC   invention is used for screening candidate binding partner(s) for binding
CC   to test molecule. It can also be used to detect changes in orientation or
```

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CC   conformation of the probe and/or target. The present sequence is an
CC   oligonucleotide related to the invention
XX
SQ   Sequence 25 BP; 1 A; 5 C; 3 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTT 2182
              ||||||||||||||||| |
Db          5 CTTTTTTTTTTTTTTTCT 22


RESULT 2447
AAD57848/c
ID   AAD57848 standard; DNA; 25 BP.
XX
AC   AAD57848;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Oligonucleotide related to the invention.
XX
KW   Nonlinear optical technique; screening; ss.
XX
OS   Unidentified.
XX
PN   WO2003064991-A2.
XX
PD   07-AUG-2003.
XX
PF   17-JUL-2002; 2002WO-US022681.
XX
PR   17-JUL-2001; 2001US-0306040P.
PR   23-OCT-2001; 2001US-0347821P.
PR   06-FEB-2002; 2002US-0354668P.
XX
PA   (SALA/) SALAFSKY J S.
XX
PI   Salafsky JS;
XX
DR   WPI; 2003-646172/61.
XX
PT   Screening candidate binding partner(s) for binding to test molecule by
PT   applying external force field to sample in homogeneous phase,
PT   illuminating sample with light beam(s) at fundamental frequencies, and
PT   measuring physical properties.
XX
PS   Disclosure; Page 146; 146pp; English.
XX
CC   The present invention relates to a method for detecting interactions
CC   between biological components using a nonlinear optical technique. The
CC   invention is used for screening candidate binding partner(s) for binding
CC   to test molecule. It can also be used to detect changes in orientation or
CC   conformation of the probe and/or target. The present sequence is an
CC   oligonucleotide related to the invention
XX
SQ   Sequence 25 BP; 1 A; 5 C; 3 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2802
              || |||||||||||||||
Db         23 GAGAAAAAAAAAAAAAA 6


RESULT 2448
ACF04465
ID   ACF04465 standard; DNA; 25 BP.
XX
AC   ACF04465;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Real time PCR targeting IL-1ra probe P291.
XX
KW   Nucleic acid level determination; PCR; primer; probe; DNA quantification;
KW   gene therapy; immunosuppressive; anti-HIV; antiarthritic;
KW   neuroprotective; cytostatic; antiallergic; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "modified by 6FAM"
FT   modified_base    25
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "modified by TAMRA-p"
XX
PN   WO2003060119-A2.
XX
PD   24-JUL-2003.
XX
PF   20-JAN-2003; 2003WO-EP000493.
XX
PR   18-JAN-2002; 2002EP-00447009.
XX
PA   (ULBR ) UNIV LIBRE BRUXELLES.
XX
PI   Stordeur P,  Goldman M;
XX
DR   WPI; 2003-598531/56.
XX
PT   Quantifying in vivo RNA from a biological sample for producing a
PT   medicament for treating immune related disease by determining in vivo
PT   levels of transcripts using nucleic acid/reverse transcription-PCR
PT   reagent mix in an automated setup.
XX
PS   Disclosure; Page 42; 83pp; English.
XX
CC   The present invention relates to a method of quantifying in vivo RNA from
CC   a biological sample. This involves collecting the biological sample in a
CC   tube comprising a compound inhibiting RNA degradation and/or gene
CC   induction, forming a precipitate comprising nucleic acids, separating the
CC   precipitate from the supernatant, dissolving the precipitate using a
CC   buffer, forming a suspension, isolating nucleic acids from the suspension
CC   using an automated device, dispersing or distributing a reagent mix for
CC   reverse transcription (RT)-PCR using an automated device, dispersing or
CC   distributing the nucleic acids isolated within the dispersed reagent mix
CC   using an automated device and determining the in vivo levels of
CC   transcripts using the nucleic acid and RT-PCR reagent mix of the previous
CC   step in an automated setup. The method is useful for monitoring or
CC   detecting changes in in vivo nucleic acids levels in a biological agent
CC   present, such as eukaryotic or prokaryotic cells, viruses or phages in a
CC   biological sample or for producing a medicament for treating immune
CC   related disease, e.g., autoimmunity, rheumatoid arthritis, multiple
CC   sclerosis, cancer, immunodeficiencies such as AIDS, allergy, graft
CC   rejection or Graft versus Host Disease. The present sequence is a PCR
CC   primer/probe used in the exemplification of the invention
XX
SQ   Sequence 25 BP; 6 A; 6 C; 8 G; 5 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1458 GAGACCAGAGTCCAGCTG 1475
              ||||||||| ||||||||
Db          8 GAGACCAGACTCCAGCTG 25
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RESULT 2449
AAT93819/c
ID   AAT93819 standard; DNA; 26 BP.
XX
AC   AAT93819;
XX
DT   25-MAR-2003  (revised)
DT   24-FEB-1998  (first entry)
XX
DE   Antitumoural phosphodiester oligonucleotide 9 with cytotoxic activity.
XX
KW   Phosphodiester; selective binding; cell viability; growth;
KW   tumoural cell line; cytotoxic activity; tumour cell; lymphoma;
KW   lymphoblastic tumour; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .26
FT                   /*tag=  a
FT                   /note= "phosphodiester oligonucleotide"
XX
PN   WO9720924-A1.
XX
PD   12-JUN-1997.
XX
PF   04-DEC-1996;   96WO-EP005388.
XX
PR   04-DEC-1995;   95IT-MI002539.
XX
PA   (SAIC-) SAICOM SRL.
XX
PI   Scaggiante B,  Quadrifoglio F;
XX
DR   WPI; 1997-319771/29.
XX
PT   New phospho:di:esteric oligo:nucleotide(s) - which exert a specific and
PT   selective cytotoxic effect on tumour cells, for treating both solid and
PT   liquid tumours.
XX
PS   Claim 10; Page 5; 38pp; English.
XX
CC   Novel phosphodiesteric oligonucleotides AAT93811-27 are based on the
CC   generic formula, in the 3'-5' or 5'-3' direction: (GaTa')a''-(GbTb')b''-
CC   (GcTc')c''-(GdTd')d''-(GeTe')e''-(GfTf')f''- (G-gTg')g''-N', where: N and
CC   N' = T or G, equal or different from each other; x = 0-8, equal or
CC   different from each other; a, b, c, d, e, f, and g = 0-10, equal or
CC   different from each other; a', b', c', d', e', f', and g' = 0-30, equal
CC   or different from each other; a'', b'', c'', d'', e'', f'', and g'' = 1-
CC   16, equal or different from each other; The oligonucleotides are believed
CC   to selectively bind and sequester some proteins which are essential to
CC   the viability and growth of tumoural cell line. They have specific and
CC   selective cytotoxic activity against tumour cells, and can be used for
CC   treating tumours of the liquid type, in particular of lymphoblastic
CC   origin, and of solid type, in particular lymphomas. The present
CC   phosphodiester oligonucleotide, at a concentration of 15 micromolar,
CC   reduced growth of CCRF-CEM tumoural cells by 76%, which is detectable 48
CC   hours after administration. (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ   Sequence 26 BP; 0 A; 0 C; 2 G; 24 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 26;
  Best Local Similarity   76.9%;  Pred. No. 3e+03;
  Matches   20;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   | |||||||| ||||||||
Db         26 AAAAAAAACAAAAAAAACAAAAAAAA 1


RESULT 2450
AAX23568
ID   AAX23568 standard; DNA; 27 BP.
XX
AC   AAX23568;
XX
DT   18-JUN-1999  (first entry)
XX
DE   Deletion sequence oligonucleotide 21.
XX
KW   Deletion sequence oligonucleotide; sensor array; eukaryotic pathogen;
KW   probe; cellular adhesion modulator; cellular proliferation modulator;
KW   human retrovirus; human immunodeficiency virus; non-human retrovirus;
KW   HIV; primer; ss.
XX
OS   Synthetic.
XX
PN   WO9911820-A1.
XX
PD   11-MAR-1999.
XX
PF   01-SEP-1998;   98WO-US018084.
XX
PR   02-SEP-1997;   97US-00923771.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Chen D,  Srivatsa GS;
XX
DR   WPI; 1999-205198/17.
XX
PT   New compositions comprising sensor arrays made up of unique probe
PT   oligonucleotides - useful for characterizing a sample of target deletion
PT   oligonucleotides.
XX
PS   Example 1; Page 96; 163pp; English.
XX
CC   This invention describes a novel composition comprising a number of
CC   sensor arrays, where each array comprises a unique probe oligonucleotide,
CC   which is the reverse complement of part of a unique target
CC   oligonucleotide present in a mixture of target deletion sequence
CC   oligonucleotides. The compositions form a method for characterizing a
CC   sample of target deletion oligonucleotides which are labelled and
CC   hybridize with the probe oligonucleotides of the sensor arrays. Such
CC   oligonucleotides and their targets are represented in AAX23548-X23709.
CC   Oligonucleotides characterized by the method form pharmaceutical
CC   compositions that are useful for modulating cellular adhesion or
CC   proliferation, and being active against a eukaryotic pathogen, a human
CC   retrovirus, a human immunodeficiency virus (HIV), or a non-human
CC   retrovirus, including influenza virus, Epstein-Barr virus, Respiratory
CC   Syncytial Virus or cytomegalovirus (CMV). The compositions enable
CC   characterization of deletion sequence oligonucleotides having related,
CC   but different nucleobase sequences, and quantification of different
CC   species of deletion sequence ("target") oligonucleotides in a mixture.
CC   Also, if the specificity of the oligonucleotide's nucleobase sequence for
CC   its reverse complement is not modified, the method may be performed using
CC   oligodeoxynucleotides
XX
SQ   Sequence 27 BP; 7 A; 2 C; 3 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 27;
  Best Local Similarity   94.4%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTAA 2188
              |||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTCAA 18


RESULT 2451
ABL35101
ID   ABL35101 standard; DNA; 30 BP.
XX
AC   ABL35101;
XX
```

```
DT   04-APR-2002  (first entry)
XX
DE   Phosphorothioate substituted RNA/DNA hybrid oligonucleotide SEQ ID NO: 7.
XX
KW   DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
KW   infection; allergy; cancer; hypersensitivity; bio-warfare;
KW   immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
KW   immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
KW   antiinflammatory; antibacterial; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .14
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "phosphorothioate backbone"
FT   misc_RNA         1. .14
FT                    /*tag=  b
FT   misc_RNA         17. .30
FT                    /*tag=  c
XX
PN   WO200193902-A2.
XX
PD   13-DEC-2001.
XX
PF   07-JUN-2001; 2001WO-US018276.
XX
PR   07-JUN-2000; 2000US-0209797P.
XX
PA   (BIOS-) BIOSYNEXUS INC.
XX
PI   Mond JJ,  Flora M,  Klinman DM;
XX
DR   WPI; 2002-130570/17.
XX
PT   New immunostimulatory compositions comprising RNA/DNA hybrid
PT   oligonucleotides, useful for enhancing an immune response or inducing
PT   cytokines, particularly for treating diseases, e.g. cancer, allergy or
PT   HIV infection.
XX
PS   Example 1; Page 30; 68pp; English.
XX
CC   The present invention relates to an immunostimulatory composition, which
CC   comprises at least one oligonucleotide comprising both an RNA region and
CC   a DNA region. The composition is useful for enhancing an immune response
CC   or inducing cytokines. It can be used as a vaccine adjuvant and in
CC   treating diseases, including pathogenic infection, (non-)malignant
CC   tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
CC   colon, or carcinomas and sarcomas), autoimmune diseases or allergies
CC   (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
CC   hepatitis, HIV or malaria. The composition is also useful for treating,
CC   preventing or ameliorating the symptoms resulting from exposure to a bio-
CC   warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
CC   an immunostimulatory oligonucleotide described in the exemplification of
CC   the invention
XX
SQ   Sequence 30 BP; 28 A; 1 C; 1 G; 0 T; 0 U; 0 Other;

  Query Match              0.6%;  Score 16.4;  DB 1;  Length 30;
  Best Local Similarity   76.9%;  Pred. No. 3.5e+03;
  Matches   20;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
                 | ||   |||||||  ||||||||||
Db          1 AAAAAAAAAAAAAACGAAAAAAAAAA 26


RESULT 2452
AAT93816/c
ID   AAT93816 standard; DNA; 35 BP.
XX
AC   AAT93816;
XX
DT   25-MAR-2003  (revised)
DT   24-FEB-1998  (first entry)
XX
DE   Antitumoural phosphodiester oligonucleotide 6 with cytotoxic activity.
XX
KW   Phosphodiester; selective binding; cell viability; growth;
KW   tumoural cell line; cytotoxic activity; tumour cell; lymphoma;
KW   lymphoblastic tumour; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .35
FT                    /*tag=  a
FT                    /note= "phosphodiester oligonucleotide"
XX
PN   WO9720924-A1.
XX
PD   12-JUN-1997.
XX
PF   04-DEC-1996;   96WO-EP005388.
XX
PR   04-DEC-1995;   95IT-MI002539.
XX
PA   (SAIC-) SAICOM SRL.
XX
PI   Scaggiante B,  Quadrifoglio F;
XX
DR   WPI; 1997-319771/29.
XX
PT   New phospho:di:esteric oligo:nucleotide(s) - which exert a specific and
PT   selective cytotoxic effect on tumour cells, for treating both solid and
PT   liquid tumours.
XX
PS   Claim 10; Page 5; 38pp; English.
XX
CC   Novel phosphodiesteric oligonucleotides AAT93811-27 are based on the
CC   generic formula, in the 3'-5' or 5'-3' direction: (GaTa')a''-(GbTb')b''-
CC   (GcTc')c''-(GdTd')d''-(GeTe')e''-(GfTf')f''- (G-gTg')g''-N', where: N and
CC   N' = T or G, equal or different from each other; x = 0-8, equal or
CC   different from each other; a, b, c, d, e, f, and g = 0-10, equal or
CC   different from each other; a', b', c', d', e', f', and g' = 0-30, equal
CC   or different from each other; a'', b'', c'', d'', e'', f'', and g'' = 1-
CC   16, equal or different from each other; The oligonucleotides are believed
CC   to selectively bind and sequester some proteins which are essential to
CC   the viability and growth of tumoural cell line. They have specific and
CC   selective cytotoxic activity against tumour cells, and can be used for
CC   treating tumours of the liquid type, in particular of lymphoblastic
CC   origin, and of solid type, in particular lymphomas. The present
CC   phosphodiester oligonucleotide, at a concentration of 15 micromolar,
CC   reduced growth of CCRF-CEM tumoural cells by 83%, which is detectable 48
CC   hours after administration. (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ   Sequence 35 BP; 0 A; 0 C; 5 G; 30 T; 0 U; 0 Other;

  Query Match              0.6%;  Score 16.4;  DB 1;  Length 35;
  Best Local Similarity   76.9%;  Pred. No. 3.8e+03;
  Matches   20;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
                 | ||   |||||||  ||||||| |||
Db         32 AAAAAACAAAAAAACAAAAAAACAAA 7


RESULT 2453
AAX18389
ID   AAX18389 standard; DNA; 18 BP.
XX
AC   AAX18389;
XX
DT   11-MAY-1999  (first entry)
XX
```

DE RT-PCR primer of the invention SEQ ID 30.
XX
KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS Synthetic.
XX
PN JP11032765-A.
XX
PD 09-FEB-1999.
XX
PF 18-JUL-1997; 97JP-00208312.
XX
PR 18-JUL-1997; 97JP-00208312.
XX
PA (TAKI) TAKARA SHUZO CO LTD.
XX
DR WPI; 1999-183822/16.
XX
PT Peptides having at least two new nucleotides - useful as primers in RT-
PT PCR.
XX
PS Example 1; Page 12; 19pp; Japanese.
XX
CC This sequence represents a primer of the invention. The invention relates
CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC natural number indicating the repetition of alpha; beta, delta = V or N;
CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC repetition of gamma, in which thymine expressed by gamma is composed of
CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC useful as primers for RT-PCR and determination of base sequences. The new
CC sequences allow for reproductive and highly efficient analysis of gene
CC sequences
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 2 Other;

Query Match 0.6%; Score 16.2; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 1.5e+03;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2171 TTTTTTTTTTTTTTTA 2187
||||||||||||||||:
Db 1 TTTTTTTTTTTTTTTV 17

RESULT 2454
AAX18389/c
ID AAX18389 standard; DNA; 18 BP.
XX
AC AAX18389;
XX
DT 11-MAY-1999 (first entry)
XX
DE RT-PCR primer of the invention SEQ ID 30.
XX
KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS Synthetic.
XX
PN JP11032765-A.
XX
PD 09-FEB-1999.
XX
PF 18-JUL-1997; 97JP-00208312.
XX
PR 18-JUL-1997; 97JP-00208312.
XX
PA (TAKI) TAKARA SHUZO CO LTD.
XX
DR WPI; 1999-183822/16.
XX
PT Peptides having at least two new nucleotides - useful as primers in RT-
PT PCR.
XX
PS Example 1; Page 12; 19pp; Japanese.
XX
CC This sequence represents a primer of the invention. The invention relates
CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC natural number indicating the repetition of alpha; beta, delta = V or N;
CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC repetition of gamma, in which thymine expressed by gamma is composed of
CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC useful as primers for RT-PCR and determination of base sequences. The new
CC sequences allow for reproductive and highly efficient analysis of gene
CC sequences
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 2 Other;

Query Match 0.6%; Score 16.2; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 1.5e+03;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAAAAAA 2801
:||||||||||||||||
Db 17 BAAAAAAAAAAAAAAA 1

RESULT 2455
AAZ26249
ID AAZ26249 standard; DNA; 21 BP.
XX
AC AAZ26249;
XX
DT 30-NOV-1999 (first entry)
XX
DE Human polymorphic region 438.
XX
KW Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW cell viability; loss of heterozygosity; precancerous condition; ASI;
KW allele specific inhibitor; somatic cell; diagnosis; prevention;
KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW graft versus host disease; malignant cell removal; bone marrow; ss.
XX
OS Homo sapiens.
XX
PN WO9841648-A2.
XX
PD 24-SEP-1998.
XX
PF 19-MAR-1998; 98WO-US005419.
XX
PR 20-MAR-1997; 97US-0041057P.
XX
PA (VARI-) VARIAGENICS INC.
XX
PI Housman D, Ledley FD, Stanton VP;
XX
DR WPI; 1998-521232/44.
XX
PT Identifying target genes for allele-specific drugs - used for diagnosis,
PT prevention and treatment of, e.g. cancers, atherosclerotic plaque,
PT dysplastic lesions, endometriosis or graft versus host disease.
XX
PS Disclosure; Fig 7; 605pp; English.
XX
CC This invention describes a novel method for identifying an inhibitor
CC potentially useful for treatment of cancer, where the inhibitor is active
CC on a gene vital for cell growth or viability, and where the gene is
CC subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC used for preventing the development of cancer in a patient having a

CC precancerous condition, by administering to the patient a first allele
CC specific inhibitor (ASI) targeted to an allele of a first essential gene
CC present in cells of the precancerous condition, where the normal somatic
CC cells of the patient are heterozygous for the first gene, the inhibitor
CC is active on at least one but less than all allelic forms of the gene
CC present in a population and targets only one allelic form present in the
CC normal somatic cells, and the first gene. The products and methods can be
CC used in the diagnosis, prevention and treatment of LOH disorders, e.g.
CC cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
CC lesions, benign tumours, endometriosis, polycystic kidney disease, and
CC graft versus host disease. The method can also be used to remove
CC malignant cells from bone marrow transplants. AAZ25812-Z26825 represent
CC human polymorphic sites described in the method of the invention
XX
SQ Sequence 21 BP; 13 A; 1 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.1e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2776 GTTAGAATTGAAAAAAAAAAA 2796
||||| || ||||||||||||
Db 1 GTTAGCTTTAAAAAAAAAAAA 21

RESULT 2456
AAZ09196
ID AAZ09196 standard; DNA; 21 BP.
XX
AC AAZ09196;
XX
DT 19-OCT-1999 (first entry)
XX
DE Oligonucleotide 8 for DNA analysis.
XX
KW Primer; DNA analysis; amplification; hybridisation; ss.
XX
OS Synthetic.
XX
PN JP11196874-A.
XX
PD 27-JUL-1999.
XX
PF 14-JAN-1998; 98JP-00005399.
XX
PR 14-JAN-1998; 98JP-00005399.
XX
PA (HITA) HITACHI LTD.
XX
DR WPI; 1999-496652/42.
XX
PT Analysis of DNA fragment - comprises addition of known common
PT oligonucleotide, amplification of resultant DNA fragment and analysis and
PT labelling of amplified DNA.
XX
PS Example 1; Page 12; 17pp; Japanese.
XX
CC This invention descibes a novel method for the analysis of a DNA fragment
CC which comprises: (i) addition of a known common oligonucleotide sequence
CC to at least one terminal of each DNA fragment, (ii) amplification of the
CC resultant DNA fragment as a primer using a first common primer containing
CC a complementary nucleotide sequence to the above mentioned known common
CC oligonucleotide sequence, a second common primer containing a
CC complementary nucleotide sequence to the prepared known common
CC oligonucleotide sequence optionally having been introduced with
CC complementary nucleotide sequence at a terminal, and a specific primer
CC capable of hybridisation with a DNA fragment containing whole or part of
CC the gene having known sequence, to give amplified DNA, (iii) analysis of
CC the amplified DNA to find the information of the DNA fragment, in which
CC the specific primer is designed to prepare fragments of the common first
CC and second primers and to give short fragment of amplified DNA and (iv)
CC labelling them to make their differentiation. Differentiation of
CC informations of known and unknown genes readily provides information of
CC unknown gene and simultaneous monitoring of signals derived from minor
CC genes. Furthermore, labelling of DNAs according to functions of known
CC genes can be performed. AAZ09189-Z09201 represent oligonucleotide primers
CC used to illustrate the method of the invention
XX
SQ Sequence 21 BP; 0 A; 0 C; 3 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.1e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2161 TCTCCTTTTTTTTTTTTTTT 2181
| | ||||||||||||||||||
Db 1 TGTGGTTTTTTTTTTTTTTT 21

RESULT 2457
AAZ73804
ID AAZ73804 standard; DNA; 21 BP.
XX
AC AAZ73804;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human biallelic marker downstream amplification primer SEQ ID NO:8160.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB000822.
XX
PR 21-APR-1998; 98US-0082614P.
PR 23-NOV-1998; 98US-0109732P.
XX
PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
DR WPI; 2000-013267/01.
XX
PT Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
XX
PS Claim 8; Page 1970; 2745pp; English.
XX
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention
XX
SQ Sequence 21 BP; 6 A; 7 C; 1 G; 7 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.2; DB 1; Length 21;

```
  Best Local Similarity   85.7%;  Pred. No. 2.1e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1567 AAAAATCCTTCTCCACCGCAC 1587
              || |||| |||||||| ||||
Db          1 AATAATCTTTCTCCACTGCAC 21


RESULT 2458
AAA62856
ID   AAA62856 standard; DNA; 21 BP.
XX
AC   AAA62856;
XX
DT   24-OCT-2000  (first entry)
XX
DE   PCR primer used for RANTES promoter DNA fragment amplification.
XX
KW   Human; regulated upon activation normal T cell expressed and secreted;
KW   RANTES; single nucleotide polymorphism; SNP; chemokine; diagnose; detect;
KW   HIV; asthma; inflammatory disease; PCR primer; promoter; ss.
XX
OS   Homo sapiens.
XX
PN   WO200034516-A1.
XX
PD   15-JUN-2000.
XX
PF   09-DEC-1999;   99WO-GB004152.
XX
PR   10-DEC-1998;   98GB-00027032.
PR   29-SEP-1999;   99GB-00022984.
XX
PA   (UYMA-) UNIV VICTORIA MANCHESTER.
XX
PI   Hajeer A,  Ollier W;
XX
DR   WPI; 2000-423445/36.
XX
PT   Diagnosing or detecting a predisposition to a disease or disorder in
PT   vitro for treating asthma and HIV infection involves examining the
PT   presence of genetic polymorphism in RANTES gene promoter.
XX
PS   Claim 12; Page 40; 58pp; English.
XX
CC   The present invention relates to a method for detecting or diagnosing a
CC   predisposition to a disease or disorder associated with abnormal RANTES
CC   gene expression in vitro. The method involves examining the RANTES gene
CC   promoter to detect the presence of a genetic polymorphism. Also included
CC   in the invention is a method of treating individuals who either have or
CC   are pre-disposed to diseases or disorders associated with abnormal RANTES
CC   gene expression by administering to individuals who have a RANTES
CC   promoter polymorphism as determined by the method, a modulator of RANTES
CC   activity. RANTES (regulated upon activation normal T cell expressed and
CC   secreted) belongs to the superfamily of pro-inflammatory cytokines called
CC   chemokines. RANTES is involved in the attraction and recruitment of
CC   monocytes, memory T cells, basophils, and natural killer cells to sites
CC   of inflammation. The RANTES gene is located on the long arm of chromosome
CC   17 at 17Q 11.2-q12. The method is useful for diagnosing and detecting
CC   inflammatory diseases, asthma and HIV infection and also for diagnosing
CC   patients having a predisposition to develop these diseases. Modulators of
CC   RANTES activity are useful for treating individuals who either have or
CC   are predisposed to diseases or disorders associated with abnormal RANTES
CC   gene expression such as asthma, and HIV, and other inflammatory diseases.
CC   This sequence represents a PCR primer used to amplify a fragment of the
CC   human RANTES promoter sequence. The fragment of DNA amplified, contains
CC   the area surrounding a single nucleotide polymorphism (SNP) at position -
CC   403. The primer is used in the method of the invention
XX
SQ   Sequence 21 BP; 5 A; 3 C; 3 G; 10 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 21;
  Best Local Similarity   85.7%;  Pred. No. 2.1e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2261 TGCATATTTATTTCAGATGTT 2281
              ||| |||| ||| ||||||||
Db          1 TGCTTATTCATTACAGATGTT 21


RESULT 2459
AAH89080/c
ID   AAH89080 standard; DNA; 21 BP.
XX
AC   AAH89080;
XX
DT   27-FEB-2002  (first entry)
XX
DE   Human polymorphic oligonucleotide L27558 fragment.
XX
KW   Human; single nucleotide polymorphic; SNP; forensic science;
KW   paternity testing; phenotypic trait; genetic mapping; animal breeding;
KW   plant breeding; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Variation       replace(11,c)
FT                   /*tag=  a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO200134840-A2.
XX
PD   17-MAY-2001.
XX
PF   10-NOV-2000; 2000WO-US030766.
XX
PR   10-NOV-1999;   99US-0164596P.
XX
PA   (GLAX ) GLAXO GROUP LTD.
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Au K,  Chen J,  Patil N,  Thomas D;
XX
DR   WPI; 2001-335945/35.
XX
PT   New polymorphic sites derived from the human genome are useful to
PT   determine sites correlating with phenotypic traits, particularly disease,
PT   and also in forensics and paternity testing.
XX
PS   Claim 82; Page 13; 43pp; English.
XX
CC   The present invention relates to human oligonucleotides comprising a
CC   single nucleotide polymorphic site (SNP: AAH88797-AAH89219). The present
CC   sequence is one such oligonucleotide. The oligonucleotides can be used in
CC   forensics, paternity testing, correlation of polymorphisms with
CC   phenotypic traits, genetic mapping of phenotypic traits and marker
CC   assisted breeding of animals and crop plants
XX
SQ   Sequence 21 BP; 4 A; 7 C; 6 G; 4 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 21;
  Best Local Similarity   85.7%;  Pred. No. 2.1e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        573 TGAGCGCCCGCAGGGATGCCT 593
              ||||| || ||||||| ||||
Db         21 TGAGCTCCTGCAGGGAAGCCT 1


RESULT 2460
ABX79739/c
ID   ABX79739 standard; cDNA; 21 BP.
XX
AC   ABX79739;
XX
```

```
DT   17-APR-2003  (first entry)
XX
DE   EST polymorphic DNA repeat polynucleotide #64.
XX
KW   EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
KW   polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
KW   Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
KW   Haw River syndrome; Huntington's disease; fragile-X syndrome;
KW   Fredreich's ataxis; myotonic dystrophy; hyperandrogenaemia;
KW   spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
XX
OS   Homo sapiens.
XX
PN   US6472154-B1.
XX
PD   29-OCT-2002.
XX
PF   31-DEC-1999;   99US-00475947.
XX
PR   31-DEC-1999;   99US-00475947.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Garner HR,  Wren JD,  Minna JD,  Fondon JW;
XX
DR   WPI; 2003-208818/20.
XX
PT   Identifying a candidate polymorphic repeat within a coding sequence, for
PT   understanding or treating genetic disease, comprises detecting tandem
PT   repeats in a target coding sequence and scoring the repeats for
PT   polymorphic probability.
XX
PS   Example; Col 273; 588pp; English.
XX
CC   The invention discloses a method for identifying a candidate polymorphic
CC   repeat within a coding sequence (expressed sequence tag, EST), which
CC   comprises detecting tandem repeats in a target coding sequence, scoring
CC   the repeats for polymorphic probability and generating a dataset
CC   correlating the repeats with polymorphic probability to identify a
CC   candidate polymorphic repeat. The computational methods (polymorphic
CC   marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
CC   useful for identifying and detecting candidate polymorphic repeats in
CC   human genes, which can be used to understand, treat or eliminate genetic
CC   diseases, predispositions or adverse drug-treatment reactions. Examples
CC   of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
CC   syndrome, Huntington's disease, fragile-X syndrome, Fredreich's ataxis,
CC   myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
CC   spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
CC   the polymorphic repeats identified for a search of human ESTs
XX
SQ   Sequence 21 BP; 8 A; 9 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 21;
  Best Local Similarity   85.7%;  Pred. No. 2.1e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1938 AGGTAATGGTTGGTTTTTGTG 1958
              ||| |||||| ||||||| ||
Db         21 AGGGAATGGTGGGTTTTTCTG 1

RESULT 2461
AAA26585
ID   AAA26585 standard; DNA; 22 BP.
XX
AC   AAA26585;
XX
DT   23-JUN-2000  (first entry)
XX
DE   Human HPC1 mutation screening PCR primer SEQ ID NO:129.
XX
KW   Human; prostate cancer predisposing gene; HPC1; chromosome 1;
KW   susceptibility; tumour suppressor; prostate cancer; cytostatic;
KW   gene therapy; mutant; screening; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200012694-A1.
XX
PD   09-MAR-2000.
XX
PF   26-AUG-1999;   99WO-US019508.
XX
PR   26-AUG-1998;   98US-0098183P.
XX
PA   (MYRI-) MYRIAD GENETICS INC.
XX
PI   Tavtigian S,  Teng DHF,  Perry WL,  Schroeder MM,  Simard J;
PI   Rommens JM;
XX
DR   WPI; 2000-270819/23.
XX
PT   Novel human prostate cancer predisposing gene in which somatic and
PT   germline mutations correlate with prostate cancer, useful in gene therapy
PT   and for diagnosis and prognosis of predisposition to prostate cancer.
XX
PS   Example 8; Page 72; 159pp; English.
XX
CC   The present invention describes a human prostate cancer susceptibility
CC   gene, designated the human prostate cancer predisposing gene 1 (HPC1).
CC   AAA26459 to AAA26510 represent nucleotide sequences from the HPC1 gene.
CC   The HPC1 gene sequences are used as diagnostic molecules since they can
CC   determine a predisposition to cancers especially, prostate cancer.
CC   Nucleic acid probes from the present invention are used to detect
CC   mismatches of the HPC1 gene or mRNA. Primers from the present invention
CC   can be used for determining the nucleotide sequence of a particular HPC1
CC   allele. The mutations in the HPC1 allele which lead to an altered
CC   function of HPC1 are used in diagnostic and prognostic methods to
CC   determine a predisposition to cancer. HPC1 genes are also used in gene
CC   therapy to treat cancer. The HPC1 gene can be found in the HPC1 region of
CC   human chromosome 1, bound by the markers mM.GAAA.158;23.4 and
CC   mM.GA57e15.S16. AAA26513 to AAA26521 represent oligonucleotides used in
CC   hybrid selection in an example from the present invention. AAA26522 to
CC   AAA26537 represent PCR primers for the HPC1 gene, and AAA26538 to
CC   AAA26658 represent PCR primers used in mutation screening of the HPC1
CC   gene. AAA26659 to AAA26662 encode the putative protein sequences given in
CC   AAY82362 to AAY82365 from HPC1
XX
SQ   Sequence 22 BP; 6 A; 6 C; 3 G; 7 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 22;
  Best Local Similarity   85.7%;  Pred. No. 2.3e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        779 CTGAACCTCCCCTGTCAGAAG 799
              ||||| ||||||| | |||||
Db          1 CTGAATCTCCCCTATTAGAAG 21

RESULT 2462
AAC86203/c
ID   AAC86203 standard; DNA; 22 BP.
XX
AC   AAC86203;
XX
DT   28-FEB-2001  (first entry)
XX
DE   Primer #3 used to amplify BRCA1.
XX
KW   BRCA1; estrogen signalling pathway; ESP; cancer; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200066767-A1.
XX
PD   09-NOV-2000.
```

```
XX
PF   28-APR-2000; 2000WO-US011442.
XX
PR   30-APR-1999;   99US-0131841P.
PR   27-APR-2000; 2000US-00559025.
XX
PA   (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.
XX
PI   Goldberg ID,  Rosen EM,  Fan S;
XX
DR   WPI; 2000-687545/67.
XX
PT   Preventing, diagnosing and treating cancers associated with defects in
PT   the estrogen signaling pathway, especially breast, ovarian and prostate
PT   cancers.
XX
PS   Example; Page 42; 82pp; English.
XX
CC   The present invention relates to identifying modulators of the estrogen
CC   signaling pathway (ESP), identifying individuals at risk of developing
CC   cancer due to genetic mutations in genes (e.g. the BRCA1 gene) involved
CC   in the ESP and treating cancers using modulators of the ESP
XX
SQ   Sequence 22 BP; 11 A; 4 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 22;
  Best Local Similarity   85.7%;  Pred. No. 2.3e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1095 CTGTTCATTTGGCTAGGGACT 1115
              ||||||||||||||| |  |||
Db         22 CTGTTCATTTGGCTTGTTACT 2


RESULT 2463
AAT08689
ID   AAT08689 standard; cDNA; 23 BP.
XX
AC   AAT08689;
XX
DT   06-SEP-1996  (first entry)
XX
DE   CRH related G-protein coupled receptor degenerate PCR primer #14.
XX
KW   Human; corticotropin; releasing hormone; CRH; skeletal muscle;
KW   G-protein coupled receptor; poly(A)+ RNA; derived; mouse; transgenic;
KW   mammal; identification; agonist; antagonist; therapeutics; development;
KW   treatment; anorexia nervosa; irritable bowel syndrome; HIV;
KW   Alzheimer's disease; antibody; vaccine preparation;
KW   antisense oligonucleotide; expression; modulation; corticotrophin;
KW   degenerate; PCR primer; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   6
FT                   /*tag=  a
FT                   /mod_base= i
FT   modified_base   12
FT                   /*tag=  b
FT                   /mod_base= i
XX
PN   EP695802-A2.
XX
PD   07-FEB-1996.
XX
PF   30-MAY-1995;   95EP-00303678.
XX
PR   10-JUN-1994;   94US-00259265.
XX
PA   (PFIZ ) PFIZER INC.
XX
PI   De Wet JR;
XX
DR   WPI; 1996-088925/10.
XX
PT   DNA encoding Human corticotropin releasing hormone receptor-related G
PT   protein-coupled receptor - useful for studies and possibly treatment of
PT   stress related illnesses.
XX
PS   Example; Page 6; 13pp; English.
XX
CC   The present sequence is a degenerate PCR primer, for the cDNA mol. which
CC   encodes human corticotropin releasing hormone (CRH) related G-protein
CC   coupled receptor. The cDNA was derived from a human brain and skeletal
CC   muscle poly(A)+ RNA, using Superscript II MLV reverse transcriptase
CC   (BRL), and oligo d(T) 12-18 as the primer. Transgenic animals, which
CC   express the CRH receptor, can be produced by inserting the cDNA into the
CC   embryonic stem cells of mice, or other mammals. The CRH receptor can be
CC   used to identify agonists and antagonists, and in the development of
CC   therapeutic cpds. for the treatment of, e.g. anorexia nervosa, irritable
CC   bowel syndrome, HIV or Alzheimer's disease. Anti-CRH receptor antibodies
CC   can be used in vaccine prepns., and oligonucleotides antisense to the
CC   cDNA can be used to modulate its expression
XX
SQ   Sequence 23 BP; 6 A; 3 C; 0 G; 4 T; 0 U; 10 Other;

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 23;
  Best Local Similarity   52.2%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    8;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2601 AACTCTCTGTTCAGAAAGCAATA 2623
              | :|| :::|| |::||:||:||
Db          1 ACYTCNYWRTTNARRAARCARTA 23


RESULT 2464
AAH45458/c
ID   AAH45458 standard; DNA; 23 BP.
XX
AC   AAH45458;
XX
DT   07-SEP-2001  (first entry)
XX
DE   PCR primer specific for transcriptional activator subunit 49 cDNA.
XX
KW   Human; transcriptional activator subunit 49; muscular dystrophy;
KW   genesis dysfunction; cancer; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138370-A1.
XX
PD   31-MAY-2001.
XX
PF   20-NOV-2000; 2000WO-CN000474.
XX
PR   24-NOV-1999;   99CN-00124101.
XX
PA   (BIOR-) BIOROAD GENE DEV LTD SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2001-355890/37.
XX
PT   New transcriptional activator subunit 49 and polynucleotide encoding it,
PT   for diagnosing and treating muscular dystrophy, genesis dysfunction and
PT   cancer.
XX
PS   Example 3; Page 9; 29pp; Chinese.
XX
CC   This invention relates to human transcriptional activator subunit 49
CC   protein and cDNA sequences. The invention includes a vector containing
CC   the cDNA sequence, a host cell transformed with the vector, and an
CC   antibody directed to the transcriptional activator subunit 49 protein.
CC   The protein and polynucleotide are applicable in the diagnosis and
```

```
CC   treatment of muscular dystrophy, genesis dysfunction and cancer. Use of
CC   the protein and polynucleotide can cause muscular and cytostatic
CC   activity. The present sequence represents a PCR primer specific for cDNA
CC   encoding the human transcriptional activator subunit 49 protein
XX
SQ   Sequence 23 BP; 1 A; 6 C; 4 G; 12 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 23;
  Best Local Similarity   85.7%;  Pred. No. 2.6e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1502 GAGAAACACAGGAAATAAAAT 1522
              |||||||| ||| || |||||
Db         23 GAGAAACAGAGGCAACAAAAT 3


RESULT 2465
AAL46192
ID   AAL46192 standard; DNA; 23 BP.
XX
AC   AAL46192;
XX
DT   11-JUL-2002  (first entry)
XX
DE   Human liver cancer expressed protein PP3731 PCR primer #1.
XX
KW   Human; liver cancer; hepatoma; PP367; PP1597; PP1729; PP3476; PP3731;
KW   PP3856; PP3958; PP3971; PP4519; PP5241; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1329064-A.
XX
PD   02-JAN-2002.
XX
PF   20-JUN-2000; 2000CN-00116616.
XX
PR   20-JUN-2000; 2000CN-00116616.
XX
PA   (SHAN-) SHANGHAI INST TUMOR.
XX
PI   Gu J,  Yang S;
XX
DR   WPI; 2002-330564/37.
XX
PT   Novel human protein with expression difference in liver cancer tissue
PT   useful for detecting cancers, such as hepatoma.
XX
PS   Example 2; Page 14 (Disclosure); 40pp; Chinese.
XX
CC   The present invention provides the protein and coding sequences of a
CC   number of human protein which are differentially expressed in hepatoma
CC   tissues, and can thus be used to detect liver cancers. These are
CC   designated PP367, PP1597, PP1729, PP3476, PP3731, PP3856, PP3958, PP3971,
CC   PP4519 and PP5241. The present sequence is a PCR primer for a coding
CC   sequence of the invention
XX
SQ   Sequence 23 BP; 3 A; 12 C; 3 G; 5 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 23;
  Best Local Similarity   85.7%;  Pred. No. 2.6e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        302 CTCTCCCACACTGGAGTCGCC 322
              |||||||| |||  |||||||
Db          2 CTCTCCCAGACTCCAGTCGCC 22


RESULT 2466
ABK91269
ID   ABK91269 standard; DNA; 24 BP.
XX
AC   ABK91269;
XX
DT   05-NOV-2002  (first entry)
XX
DE   Leukaemia related protein 24.09 specific RT-PCR primer #2.
XX
KW   Leukaemia related protein; leukaemia; lymphoma; primer; ss; haemopathy;
KW   growth development disturbance disease; reverse transcription; RT-PCR.
XX
OS   Unidentified.
XX
PN   CN1341647-A.
XX
PD   27-MAR-2002.
XX
PF   07-SEP-2000; 2000CN-00125055.
XX
PR   07-SEP-2000; 2000CN-00125055.
XX
PA   (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-520722/56.
XX
PT   Novel leukemia related protein 24.09.
XX
PS   Example 3; Page 17 (disclosure); 32pp; Chinese.
XX
CC   This invention relates to the DNA and protein sequences of leukemia
CC   related protein 24.09. The invention also comprises methods for producing
CC   the protein using recombinant DNA technology and antagonists of the
CC   protein which may be used for inhibiting the action of the protein. The
CC   sequences of the invention may be used for treating several diseases such
CC   as leukaemia, lymphoma, other haemopathy and growth development
CC   disturbance disease. The present sequence represents a reverse
CC   transcription (RT) PCR primer used to isolate the leukaemia related
CC   protein cDNA 24.09 of the invention
XX
SQ   Sequence 24 BP; 4 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 24;
  Best Local Similarity   85.7%;  Pred. No. 2.8e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAACT 2190
              | ||||||||||||||| || |
Db          2 TGTTTTTTTTTTTTTTCAATT 22


RESULT 2467
ABA98547/c
ID   ABA98547 standard; DNA; 24 BP.
XX
AC   ABA98547;
XX
DT   30-APR-2002  (first entry)
XX
DE   Insulin-like growth factor binding protein 16.17 PCR primer #1.
XX
KW   Insulin-like growth factor; binding protein; cytostatic; gene therapy;
KW   cancer; PCR primer; ss.
XX
OS   Unidentified.
XX
PN   WO200212301-A1.
XX
PD   14-FEB-2002.
XX
PF   11-JUN-2001; 2001WO-CN000947.
XX
PR   14-JUN-2000; 2000CN-00116509.
XX
PA   (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
```

```
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-172131/22.
XX
PT   Insulin-like growth factor binding protein 16.17 and encoding
PT   polynucleotide, used in diagnosis and treatment of cancer.
XX
PS   Example 2; Page 12; 37pp; Chinese.
XX
CC   The present invention relates to insulin-like growth factor binding
CC   protein 16.17 (see AAM48365). The binding protein and its coding sequence
CC   are useful for the diagnosis and treatment of cancer. The present
CC   sequence is a PCR primer, which was used in an example from the invention
XX
SQ   Sequence 24 BP; 1 A; 3 C; 1 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 24;
  Best Local Similarity   85.7%;  Pred. No. 2.8e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAAA 2804
              | |||||||||||||| ||| |
Db         24 TCAAAAAAAAAAAAAAGAAAGA 4


RESULT 2468
ABV77761
ID   ABV77761 standard; DNA; 24 BP.
XX
AC   ABV77761;
XX
DT   03-FEB-2003  (first entry)
XX
DE   Human DNA-PK interaction protein 9.9 PCR primer #2.
XX
KW   Human; DNA-PK interaction protein 9.9; cancer; HIV infection; cytostatic;
KW   anti-HIV; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1351066-A.
XX
PD   29-MAY-2002.
XX
PF   26-OCT-2000; 2000CN-00125835.
XX
PR   26-OCT-2000; 2000CN-00125835.
XX
PA   (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-609430/66.
XX
PT   New polypeptide-human DNA-PK interaction protein 9.9 for treating
PT   diseases, such as, cancer, and human immunodeficiency virus infection.
XX
PS   Example 2; Page 16 (Disclosure); 31pp; Chinese.
XX
CC   The present invention relates to human DNA-PK interaction protein 9.9.
CC   The protein can be used for treating diseases such as cancer and HIV
CC   infection. The present sequence is a PCR primer, which was used in an
CC   example from the invention
XX
SQ   Sequence 24 BP; 4 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 24;
  Best Local Similarity   85.7%;  Pred. No. 2.8e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTAACT 2190
              | |||||||||||||||  || |
Db          1 TGTTTTTTTTTTTTTTGAAAT 21


RESULT 2469
AAV48089
ID   AAV48089 standard; DNA; 24 BP.
XX
AC   AAV48089;
XX
DT   27-OCT-1998  (first entry)
XX
DE   Oligonucleotide 25-P.
XX
KW   In situ translation; RNA-protein fusion; binding reagent; antibody;
KW   industrial catalyst; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   24
FT                   /*tag=  a
FT                   /note= "Puromycin"
XX
PN   WO9831700-A1.
XX
PD   23-JUL-1998.
XX
PF   14-JAN-1998;   98WO-US000807.
XX
PR   21-JAN-1997;   97US-0035963P.
PR   06-NOV-1997;   97US-0064491P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Szostak JW,  Roberts RW,  Liu R;
XX
DR   WPI; 1998-414032/35.
XX
PT   Selection of specific protein by screening protein-RNA fusions generated
PT   in vitro or in situ - useful for, e.g. identifying enzymes and antibodies
PT   with altered properties, potentially useful as catalysts or for therapy
PT   or diagnosis.
XX
PS   Disclosure; Page 39; 94pp; English.
XX
CC   The Oligonucleotides AAV48087, AAV48089-V48091 and AAV48096-V48098 and
CC   variations were used to generate RNA-protein fusions. These were used in
CC   the selection of a specific protein or RNA, by in vitro or in situ
CC   translation of candidate RNA molecules to produce RNA-protein fusions,
CC   then selecting specific RNA protein fusions. The method is used to select
CC   proteins (or DNA encoding them) having altered properties, e.g. for
CC   identification of new binding reagents, to identify improved human
CC   antibodies or new enzymes. These proteins are potentially useful in
CC   diagnosis and therapy, or as industrial catalysts. The methods allow many
CC   rounds of selection and amplification to be performed, resulting in
CC   enrichment of even very rare molecules and allowing isolation of proteins
CC   that bind specifically to almost any compound or catalyse almost any
CC   reaction
XX
SQ   Sequence 24 BP; 0 A; 4 C; 3 G; 16 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 24;
  Best Local Similarity   85.7%;  Pred. No. 2.8e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTTTTT 2182
              | |  ||||||||||||||||
Db          1 CGCGGTTTTTTTTTTTTTTTT 21


RESULT 2470
AAL51806/c
ID   AAL51806 standard; DNA; 24 BP.
```

```
XX
AC   AAL51806;
XX
DT   24-APR-2003  (first entry)
XX
DE   Short chain dehydrogenase 9-35 PCR primer #2.
XX
KW   PCR; primer; ss; short chain dehydrogenase; 9.35; cancer; HIV.
XX
OS   Unidentified.
XX
PN   CN1363664-A.
XX
PD   14-AUG-2002.
XX
PF   05-JAN-2001; 2001CN-00105049.
XX
PR   05-JAN-2001; 2001CN-00105049.
XX
PA   (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-751778/82.
XX
PT   Polypeptide-short-chain dehydrogenase 9.35 and polynucleotide for coding
PT   it.
XX
PS   Example 2; Page 17 (Disclosure); 32pp; Chinese.
XX
CC   The invention comprises the amino acid and coding sequence of a short
CC   chain dehydrogenase 9.35. The DNA and protein sequences of the invention
CC   are useful for treating cancer and HIV infection. The present DNA
CC   sequence represents a PCR primer for the short chain dehydrogenase 9.35
CC   gene
XX
SQ   Sequence 24 BP; 2 A; 3 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 24;
  Best Local Similarity   85.7%;  Pred. No. 2.8e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAAA 2804
              | ||||  ||||||||||||
Db         21 TCAAAAGGAAAAAAAAAAAAA 1


RESULT 2471
AAZ07017/c
ID   AAZ07017 standard; DNA; 24 BP.
XX
AC   AAZ07017;
XX
DT   09-NOV-1999  (first entry)
XX
DE   Murine alpha-L-iduronidase genomic DNA oligonucleotide #3.
XX
KW   Murine; mouse; alpha-L-iduronidase; IDUA; hepatic sulphate transporter;
KW   SAT-1; mucopolysaccharidosis type I; MPS I; transgenic mouse;
KW   cell-specific targeting system; tissue-specific targeting system;
KW   lysosomal disorder; ss.
XX
OS   Mus sp.
XX
PN   CA2205710-A.
XX
PD   20-NOV-1997.
XX
PF   20-MAY-1997;   97CA-02205710.
XX
PR   20-MAY-1996;   96US-0017156P.
XX
PA   (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI   Jirik F,  Clarke LA;
XX
DR   WPI; 1999-494691/42.
XX
PT   New transgenic mouse, useful for modeling lysosomal disorders and testing
PT   cell- or tissue-specific targeting systems.
XX
PS   Example 3; Page 12; 20pp; English.
XX
CC   The present invention describes a mouse (I), homozygous for a disruption
CC   in the alpha-L-iduronidase (IDUA) gene but with normal expression of the
CC   hepatic sulphate transporter SAT-1 gene. (I) is used to evaluate
CC   therapeutic agents for use in treating mucopolysaccharidosis Type I (MPS
CC   I) by administering the agent to (I) and evaluating the mouse for
CC   pathology associated with iduronidase deficiency. (I) may also be used to
CC   evaluate the ability of a targeting system to deliver a therapeutic agent
CC   to a specific tissue or organ in the mouse using the same techniques.
CC   Targeting systems which may be tested using this regime include a target-
CC   specific label, a viral expression vector or a liposome coupled to
CC   iduronidase. (I) may also be used as a general model for studying the
CC   pathology of MPS I. The SAT-1 gene overlaps with the IDUA gene but in (I)
CC   the expression of the SAT-1 gene is unaffected. Therefore any
CC   pathological effects observed in (I) are due solely to the disruption of
CC   the IDUA gene. The present sequence represents a IDUA genomic DNA
CC   oligonucleotide used in the exemplification of the present invention
XX
SQ   Sequence 24 BP; 20 A; 4 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 24;
  Best Local Similarity   85.7%;  Pred. No. 2.8e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              |||| |||||| |||||| ||
Db         22 TTTTGTTTTTTGTTTTTTGTT 2


RESULT 2472
AAF70467
ID   AAF70467 standard; DNA; 24 BP.
XX
AC   AAF70467;
XX
DT   20-APR-2001  (first entry)
XX
DE   Human DRD2 exon 5 PCR primer SEQ ID NO:210.
XX
KW   Human; dopamine receptor D2; DRD2; polymorphism; allele specific;
KW   drug target isogene; detection; single nucleotide polymorphism; SNP;
KW   genotype; schizophrenia; Parkinson's disease; myoclonus dystonia; MD;
KW   probe; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200105832-A1.
XX
PD   25-JAN-2001.
XX
PF   19-JUL-2000; 2000WO-US019644.
XX
PR   19-JUL-1999;   99US-0144493P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Chew A,  Denton RR,  Duda A,  Nandabalan K,  Stephens JC;
XX
DR   WPI; 2001-091967/10.
XX
PT   Polynucleotides comprising single nucleotide polymorphisms in the human
PT   dopamine receptor D2, useful for detecting mutations associated with,
PT   e.g. schizophrenia, Parkinson's and myoclonus dystonia.
```

```
XX
PS   Example 1A; Page 37; 135pp; English.
XX
CC   The present invention describes polynucleotides comprising single
CC   nucleotide polymorphisms (SNPs) in the human dopamine receptor D2 (DRD2).
CC   The polynucleotides may be used in assays to detect and characterise
CC   polymorphisms in DRD2 that affect its expression and activity and are
CC   involved in disorders such as schizophrenia, Parkinson's and myoclonus
CC   dystonia (MD). This information would be useful for studying the
CC   biological function of DRD2 as well as in identifying drugs targeting
CC   this protein for the treatment of disorders related to its abnormal
CC   expression or function. Polymorphisms in the DRD2 gene affect the
CC   expression of active and functional polypeptides. Therefore it is
CC   advantageous to detect polymorphisms in the DRD2 gene and how those
CC   polymorphisms are combined in different copies of the gene. AAF70261 to
CC   AAF70308 represent human DRD2 allele specific oligonucleotide probes, and
CC   AAF70309 to AAF70404 represent human DRD2 allele specific oligonucleotide
CC   primers which are used in the detection of DRD2 polymorphisms. AAF70405
CC   to AAF70452 represent oligonucleotide primers for the detection of human
CC   DRD2 polymorphisms which are given in the exemplification of the present
CC   invention. AAF70453 to AAF70538 represent PCR primers for the human DRD2
CC   gene which are used in examples from the present invention
XX
SQ   Sequence 24 BP; 2 A; 9 C; 2 G; 11 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 24;
  Best Local Similarity   85.7%;  Pred. No. 2.8e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1330 CTGCTTGTCTCATTTCAGCCT 1350
              ||  |||||||||| ||||||
Db          1 CTTTTTGTCTCATTCCAGCCT 21


RESULT 2473
ABS57731
ID   ABS57731 standard; DNA; 24 BP.
XX
AC   ABS57731;
XX
DT   03-FEB-2003  (first entry)
XX
DE   Human zinc finger protein 41.58 RT-PCR primer #2.
XX
KW   Human; zinc finger protein 41.58; solid tumour; nervous system disease;
KW   malignant disease of blood; development disturbance; HIV;
KW   human immunodeficiency virus; reverse transcriptase PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1345879-A.
XX
PD   24-APR-2002.
XX
PF   29-SEP-2000; 2000CN-00125607.
XX
PR   29-SEP-2000; 2000CN-00125607.
XX
PA   (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-529900/57.
XX
PT   New polypeptide-human zinc finger protein 41.58 for treating solid tumor,
PT   nervous system disease, malignant disease of blood, development
PT   disturbance and human immunodeficiency virus infection.
XX
PS   Example 3; Page 17 (Disclosure); 33pp; Chinese.
XX
CC   The present invention discloses a new polypeptide-human zinc finger
CC   protein 41.58, a polynucleotide encoding the polypeptide and producing
CC   the polypeptide by using DNA recombination technology. The polypeptide is
CC   useful for curing several diseases, such as solid tumour, nervous system
CC   disease, malignant disease of blood, development disturbance and human
CC   immunodeficiency virus (HIV) infection by using the polypeptide. The
CC   invention also discloses an antagonist for resisting the polypeptide and
CC   its therapeutic action, and also discloses application of a
CC   polynucleotide encoding the new human zinc finger protein 41.58. This
CC   sequence represents a reverse transcriptase PCR primer used to isolate
CC   DNA encoding the novel human zinc finger protein 41.58
XX
SQ   Sequence 24 BP; 3 A; 1 C; 4 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 24;
  Best Local Similarity   85.7%;  Pred. No. 2.8e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTAACT 2190
              |||||||||||||||| || |
Db          2 TGTTTTTTTTTTTTTGAAGT 22


RESULT 2474
ABS57731/c
ID   ABS57731 standard; DNA; 24 BP.
XX
AC   ABS57731;
XX
DT   03-FEB-2003  (first entry)
XX
DE   Human zinc finger protein 41.58 RT-PCR primer #2.
XX
KW   Human; zinc finger protein 41.58; solid tumour; nervous system disease;
KW   malignant disease of blood; development disturbance; HIV;
KW   human immunodeficiency virus; reverse transcriptase PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1345879-A.
XX
PD   24-APR-2002.
XX
PF   29-SEP-2000; 2000CN-00125607.
XX
PR   29-SEP-2000; 2000CN-00125607.
XX
PA   (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-529900/57.
XX
PT   New polypeptide-human zinc finger protein 41.58 for treating solid tumor,
PT   nervous system disease, malignant disease of blood, development
PT   disturbance and human immunodeficiency virus infection.
XX
PS   Example 3; Page 17 (Disclosure); 33pp; Chinese.
XX
CC   The present invention discloses a new polypeptide-human zinc finger
CC   protein 41.58, a polynucleotide encoding the polypeptide and producing
CC   the polypeptide by using DNA recombination technology. The polypeptide is
CC   useful for curing several diseases, such as solid tumour, nervous system
CC   disease, malignant disease of blood, development disturbance and human
CC   immunodeficiency virus (HIV) infection by using the polypeptide. The
CC   invention also discloses an antagonist for resisting the polypeptide and
CC   its therapeutic action, and also discloses application of a
CC   polynucleotide encoding the new human zinc finger protein 41.58. This
CC   sequence represents a reverse transcriptase PCR primer used to isolate
CC   DNA encoding the novel human zinc finger protein 41.58
XX
SQ   Sequence 24 BP; 3 A; 1 C; 4 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 24;
  Best Local Similarity   85.7%;  Pred. No. 2.8e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;
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```
Qy       2781 AATTGAAAAAAAAAAAAAAA 2801
              | || ||||||||||||||| |
Db         22 ACTTCAAAAAAAAAAAAAACA 2
```

RESULT 2475
ABV74853/c
ID ABV74853 standard; DNA; 24 BP.
XX
AC ABV74853;
XX
DT 05-FEB-2003 (first entry)
XX
DE Protein 16.17 PCR primer #2.
XX
KW Protein 16.17; colipase; cancer; HIV infection; cytostatic; anti-HIV;
KW PCR; primer; ss.
XX
OS Unidentified.
XX
PN CN1351027-A.
XX
PD 29-MAY-2002.
XX
PF 26-OCT-2000; 2000CN-00125840.
XX
PR 26-OCT-2000; 2000CN-00125840.
XX
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-619851/67.
XX
PT New polypeptide-protein 16.17 containing colipase characteristics for
PT treating diseases such as cancer and human immunodeficiency virus
PT infection.
XX
PS Example 3; Page 26 (Disclosure); 31pp; Chinese.
XX
CC The present invention relates to protein 16.17 (see ABB98830), which
CC contains colipase characteristics. The protein and its coding sequence
CC are useful for treating diseases such as cancer and HIV infection. The
CC present sequence is a PCR primer, which was used in an example from the
CC invention. Note: The present sequence, SEQ ID 4, shown in the sequence
CC listing differs from the SEQ ID 4 shown in the disclosure (see ABV74866)
XX
SQ Sequence 24 BP; 3 A; 1 C; 3 G; 17 T; 0 U; 0 Other;

 Query Match 0.6%; Score 16.2; DB 1; Length 24;
 Best Local Similarity 85.7%; Pred. No. 2.8e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       2784 TGAAAAAAAAAAAAAAAAAA 2804
              |||  | ||||||||||||||
Db         24 TGACTACAAAAAAAAAAAAAA 4
```

RESULT 2476
ABK67211
ID ABK67211 standard; DNA; 24 BP.
XX
AC ABK67211;
XX
DT 02-JUL-2002 (first entry)
XX
DE Human gene specific PCR primer #1299.
XX
KW Primer; ss; DNA microarray; differential expression analysis; human.
XX
OS Homo sapiens.
XX
PN US6352829-B1.
XX
PD 05-MAR-2002.
XX
PF 05-JAN-1999; 99US-00225928.
XX
PR 21-MAY-1997; 97US-00859998.
XX
PA (CLON-) CLONTECH LAB INC.
XX
PI Chenchik A, Jokhadze G, Bibilashvilli R;
XX
DR WPI; 2002-314699/35.
XX
PT Producing sub-population of labeled nucleic acids, useful for analyzing
PT differences in RNA profiles between several different physiological
PT sources, using set of distinct gene specific primers.
XX
PS Example 3; SEQ ID NO 1299; 11pp; English.
XX
CC The invention relates to producing a sub-population of labeled nucleic
CC acids (NAs) comprising contacting a NA sample from a physiological
CC source, with a pool of 50 distinct gene specific primers under suitable
CC conditions to enzymatically generate sub-population of NAs, where each
CC gene specific primer has a sequence complementary to a distinct mRNA, and
CC each labeled NA is generated using a single gene specific primer. The
CC method is useful for producing a sub-population of labeled NAs which is
CC useful for analysing the differences in the RNA profiles between several
CC different physiological sources, where the method comprises producing
CC subpopulation of labeled NAs for the different physiological sources,
CC comprising the populations for each physiological source to identify
CC differences in the population, where the comparison is preferably
CC performed by hybridising the labeled NAs for each of the distinct
CC physiological sources to an array of probe NAs stably associated with the
CC surface of a substrate to produce a hybridisation pattern for each of the
CC sources, and comparing the patterns for each of the sources, where
CC differential gene expression assays are utilised in differential
CC expression analysis of diseased a normal tissue e.g. neoplastic a normal
CC tissue, or different tissue or subtissue types. The present sequence is a
CC human gene specific PCR primer used in the method of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from USPTO
CC at http.wipo.seqdata.uspto.gov/sequence.html?DocID=6352829B1
XX
SQ Sequence 24 BP; 4 A; 10 C; 6 G; 4 T; 0 U; 0 Other;

 Query Match 0.6%; Score 16.2; DB 1; Length 24;
 Best Local Similarity 85.7%; Pred. No. 2.8e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       266 TCCGCCGGGCAGCACCTCTAC 286
             ||||||| ||||||| || ||
Db         1 TCCGCCGTGCAGCACGTCAAC 21
```

RESULT 2477
ABQ77631/c
ID ABQ77631 standard; DNA; 24 BP.
XX
AC ABQ77631;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human Hsmar1 protein 15.95 RT-PCR primer, SEQ ID NO:4.
XX
KW Human; Hsmar1 protein 15.95; mariner1 transposase;
KW recombinant production; gene therapy; tumour; cancer;
KW embryonic development disorder; diabetes; menstrual disorder;
KW peptic ulcer; arrhythmia; anaemia; cytostatic; cardiant;
KW reverse transcription-PCR; RT-PCR; primer; ss.
XX
OS Homo sapiens.
XX

PN CN1341642-A.
XX
PD 27-MAR-2002.
XX
PF 05-SEP-2000; 2000CN-00125027.
XX
PR 05-SEP-2000; 2000CN-00125027.
XX
PA (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-520718/56.
XX
PT A human Hsmar1 polypeptide 15.95, useful for curing e.g. tumors and
PT diabetes.
XX
PS Example 3; Page 19 (Disclosure); 32pp; Chinese.
XX
CC The invention relates to human marinerl transposase (Hsmarl) protein
CC 15.95 (ABB09530) and nucleic acids encoding it (ABQ77629). The protein
CC has a molecular weight of 15.95 kD and has 84% identity and 91% homology
CC over a 145 amino acid stretch with human marinerl transposase given in
CC GenBank accession number U52077. The invention also relates to a method
CC for the recombinant production of the protein, an antagonist of the
CC protein, and the use of the protein, gene and antagonist in therapeutic
CC applications. Hsmarl protein 15.95 can be used in the treatment of a
CC variety of diseases such as embryonic development disorders, tumours,
CC diabetes, menstrual disorders, peptic ulcers, arrhythmia, anaemia and
CC epilepsy. The present sequence represents cDNA encoding human Hsmarl
CC protein 15.95. Sequences ABQ77630-ABQ77631 represent reverse
CC transcription-PCR (RT-PCR) primers used in an exemplification of the
CC invention to isolate human Hsmarl protein 15.95 cDNA
XX
SQ Sequence 24 BP; 3 A; 3 C; 3 G; 15 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.2; DB 1; Length 24;
Best Local Similarity 85.7%; Pred. No. 2.8e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       2783 TTGAAAAAAAAAAAAAAAAA 2803
              |||  |||||||||||||| |
Db         22 TTGGCAAAAAAAAAAAAAACA 2
```

RESULT 2478
ABL56411
ID ABL56411 standard; DNA; 24 BP.
XX
AC ABL56411;
XX
DT 22-JUL-2002 (first entry)
XX
DE PCR primer F used to detect mutation N1303K causing cystic fibrosis.
XX
KW Mutation; solid phase amplification; haemochromatosis; cancer;
KW sickle-cell anaemia; beta-thalassemia; alpha-thalassemia; polymorphism;
KW cystic fibrosis; haemophilia; neurodegeneration; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200212557-A1.
XX
PD 14-FEB-2002.
XX
PF 08-AUG-2001; 2001WO-FR002574.
XX
PR 08-AUG-2000; 2000FR-00010425.
XX
PA (NUCL-) NUCLEICA.
XX
PI Cailloux F, Gobron S;
XX
DR WPI; 2002-269096/31.
XX
PT Detecting mutations in nucleic acid, useful e.g. for diagnosing
PT hemochromatosis, by solid phase amplification to incorporate exonuclease
PT resistant nucleotide.
XX
PS Example 3; Fig 3; 43pp; French.
XX
CC PCR primers ABL56411-12 and probe ABL56413 were used to detect a mutation
CC responsible for cystic fibrosis. The primers and probe are used to
CC demonstrate the method of the invention. The specification describes a
CC method for detecting a mutation at position n in a target nucleic acid by
CC solid phase amplification process. The region of interest is amplified on
CC at least two separate supports (A, B) using at least one primer linked,
CC at its 5'-end, to the supports. The DNA strands are then separated and
CC strands in the suspension removed by washing. Bound DNA sequences are
CC hybridized to a probe, the 3'-end of which hybridizes up to, at most,
CC position n-1. The probe is elongated by adding complementary nucleotides
CC in the 5' to 3' direction, using a DNA polymerase and a nucleotide
CC derivative (dNTP*) that is resistant to exonuclease. The dNTP* used is
CC complementary to the mutation for support A but to the wild type for
CC support B. Products are digested with an exonuclease so that only probes
CC elongated by dNTP* are not degraded. The supports are then washed and non
CC -degraded probes detected (in)directly. The method is used to detect
CC mutations associated with disease, especially haemochromatosis; sickle-
CC cell anaemia; alpha or beta-thalassemia; cystic fibrosis; haemophilia;
CC neurodegeneration and cancer. The method is also used to study
CC polymorphisms of gene or an entire genetic region and for detecting
CC and/or identifying genetically modified organisms
XX
SQ Sequence 24 BP; 0 A; 6 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.2; DB 1; Length 24;
Best Local Similarity 85.7%; Pred. No. 2.8e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       2156 TTTTTTCTCCTTTTTTTTTT 2176
              ||| |||| ||||| ||||||
Db          2 TTTCTTCTTCTTTTCTTTTT 22
```

RESULT 2479
AAK99651
ID AAK99651 standard; DNA; 24 BP.
XX
AC AAK99651;
XX
DT 08-JUL-2002 (first entry)
XX
DE Human alpha 2, 3-sialyltransferase (ST3 GalVI) 9-13 cDNA PCR primer 1.
XX
KW Human alpha 2, 3-sialyltransferase; ST3 GalVI 9-13; DNA recombination;
KW immunological deficiency; inflammation; tumour; human; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN CN1329158-A.
XX
PD 02-JAN-2002.
XX
PF 21-JUN-2000; 2000CN-00116664.
XX
PR 21-JUN-2000; 2000CN-00116664.
XX
PA (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-292825/34.
XX
PT New polypeptide-human alpha 2,3-sialytransferase (ST3 GalVI) 9.13 for
PT treating several diseases, such as immunological deficiency, various
PT inflammations and tumors.

```
XX
PS   Example 2; Page 20 Disclosure; 36pp; Chinese.
XX
CC   The present invention relates to a novel polypeptide-human alpha 2, 3-
CC   sialyltransferase (ST3 GalVI) 9.13, the polynucleotide encoding the
CC   polypeptide and producing the polypeptide by using a DNA recombination
CC   technique. The invention also discloses the method for curing several
CC   diseases, such as immunological deficiency, various inflammations and
CC   tumours by using the polypeptide. The invention also discloses an
CC   antagonist for resisting the polypeptide and its therapeutic action, and
CC   also discloses the application of the polynucleotide encoding the novel
CC   human alpha 2.3-sialyltransferase (ST3 GalVI) 9.13. This polynucleotide
CC   sequence represents a PCR primer of the cDNA encoding the human alpha 2.3
CC   -sialyltransferase (ST3 GalVI) 9.13 protein of the invention
XX
SQ   Sequence 24 BP; 4 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 24;
  Best Local Similarity   85.7%;  Pred. No. 2.8e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTA 2187
              |||||| ||||| ||| ||||
Db          3 TTTTTTATTTTTATTTATTTA 23


RESULT 2480
ABZ21302
ID   ABZ21302 standard; DNA; 24 BP.
XX
AC   ABZ21302;
XX
DT   24-FEB-2003  (first entry)
XX
DE   DNA binding protein (RCCI) 10.45 related primer 1.
XX
KW   DNA binding protein; RCCI; 10.45; malignant tumour; haemopathy;
KW   inflammation; immunological disease; human immunodeficiency virus; HIV;
KW   PCR; primer; ss.
XX
OS   Unidentified.
XX
PN   CN1351992-A.
XX
PD   05-JUN-2002.
XX
PF   02-NOV-2000; 2000CN-00127118.
XX
PR   02-NOV-2000; 2000CN-00127118.
XX
PA   (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-714393/78.
XX
PT   New DNA binding protein 10.45 polypeptide for treating malignant tumors,
PT   hemopathy, inflammations, immunological diseases, and human
PT   immunodeficiency virus infection.
XX
PS   Example 2; Page 16 (disclosure); 32pp; Chinese.
XX
CC   The present invention discloses a new kind of polypeptide, RCCI protein
CC   10.45, a polynucleotide encoding the polypeptide and a DNA recombination
CC   process to produce this polypeptide. The present invention also discloses
CC   applying the polypeptide to treat various diseases, such as malignant
CC   tumours, haemopathy, inflammations, immunological diseases, and human
CC   immunodeficiency virus (HIV) infection. The present invention also
CC   discloses an antagonist resisting the polypeptide and its treatment
CC   effect. The present invention also discloses application of the
CC   polynucleotide encoding the new RCCI protein 10.45. The current sequence
CC   represents a DNA binding RCCI protein 10.45 related PCR primer
XX
SQ   Sequence 24 BP; 0 A; 0 C; 6 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 24;
  Best Local Similarity   85.7%;  Pred. No. 2.8e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||  ||| |||||||
Db          2 TTTTTTTTGGTTTGTTTTTT 22


RESULT 2481
ABQ77543
ID   ABQ77543 standard; DNA; 24 BP.
XX
AC   ABQ77543;
XX
DT   01-OCT-2002  (first entry)
XX
DE   Human red blood cell cytoplasmic protein 15.29 RT-PCR primer, SEQ ID:3.
XX
KW   Human; red blood cell cytoplasmic protein 15.29; erythrocyte;
KW   recombinant production; gene therapy; cerebral anoxia;
KW   respiratory adynamia; arrhythmia; intestinal palsy; anaemia; haemostatic;
KW   cardiant; reverse transcription-PCR; RT-PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1339497-A.
XX
PD   13-MAR-2002.
XX
PF   23-AUG-2000; 2000CN-00119732.
XX
PR   23-AUG-2000; 2000CN-00119732.
XX
PA   (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-472206/51.
XX
PT   New polypeptide-human red blood cell cytoplasmic protein 15.29 for
PT   treating anaerobic cerebral disease, respiratory adynamia, arrhythmia,
PT   intestinal palsy, and anemia.
XX
PS   Example 2; Page 16 (Disclosure); 32pp; Chinese.
XX
CC   The invention relates to human red blood cell cytoplasmic protein 15.29
CC   (AAM49384) and nucleic acids encoding it (ABQ77542). The protein has a
CC   molecular weight of 15 kD. The invention also relates to a method for the
CC   recombinant production of the protein, an antagonist of the protein, and
CC   the use of the protein, gene and antagonist in therapeutic applications.
CC   Red blood cell cytoplasmic protein 15.29 can be used in the treatment of
CC   a variety of diseases such as cerebral anoxia, respiratory adynamia,
CC   arrhythmia, intestinal palsy and anaemia. Sequences ABQ77543- ABQ77544
CC   represent reverse transcription-PCR (RT-PCR) primers used in an
CC   exemplification of the invention to isolate human red blood cell
CC   cytoplasmic protein 15.29 cDNA
XX
SQ   Sequence 24 BP; 3 A; 3 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 24;
  Best Local Similarity   85.7%;  Pred. No. 2.8e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||  |||| |
Db          4 TTTTTTTTTTTTTCCTTTGA 24


RESULT 2482
ABQ77543/c
```

ID ABQ77543 standard; DNA; 24 BP.
XX
AC ABQ77543;
XX
DT 01-OCT-2002 (first entry)
XX
DE Human red blood cell cytoplasmic protein 15.29 RT-PCR primer, SEQ ID:3.
XX
KW Human; red blood cell cytoplasmic protein 15.29; erythrocyte;
KW recombinant production; gene therapy; cerebral anoxia;
KW respiratory adynamia; arrhythmia; intestinal palsy; anaemia; haemostatic;
KW cardiant; reverse transcription-PCR; RT-PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN CN1339497-A.
XX
PD 13-MAR-2002.
XX
PF 23-AUG-2000; 2000CN-00119732.
XX
PR 23-AUG-2000; 2000CN-00119732.
XX
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-472206/51.
XX
PT New polypeptide-human red blood cell cytoplasmic protein 15.29 for
PT treating anaerobic cerebral disease, respiratory adynamia, arrhythmia,
PT intestinal palsy, and anemia.
XX
PS Example 2; Page 16 (Disclosure); 32pp; Chinese.
XX
CC The invention relates to human red blood cell cytoplasmic protein 15.29
CC (AAM49384) and nucleic acids encoding it (ABQ77542). The protein has a
CC molecular weight of 15 kD. The invention also relates to a method for the
CC recombinant production of the protein, an antagonist of the protein, and
CC the use of the protein, gene and antagonist in therapeutic applications.
CC Red blood cell cytoplasmic protein 15.29 can be used in the treatment of
CC a variety of diseases such as cerebral anoxia, respiratory adynamia,
CC arrhythmia, intestinal palsy and anaemia. Sequences ABQ77543- ABQ77544
CC represent reverse transcription-PCR (RT-PCR) primers used in an
CC exemplification of the invention to isolate human red blood cell
CC cytoplasmic protein 15.29 cDNA
XX
SQ Sequence 24 BP; 3 A; 3 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.2; DB 1; Length 24;
Best Local Similarity 85.7%; Pred. No. 2.8e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2784 TGAAAAAAAAAAAAAAAAAAA 2804
| |||| ||||||||||||
Db 24 TCAAAAGGAAAAAAAAAAAAA 4

RESULT 2483
AAS19218/c
ID AAS19218 standard; DNA; 24 BP.
XX
AC AAS19218;
XX
DT 09-APR-2002 (first entry)
XX
DE Kringle protein 14, RT-PCR primer #2.
XX
KW Kringle protein 14; cytostatic; haemostatic; virucide; immunomodulatory;
KW antiinflammatory; malignant tumour; haemopathy; inflammation; primer;
KW human immunodeficiency virus; HIV; immunological disease; RT-PCR; ss;
KW reverse transcriptase PCR.
XX
OS Unidentified.
XX
PN WO200192318-A1.
XX
PD 06-DEC-2001.
XX
PF 21-MAY-2001; 2001WO-CN000845.
XX
PR 24-MAY-2000; 2000CN-00115849.
XX
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-090030/12.
XX
PT Kringle protein 14 and encoding polynucleotide, used in diagnosis and
PT treatment of malignant tumors, hemopathy, human immunodeficiency virus
PT infection, immunological diseases and inflammation.
XX
PS Example 2; Page 17; 37pp; Chinese.
XX
CC The invention relates to an isolated polypeptide (I) of Kringle protein
CC 14 and the polynucleotide (II) encoding (I). (I) and (II) are used in
CC diagnosis and treatment of malignant tumour, haemopathy, human
CC immunodeficiency virus (HIV) infection, immunological diseases and
CC various inflammations. The present sequence represents a reverse
CC transcriptase (RT)-PCR primer used to isolate the coding sequence of
CC kringle protein 14 as described in the invention
XX
SQ Sequence 24 BP; 20 A; 3 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.2; DB 1; Length 24;
Best Local Similarity 85.7%; Pred. No. 2.8e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2186
|| |||||| ||||| |||||
Db 22 TTATTTTTTGTTTTTGTTTTT 2

RESULT 2484
ABL58652/c
ID ABL58652 standard; DNA; 24 BP.
XX
AC ABL58652;
XX
DT 17-JUL-2002 (first entry)
XX
DE Human development regulator GTP-binding protein 1 (DRG1) primer 1.
XX
KW Human; GTP-binding; GTP-binding protein 1 (DRG1) 9.35; cancer;
KW embryo development disorder; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN CN1331209-A.
XX
PD 16-JAN-2002.
XX
PF 30-JUN-2000; 2000CN-00116923.
XX
PR 30-JUN-2000; 2000CN-00116923.
XX
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-305503/35.
XX
PT Human development regulator GTP-binding protein 1 (DRG1) 9.35 polypeptide
PT and its encoding polynucleotide, for treating e.g. cancer.
XX

```
PS   Example 2; Page 18 (disclosure); 33pp; Chinese.
XX
CC   The invention relates to human development regulator GTP-binding protein
CC   1 (DRG1) 9.35 polypeptide and its encoding nucleic acid. The
CC   polynucleotide, polypeptide and its antagonist are useful for treating
CC   e.g. embryo development disorder and cancer. The current sequence
CC   represents a human development regulator GTP-binding protein 1 (DRG1)
CC   9.35 related primer
XX
SQ   Sequence 24 BP; 4 A; 2 C; 4 G; 14 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 24;
  Best Local Similarity   85.7%;  Pred. No. 2.8e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2777 TTAGAATTGAAAAAAAAAAAA 2797
              ||  ||| ||||||||||||||
Db         21 TTCCAATGGAAAAAAAAAAAA 1


RESULT 2485
ABZ25620
ID   ABZ25620 standard; DNA; 24 BP.
XX
AC   ABZ25620;
XX
DT   28-MAR-2003  (first entry)
XX
DE   Human zinc finger protein 11 PCR primer 1.
XX
KW   Human; zinc finger protein 11; tumour; haemopathy; HIV; inflammation;
KW   immunological disease; zinc finger; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1364768-A.
XX
PD   21-AUG-2002.
XX
PF   10-JAN-2001; 2001CN-00105125.
XX
PR   10-JAN-2001; 2001CN-00105125.
XX
PA   (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2003-000480/01.
XX
PT   New human zinc finger protein 11 and encoding polynucleotide, useful in
PT   treating cancer and as an anti-inflammatory.
XX
PS   Example 2; Page 16 (Disclosure); 32pp; Chinese.
XX
CC   The invention relates to the novel human zinc finger protein 11, and the
CC   polynucleotide encoding it. The polypeptide is useful in treating various
CC   diseases, such as malignant tumours, haemopathy, HIV Infection,
CC   immunological diseases and various inflammations. The present sequence
CC   represents a PCR primer used to amplify the human zinc finger protein 11
CC   cDNA of the invention
XX
SQ   Sequence 24 BP; 4 A; 5 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 24;
  Best Local Similarity   85.7%;  Pred. No. 2.8e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAACTTTGA 2194
              |||||| ||||||| |||| |
Db          4 TTTTTTCTTTTTTACCTTTAA 24


RESULT 2486
AAL57131/c
ID   AAL57131 standard; DNA; 24 BP.
XX
AC   AAL57131;
XX
DT   04-DEC-2003  (first entry)
XX
DE   RT-PCR primer 2 related to human zinc finger protein 61-82.
XX
KW   Human zinc finger protein 61.82; cancer; HIV infection; RT-PCR; PCR;
KW   primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1381486-A.
XX
PD   27-NOV-2002.
XX
PF   18-APR-2001; 2001CN-00112634.
XX
PR   18-APR-2001; 2001CN-00112634.
XX
PA   (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2003-258239/26.
XX
PT   Polypeptide-human zinc finger protein-61.82 and polynucleotide for coding
PT   it.
XX
PS   Example 3; Page 20; 0pp; Chinese.
XX
CC   This invention relates to a novel human zinc finger protein 61.82 and the
CC   DNA sequence encoding it. The protein of the invention may be useful for
CC   the treatment of diseases such as cancer and HIV infection. The present
CC   sequence is that of RT-PCR primer 2 related to the human zinc finger
CC   protein 61.82 of the invention and used in example 3 of the specification
XX
SQ   Sequence 24 BP; 2 A; 2 C; 3 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 24;
  Best Local Similarity   85.7%;  Pred. No. 2.8e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAAA 2803
              | |||  ||||||||||||||||
Db         24 TGGAACCAAAAAAAAAAAAAA 4


RESULT 2487
ADC10360/c
ID   ADC10360 standard; DNA; 24 BP.
XX
AC   ADC10360;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human NOVX polypeptide gene forward primer SEQ ID NO: 379.
XX
KW   ss; primer; cytostatic; antidiabetic; anorectic; cerebroprotective;
KW   neuroprotective; antiinflammatory; gene therapy; antisense therapy;
KW   thyromimetic; NOVX; pathology; cancer; diabetes; obesity;
KW   endocrine disorder; CNS disorder; inflammatory disorder;
KW   chromosome mapping; tissue typing; predictive medicine.
XX
OS   Homo sapiens.
XX
PN   WO2003000842-A2.
XX
PD   03-JAN-2003.
XX
PF   04-JUN-2002; 2002WO-US017443.
```

```
XX
PR   04-JUN-2001; 2001US-0295607P.
PR   04-JUN-2001; 2001US-0295661P.
PR   06-JUN-2001; 2001US-0296404P.
PR   06-JUN-2001; 2001US-0296418P.
PR   07-JUN-2001; 2001US-0296575P.
PR   11-JUN-2001; 2001US-0297414P.
PR   12-JUN-2001; 2001US-0295573P.
PR   12-JUN-2001; 2001US-0297567P.
PR   14-JUN-2001; 2001US-0298285P.
PR   15-JUN-2001; 2001US-0298528P.
PR   18-JUN-2001; 2001US-0299133P.
PR   19-JUN-2001; 2001US-0299230P.
PR   21-JUN-2001; 2001US-0299949P.
PR   22-JUN-2001; 2001US-0300177P.
PR   26-JUN-2001; 2001US-0300883P.
PR   28-JUN-2001; 2001US-0301530P.
PR   28-JUN-2001; 2001US-0301550P.
PR   03-JUL-2001; 2001US-0302951P.
PR   31-JUL-2001; 2001US-0308890P.
PR   14-SEP-2001; 2001US-0322297P.
PR   25-SEP-2001; 2001US-0324669P.
PR   03-DEC-2001; 2001US-0337477P.
PR   14-DEC-2001; 2001US-0341562P.
PR   21-FEB-2002; 2002US-0358656P.
PR   21-FEB-2002; 2002US-0359122P.
PR   22-FEB-2002; 2002US-0358978P.
PR   22-FEB-2002; 2002US-0359034P.
PR   22-FEB-2002; 2002US-0359035P.
PR   22-FEB-2002; 2002US-0359121P.
PR   27-FEB-2002; 2002US-0359964P.
PR   01-MAR-2002; 2002US-0360858P.
PR   12-MAR-2002; 2002US-0363430P.
PR   12-MAR-2002; 2002US-0363676P.
PR   10-APR-2002; 2002US-0371346P.
PR   10-MAY-2002; 2002US-0379444P.
PR   04-JUN-2002; 2002US-00379444.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Agee ML,  Anderson DW,  Berghs C,  Casman SJ,  Catterton E;
PI   Dipippo VA,  Edinger SR,  Eisen A,  Ellerman K,  Gangolli EA;
PI   Gerlach VL,  Gorman L,  Guo X,  Herrmann JL,  Hjalt T,  Ji W,  Kekuda R;
PI   Khramtsov NV,  Li L,  Liu X,  Malyankar UM,  Miller CE,  Millet I;
PI   Ort T,  Padigaru M,  Patturajan M,  Pena CEA,  Rastelli L,  Rieger DK;
PI   Rothenberg ME,  Shenoy SG,  Shimkets RA,  Smithson G,  Spaderna SK;
PI   Spytek KA,  Stone DJ,  Vernet CAM,  Zhong H,  Zhong M,  Alsobrook JP;
PI   Burgess CE,  Lepley DM;
XX
DR   WPI; 2003-210149/20.
XX
PT   New isolated NOVX polypeptides and nucleic acid molecules useful for
PT   treating, preventing and diagnosing pathological conditions with NOVX-
PT   associated disorders, such as cancer, obesity, diabetes and inflammatory
PT   or CNS diseases.
XX
PS   Example B; SEQ ID NO 379; 772pp; English.
XX
CC   The invention relates to novel isolated polypeptides, mature form of the
CC   polypeptide, a sequence that is 95% identical to the polypeptide or the
CC   polypeptide comprising one or more conservative substitutions. The NOVX
CC   polypeptide is useful for treating or preventing a pathology associated
CC   with the polypeptide e.g. disorders associated with aberrant expression
CC   or activity of the polypeptide, such as cancer, diabetes, obesity, and
CC   endocrine, CNS and inflammatory disorders. They can also be used in
CC   various detection and screening assays, chromosome mapping, tissue typing
CC   and predictive medicine. This sequence corresponds to a primer used to
CC   amplify and isolate the coding sequence for one of the polypeptides of
CC   the invention.
XX
SQ   Sequence 24 BP; 6 A; 7 C; 3 G; 8 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 24;
  Best Local Similarity   85.7%;  Pred. No. 2.8e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2214 GAGACTCTTTGAAATGACATG 2234
              |||||||||  | ||||||||
Db         23 GAGACTCTTGAAGATGACATG 3


RESULT 2488
AAV57477/c
ID   AAV57477 standard; DNA; 25 BP.
XX
AC   AAV57477;
XX
DT   14-DEC-1998  (first entry)
XX
DE   Cytochrome P450ox monooxygenase PCR primer SEQ ID NO:11.
XX
KW   Cytochrome P450 monooxygenase; P450ox; Sorghum bicolor (L.) Moench;
KW   Sinapis alba; biosynthetic conversion; aldoxime; nitrile; cyanohydrin;
KW   cyanogenic glycoside; transgenic plant; resistance; PCR primer; ss.
XX
OS   Synthetic.
OS   Sorghum bicolor.
XX
PN   WO9840470-A2.
XX
PD   17-SEP-1998.
XX
PF   05-MAR-1998;   98WO-EP001253.
XX
PR   07-MAR-1997;   97EP-00810132.
PR   08-DEC-1997;   97EP-00810954.
XX
PA   (NOVS ) NOVARTIS AG.
PA   (UYRO-) UNIV ROYAL VETERINARY & AGRIC.
XX
PI   Halkier BA,  Bak S,  Kahn RA,  Moeller BL;
XX
DR   WPI; 1998-520808/44.
XX
PT   Cytochrome P450 monooxygenase of the cyanogenic glycoside pathway -
PT   useful for the production of plants with improved nutritive value or pest
PT   resistance.
XX
PS   Example 5; Page 29; 32pp; English.
XX
CC   The present sequence represents a PCR primer for cytochrome P450
CC   monooxygenase from Sorghum bicolor (L.) Moench, designated P450ox.
CC   Cytochrome P450 monooxygenase catalyses: (i) the conversion of aldoxime
CC   to a nitrile; and (ii) the nitrile to the corresponding cyanohydrin. DNA
CC   encoding cytochrome P450 monooxygenase can be used to obtain transgenic
CC   plants, for the purpose of improving the nutritive value or pest
CC   resistance of the plant. Cytochrome P450 monooxygenase catalyses the
CC   conversion of aldoximes to nitriles to cyanohydrins, which are the
CC   precursors of toxic cyanogenic glycosides, so staple food such as cassava
CC   and lima beans, as well as animal feed such as white clover, can be
CC   rendered less toxic by blocking the cytochrome P450 monooxygenase
CC   activity. Introducing the enzyme to plants or to certain tissues could
CC   help reduce crop damage since the product is also toxic to insects,
CC   acarids and nematodes
XX
SQ   Sequence 25 BP; 1 A; 3 C; 3 G; 17 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 25;
  Best Local Similarity   94.1%;  Pred. No. 3e+03;
  Matches   16;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2801
              :|||||||||||||||||
Db         25 BAAAAAAAAAAAAAAAA 9
```

```
RESULT 2489
ABA03917/c
ID   ABA03917 standard; DNA; 25 BP.
XX
AC   ABA03917;
XX
DT   18-FEB-2002  (first entry)
XX
DE   Human connexin 9 PCR primer 2 SEQ ID NO:4.
XX
KW   Human; connexin 9; cytostatic; virucidal; immunomodulatory;
KW   antiinflammatory; haemostatic; malignant tumour; haemopathy;
KW   HIV infection; immunological disease; inflammation; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200181538-A2.
XX
PD   01-NOV-2001.
XX
PF   23-APR-2001; 2001WO-CN000608.
XX
PR   27-APR-2000; 2000CN-00115456.
XX
PA   (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-034440/04.
XX
PT   Human connexin 9 and encoded polynucleotide, applicable in diagnosis and
PT   treatment of malignant tumor, hemopathy, HIV infection, immunological
PT   diseases and inflammation.
XX
PS   Example 2; Page 12; 32pp; Chinese.
XX
CC   The present invention describes human connexin 9 (I). (I) has cytostatic,
CC   virucidal, immunomodulatory, antiinflammatory and haemostatic activities.
CC   (I) and the polynucleotide encoding it (II) are applicable in the
CC   diagnosis and treatment of malignant tumour, haemopathy, HIV infection,
CC   immunological diseases and various inflammations. The present sequence
CC   represents a PCR primer for human connexin 9, which is used in an example
CC   from the present invention
XX
SQ   Sequence 25 BP; 3 A; 0 C; 1 G; 21 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 25;
  Best Local Similarity   85.7%;  Pred. No. 3e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAAA 2804
             | |||||| ||||| ||||||
Db         25 TAAAAAAATAAAAATAAAAAA 5


RESULT 2490
AAC96118/c
ID   AAC96118 standard; DNA; 25 BP.
XX
AC   AAC96118;
XX
DT   26-FEB-2001  (first entry)
XX
DE   16s rRNA gene PCR primer #85.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;  99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 45; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 3 A; 2 C; 3 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 25;
  Best Local Similarity   85.7%;  Pred. No. 3e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAA 2801
              | ||  ||||||||||||||||
Db         21 AGTTCCAAAAAAAAAAAAAAA 1


RESULT 2491
AAH38027
ID   AAH38027 standard; DNA; 25 BP.
XX
AC   AAH38027;
XX
DT   14-AUG-2001  (first entry)
XX
DE   SNP specific SNPE primer SEQ ID 823.
XX
KW   Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW   SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
KW   Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW   polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW   acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW   inflammation; forensic investigation; paternity analysis; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200129262-A2.
XX
PD   26-APR-2001.
XX
PF   13-OCT-2000; 2000WO-US028436.
XX
PR   15-OCT-1999;  99US-0160096P.
XX
PA   (ORCH-) ORCHID BIOSCIENCES INC.
XX
PI   Picoult-Newburg L,  Pohl M;
XX
DR   WPI; 2001-290930/30.
XX
PT   New genotyping oligonucleotide, useful for detecting the presence,
PT   absence or identity of single polynucleotide polymorphism in a nucleic
```

PT acid sample.
XX
PS Claim 1; Page 54; 83pp; English.
XX
CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a single nucleotide
CC primer extension (SNPE) primer specific for a human SNP containing DNA
CC sequence
XX
SQ Sequence 25 BP; 18 A; 1 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.2; DB 1; Length 25;
Best Local Similarity 85.7%; Pred. No. 3e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2782 ATTGAAAAAAAAAAAAAAAAA 2802
||| | |||||||||||||| |
Db 1 ATTAAGAAAAAAAAAAAAAGA 21

RESULT 2492
AAC95728
ID AAC95728 standard; DNA; 25 BP.
XX
AC AAC95728;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA DQA1 gene PCR primer #25.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 39; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 5 A; 3 C; 1 G; 16 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.2; DB 1; Length 25;
Best Local Similarity 85.7%; Pred. No. 3e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2174 TTTTTTTTTTTTTAACTTTGA 2194
|||||||||||||||| | | |
Db 1 TTTTTTTTTTTTTAAATCTCA 21

RESULT 2493
AAC96429
ID AAC96429 standard; DNA; 25 BP.
XX
AC AAC96429;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA DQA1 gene PCR primer #31.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 51; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 5 A; 3 C; 1 G; 16 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.2; DB 1; Length 25;
Best Local Similarity 85.7%; Pred. No. 3e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       2174 TTTTTTTTTTTTTAACTTTGA 2194
              ||||||||||||||| | | |
Db          1 TTTTTTTTTTTTTAAATCTCA 21
```

RESULT 2494
AAC96256/c
ID AAC96256 standard; DNA; 25 BP.
XX
AC AAC96256;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA DPA1 gene PCR primer #13.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 48; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 3 A; 2 C; 3 G; 17 T; 0 U; 0 Other;

 Query Match 0.6%; Score 16.2; DB 1; Length 25;
 Best Local Similarity 85.7%; Pred. No. 3e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       2784 TGAAAAAAAAAAAAAAAAAAA 2804
              || | ||| |||||||||||
Db         22 TGTACAAACAAAAAAAAAAAA 2
```

RESULT 2495
AAC96779
ID AAC96779 standard; DNA; 25 BP.
XX
AC AAC96779;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA HLA-A gene PCR primer #156.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 57; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 0 A; 6 C; 1 G; 18 T; 0 U; 0 Other;

 Query Match 0.6%; Score 16.2; DB 1; Length 25;
 Best Local Similarity 85.7%; Pred. No. 3e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       2172 TTTTTTTTTTTTTTTAACTTT 2192
              |||||||||||||||  || |
Db          1 TTTTTTTTTTTTTTTCCCTGT 21
```

RESULT 2496
AAT75139
ID AAT75139 standard; DNA; 16 BP.
XX
AC AAT75139;
XX
DT 04-MAR-1998 (first entry)
XX
DE Arbitrary anchor primer HG.
XX
KW dhc-1; homocysteine; hypohomocysteinaemia; atherosclerosis; diagnosis;
KW serum; Dami cell; PCR; arbitrary primer; messenger RNA pool; ss.
XX
OS Synthetic.
XX
PN WO9725440-A2.
XX
PD 17-JUL-1997.
XX
PF 02-JAN-1997; 97WO-CA000001.
XX
PR 03-JAN-1996; 96US-00582261.
XX
PA (HAMI-) HAMILTON CIVIC HOSPITALS RES DEV INC.
XX
PI Austin RC, Hirsh J, Weitz J;
XX
DR WPI; 1997-372877/34.

```
XX
PT   Methods and polynucleotide(s) for diagnosing hyperhomocysteinaemia -
PT   and/or predisposition to develop premature atherosclerosis by detecting
PT   increased levels of serum homocysteine.
XX
PS   Disclosure; Page 22; 84pp; English.
XX
CC   Arbitrary RT-PCR primers (AAT75138-42) were used to amplify mRNA from
CC   cells exposed to hyperphysiological, normal or subphysiological levels of
CC   homocysteine. PCR products were separated on a sequencing gel and
CC   discrete fractions which were increased or decreased were identified.
CC   This method was used to identify mRNA and the corresponding cDNA which
CC   are increased in the cells of a patient having hyperhomocysteinaemia or a
CC   predisposition to homocysteine mediated atherosclerosis. These
CC   polynucleotides can be used for the diagnosis and treatment of
CC   atherosclerotic diseases and diseases of metabolism of sulphur containing
CC   amino acids (e.g. homocysteinaemia), which are associated with vascular
CC   damage and atherosclerotic disease, specifically unstable angina, acute
CC   myocardial infarction (heart attack), cerebrovascular accidents (stroke),
CC   hypertension, renal artery stenosis, aortic stenosis and deep vein
CC   occlusive disease
XX
SQ   Sequence 16 BP; 2 A; 1 C; 2 G; 11 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTG 1782
              ||||||||||||||||
Db          1 AAGCTTTTTTTTTTTG 16


RESULT 2497
AAV36965
ID   AAV36965 standard; cDNA; 16 BP.
XX
AC   AAV36965;
XX
DT   02-OCT-1998  (first entry)
XX
DE   Rat pituitary-tumour-transforming-gene anchored primer.
XX
KW   ss; pituitary-tumour-transforming gene; PTTG; pituitary tumour; PCR;
KW   cancer; oncogene; gene replacement therapy; primer; amplification.
XX
OS   Synthetic.
OS   Rattus sp.
XX
PN   WO9822587-A2.
XX
PD   28-MAY-1998.
XX
PF   21-NOV-1997;   97WO-US021463.
XX
PR   21-NOV-1996;   96US-0031338P.
XX
PA   (CEDA-) CEDARS SINAI MEDICAL CENT.
XX
PI   Melmed S,  Pei L;
XX
DR   WPI; 1998-312473/27.
XX
PT   New pituitary tumour transforming gene and protein - used for diagnosis,
PT   monitoring and treatment of tumours.
XX
PS   Example 1; Page 23; 44pp; English.
XX
CC   The primers AAV36965 and AAV36966 were used in the isolation of the
CC   pituitary-tumour transforming gene (PTTG). The PTTG encodes a polypeptide
CC   that is expressed by pituitary tumour cells and binds to anti-PTTG
CC   antibodies (Ab). Recombinant PTTG is useful as an immunogen for raising
CC   Ab, in assays and for therapy. Ab, optionally labelled, are used to
CC   detect, e.g. for monitoring treatment or in in vivo imaging, or purify
CC   human PTTG, e.g. for diagnosis of pituitary tumours and for
CC   differentiating between malignant and benign tumours in biopsy samples.
CC   Oligonucleotides and antisense oligonucleotides can also be used
CC   therapeutically to counteract or stimulate biological effects of PTTG.
CC   Many cancers express PTTG, and the nucleic acid sequence can transform
CC   cells without a complementary oncogene; it is responsible for tumour
CC   formation in the pituitary. PTTG is useful in gene replacement therapy
CC   and transgenic animals are used as models for studying pituitary tumours
CC   etc
XX
SQ   Sequence 16 BP; 2 A; 1 C; 2 G; 11 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTG 1782
              ||||||||||||||||
Db          1 AAGCTTTTTTTTTTTG 16


RESULT 2498
AAX57361
ID   AAX57361 standard; DNA; 16 BP.
XX
AC   AAX57361;
XX
DT   24-JUL-1999  (first entry)
XX
DE   P. obesus beacon PCR primer 1.
XX
KW   Beacon; hypothalamus; obese; lean; agonist; antagonist; treatment;
KW   obesity; anorexia; weight maintenance; energy imbalance; diabetes;
KW   metabolic syndrome; dyslipidemia; hypertension; insulin resistance;
KW   medicament; livestock; diagnosis; PCR primer; ss.
XX
OS   Synthetic.
OS   Psammomys obesus.
XX
PN   WO9923217-A1.
XX
PD   14-MAY-1999.
XX
PF   30-OCT-1998;   98WO-AU000902.
XX
PR   31-OCT-1997;   97AU-00000117.
PR   11-NOV-1997;   97AU-00000323.
XX
PA   (ITDI-) INT DIABETES INST.
PA   (UYDE-) UNIV DEAKIN.
XX
PI   Zimmet PZ,  Collier G;
XX
DR   WPI; 1999-337484/28.
XX
PT   New gene encoding a beacon protein associated with modulation of obesity,
PT   diabetes and metabolic energy levels.
XX
PS   Example 5; Page 51; 85pp; English.
XX
CC   This invention describes a novel beacon protein and its encoding nucleic
CC   acid which is expressed in larger amounts in hypothalamus tissue of obese
CC   animals compared to lean animals. Agonists and antagonists of beacon can
CC   be used to treat obesity, anorexia, weight maintenance, energy imbalance,
CC   diabetes, metabolic syndrome, dyslipidemia, hypertension and/or insulin
CC   resistance. The beacon protein, itself is used to manufacture medicaments
CC   for treatment of obesity, anorexia, energy imbalance or diabetes. The
CC   treatment is contemplated for both human and animals, such as those
CC   important to the livestock industry. The antibody and polynucleotides are
CC   useful in diagnosis of conditions as above. This sequence represents a
CC   PCR primer used in the method of the invention
XX
```

```
SQ   Sequence 16 BP; 2 A; 1 C; 2 G; 11 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTG 1782
              ||||||||||||||||
Db          1 AAGCTTTTTTTTTTTG 16


RESULT 2499
AAX24309
ID   AAX24309 standard; DNA; 16 BP.
XX
AC   AAX24309;
XX
DT   07-JUN-1999  (first entry)
XX
DE   Differential display PCR primer H-T11G.
XX
KW   RLMP; LMP; LIM mineralisation protein; bone mineralisation; rat;
KW   cytokine; spine fusion; fracture repair; bone grafting; osteoporosis;
KW   gene therapy; PCR; primer; ss.
XX
OS   Synthetic.
XX
PN   WO9906563-A1.
XX
PD   11-FEB-1999.
XX
PF   29-JUL-1998;   98WO-US015814.
XX
PR   30-JUL-1997;   97US-0054219P.
PR   02-APR-1998;   98US-0080407P.
XX
PA   (UYEM-) UNIV EMORY.
XX
PI   Hair G,  Boden S;
XX
DR   WPI; 1999-153793/13.
XX
PT   LIM mineralisation proteins - used to induce bone formation from
PT   osteogenic precursors, e.g. for treating osteoporosis or repairing
PT   fractures.
XX
PS   Example 9; Page 48; 67pp; English.
XX
CC   Primers H-T11G and H-AP-10 (see AAX24310) were used in differential
CC   display PCR using cDNA produced from glucocorticoid-stimulated rat
CC   osteoblasts. H-T11M was also used as the MMLV-RT primer in preparation of
CC   cDNA from cellular RNA. A 260 bp PCR product (see AAX24308) was used as a
CC   probe to screen a rat osteosarcoma (UMR 106) cDNA library. Positive
CC   clones were subjected to nested primer analysis to obtain the primer
CC   sequences necessary for amplifying full-length RLMP cDNA (see AAX24307).
CC   RLMP (see also AAW97843), or rat LIM mineralisation protein, enhances
CC   bone mineralisation in mammalian cells grown in vitro, and induces bone
CC   formation in vivo. Clinical applications include enhancement of bone
CC   repair in fractures, bone defects, bone grafting, and normal homeostasis
CC   in patients presenting with osteoporosis
XX
SQ   Sequence 16 BP; 2 A; 1 C; 2 G; 11 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTG 1782
              ||||||||||||||||
Db          1 AAGCTTTTTTTTTTTG 16


RESULT 2500
AAX19462
ID   AAX19462 standard; DNA; 16 BP.
XX
AC   AAX19462;
XX
DT   21-MAY-1999  (first entry)
XX
DE   Human senescence factor p23 H-T11 primer SEQ ID NO:4.
XX
KW   Human; senescence factor; p23; cancer; persistent inflammation;
KW   proliferative disorder; degenerative disorder; primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9907893-A1.
XX
PD   18-FEB-1999.
XX
PF   05-AUG-1998;   98WO-US016343.
XX
PR   08-AUG-1997;   97US-00908873.
XX
PA   (UNIW ) UNIV WASHINGTON.
XX
PI   Swisshelm K,  Hosier S,  Kubbies M;
XX
DR   WPI; 1999-167454/14.
XX
PT   Newly isolated nucleic acid molecule (designated p23) encoding a p23
PT   polypeptide - useful for inducing a senescence phenotype in a cell.
XX
PS   Example 1; Page 18; 44pp; English.
XX
CC   The present invention describes human senescence factor p23. An
CC   expression vector for p23 is useful for inducing a senescent phenotype in
CC   a cell (preferably eukaryotic). This may help in regulating diseases,
CC   including cancer, persistent inflammation, and various proliferative and
CC   degenerative disorders. These transgenic cells are useful in gene therapy
CC   for treating cancer, particularly where antisense oligonucleotides are
CC   useful for blocking normal or mutant p23 expression in cancer cells or
CC   other proliferating cells. Transgenic cells are also useful for producing
CC   the p23 polypeptide in large quantities. The antibodies are useful for
CC   raising antiserum against p23, and for identifying senescent cells in
CC   culture and tissue biopsies. The p23 polynucleotides are useful for
CC   modulating or altering p23 activity in a cell, and for identifying and
CC   isolating the whole gene encoding p23, and variants of p23. Assays based
CC   on p23 elements, which detect p23 levels and activity are useful as
CC   diagnostic markers for staging tumours, determining prognosis, and/or
CC   predicting therapeutic success. These elements also provide an assay for
CC   detecting chromosomal rearrangements in chromosome 3 in a human cell. The
CC   isolation of the p23 polynucleotide permits the manipulation of malignant
CC   growth in cancer. The present sequence represents a primer used in an
CC   example from the present invention
XX
SQ   Sequence 16 BP; 2 A; 1 C; 2 G; 11 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTG 1782
              ||||||||||||||||
Db          1 AAGCTTTTTTTTTTTG 16


RESULT 2501
AAX18362/c
ID   AAX18362 standard; DNA; 16 BP.
XX
AC   AAX18362;
XX
DT   11-MAY-1999  (first entry)
```

XX
DE RT-PCR primer of the invention SEQ ID 3.
XX
KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS Synthetic.
XX
PN JP11032765-A.
XX
PD 09-FEB-1999.
XX
PF 18-JUL-1997; 97JP-00208312.
XX
PR 18-JUL-1997; 97JP-00208312.
XX
PA (TAKI) TAKARA SHUZO CO LTD.
XX
DR WPI; 1999-183822/16.
XX
PT Peptides having at least two new nucleotides - useful as primers in RT-
PT PCR.
XX
PS Disclosure; Page 10; 19pp; Japanese.
XX
CC This sequence represents a primer of the invention. The invention relates
CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC natural number indicating the repetition of alpha; beta, delta = V or N;
CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC repetition of gamma, in which thymine expressed by gamma is composed of
CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC useful as primers for RT-PCR and determination of base sequences. The new
CC sequences allow for reproductive and highly efficient analysis of gene
CC sequences
XX
SQ Sequence 16 BP; 1 A; 1 C; 0 G; 14 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2784 TGAAAAAAAAAAAAAA 2799
||||||||||||||||
Db 16 TGAAAAAAAAAAAAAA 1

RESULT 2502
AAX07568
ID AAX07568 standard; cDNA; 16 BP.
XX
AC AAX07568;
XX
DT 21-JUN-1999 (first entry)
XX
DE Homo sapiens fetal kidney clone AK647 secreted protein gene 3' end.
XX
KW Secreted protein; fetal kidney; ds.
XX
OS Homo sapiens.
XX
PN WO9900405-A1.
XX
PD 07-JAN-1999.
XX
PF 29-JUN-1998; 98WO-US013530.
XX
PR 30-JUN-1997; 97US-00885610.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Jacobs K, Mccoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;
PI Evans C, Agostino MJ;
XX
DR WPI; 1999-095671/08.
XX
PT New polynucleotides encoding secreted human proteins - are derived from
PT foetal kidney or adult retina cDNA libraries, used as, e.g. potential
PT vaccines.
XX
PS Disclosure; Page 54; 76pp; English.
XX
CC The sequence is that of the 3' end of a sequence encoding a secreted
CC protein from a human fetal kidney clone AK296. Such a sequence is
CC predicted to have biological activities which would make them suitable
CC for treating, preventing or ameliorating medical conditions in humans and
CC animals, although no supporting data is given. Suggested activities
CC include nutritional activity, cytokine and cell
CC proliferation/differentiation activity, immune stimulating (e.g. as
CC vaccines) or suppressing activity, haematopoiesis regulating activity,
CC tissue growth activity, activin/inhibin activity,
CC chemotactic/chemokinetic activity, haemostatic and thrombolytic activity,
CC receptor/ligand activity, anti-inflammatory activity, cadherin/tumour
CC invasion suppressor activity, and tumour inhibition activity. It is also
CC stated to be useful for gene therapy
XX
SQ Sequence 16 BP; 16 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAA 2801
||||||||||||||||
Db 1 AAAAAAAAAAAAAAAA 16

RESULT 2503
AAX07568/c
ID AAX07568 standard; cDNA; 16 BP.
XX
AC AAX07568;
XX
DT 21-JUN-1999 (first entry)
XX
DE Homo sapiens fetal kidney clone AK647 secreted protein gene 3' end.
XX
KW Secreted protein; fetal kidney; ds.
XX
OS Homo sapiens.
XX
PN WO9900405-A1.
XX
PD 07-JAN-1999.
XX
PF 29-JUN-1998; 98WO-US013530.
XX
PR 30-JUN-1997; 97US-00885610.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Jacobs K, Mccoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;
PI Evans C, Agostino MJ;
XX
DR WPI; 1999-095671/08.
XX
PT New polynucleotides encoding secreted human proteins - are derived from
PT foetal kidney or adult retina cDNA libraries, used as, e.g. potential
PT vaccines.
XX
PS Disclosure; Page 54; 76pp; English.
XX
CC The sequence is that of the 3' end of a sequence encoding a secreted
CC protein from a human fetal kidney clone AK296. Such a sequence is
CC predicted to have biological activities which would make them suitable

```
CC   for treating, preventing or ameliorating medical conditions in humans and
CC   animals, although no supporting data is given. Suggested activities
CC   include nutritional activity, cytokine and cell
CC   proliferation/differentiation activity, immune stimulating (e.g. as
CC   vaccines) or suppressing activity, haematopoiesis regulating activity,
CC   tissue growth activity, activin/inhibin activity,
CC   chemotactic/chemokinetic activity, haemostatic and thrombolytic activity,
CC   receptor/ligand activity, anti-inflammatory activity, cadherin/tumour
CC   invasion suppressor activity, and tumour inhibition activity. It is also
CC   stated to be useful for gene therapy
XX
SQ   Sequence 16 BP; 16 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db         16 TTTTTTTTTTTTTTTT 1


RESULT 2504
AAC66068
ID   AAC66068 standard; DNA; 16 BP.
XX
AC   AAC66068;
XX
DT   22-FEB-2001  (first entry)
XX
DE   DNA chip primer #4.
XX
KW   DNA chip; primer; nucleoside derivative; photolabile protecting group;
KW   photolithographic nucleic acid chip; ss.
XX
OS   Synthetic.
XX
PN   WO200061594-A2.
XX
PD   19-OCT-2000.
XX
PF   07-APR-2000; 2000WO-DE001148.
XX
PR   08-APR-1999;   99DE-01015867.
PR   28-JAN-2000; 2000DE-01003631.
XX
PA   (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI   Beier M,  Hoheisel J;
XX
DR   WPI; 2000-679457/66.
XX
PT   New nucleoside derivatives with photolabile protecting groups, useful in
PT   oligonucleotide synthesis, particularly on solid phases, e.g. for
PT   hybridization testing.
XX
PS   Disclosure; Fig 9; 48pp; German.
XX
CC   This invention describes nucleoside derivatives (I) with photolabile
CC   protecting groups. (I) are used to synthesize oligonucleotides using the
CC   photolithographic nucleic acid chip method, particularly where these are
CC   intended for performing enzymatic reactions initiated from a free 3'-
CC   hydroxy (especially solid-phase polymerase reactions or ligase reactions,
CC   but also reverse transcription, cDNA synthesis etc.), also for
CC   hybridization testing, sequencing and in DNA computing. (I) are produced
CC   with high selectivity by reaction with a mild acylating agent that has
CC   high specificity for the 3'-position, without significant side-reactions
CC   (cf. more reactive acylating agents such as chloroformates)
XX
SQ   Sequence 16 BP; 16 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db          1 AAAAAAAAAAAAAAAA 16


RESULT 2505
AAC66068/c
ID   AAC66068 standard; DNA; 16 BP.
XX
AC   AAC66068;
XX
DT   22-FEB-2001  (first entry)
XX
DE   DNA chip primer #4.
XX
KW   DNA chip; primer; nucleoside derivative; photolabile protecting group;
KW   photolithographic nucleic acid chip; ss.
XX
OS   Synthetic.
XX
PN   WO200061594-A2.
XX
PD   19-OCT-2000.
XX
PF   07-APR-2000; 2000WO-DE001148.
XX
PR   08-APR-1999;   99DE-01015867.
PR   28-JAN-2000; 2000DE-01003631.
XX
PA   (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI   Beier M,  Hoheisel J;
XX
DR   WPI; 2000-679457/66.
XX
PT   New nucleoside derivatives with photolabile protecting groups, useful in
PT   oligonucleotide synthesis, particularly on solid phases, e.g. for
PT   hybridization testing.
XX
PS   Disclosure; Fig 9; 48pp; German.
XX
CC   This invention describes nucleoside derivatives (I) with photolabile
CC   protecting groups. (I) are used to synthesize oligonucleotides using the
CC   photolithographic nucleic acid chip method, particularly where these are
CC   intended for performing enzymatic reactions initiated from a free 3'-
CC   hydroxy (especially solid-phase polymerase reactions or ligase reactions,
CC   but also reverse transcription, cDNA synthesis etc.), also for
CC   hybridization testing, sequencing and in DNA computing. (I) are produced
CC   with high selectivity by reaction with a mild acylating agent that has
CC   high specificity for the 3'-position, without significant side-reactions
CC   (cf. more reactive acylating agents such as chloroformates)
XX
SQ   Sequence 16 BP; 16 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db         16 TTTTTTTTTTTTTTTT 1


RESULT 2506
AAC87710
ID   AAC87710 standard; DNA; 16 BP.
XX
AC   AAC87710;
XX
DT   01-MAR-2001  (first entry)
XX
```

DE MMLV reverse transcriptase PCR primer H-T11G SEQ ID NO:4.
XX
KW LIM mineralisation protein; LMP; bone formation; osteopathic;
KW osteogenic precursor cell; gene therapy; metabolic bone disease;
KW osteoporosis; bone degenerative disease; PCR primer; ss.
XX
OS Moloney murine leukemia virus.
XX
PN WO200066178-A1.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US011664.
XX
PR 30-APR-1999; 99US-0132021P.
XX
PA (UYEM-) UNIV EMORY.
XX
PI Boden SD, Hair GA;
XX
DR WPI; 2000-672828/65.
XX
PT New nucleic acid encoding a human LIM mineralization protein for inducing
PT or inhibiting bone formation, fusing a spine, stimulating production of
PT an osteogenic cell, or treating bone conditions, such as, osteoporosis.
XX
PS Example 9; Page 61; 84pp; English.
XX
CC The present invention specifically describes the human LIM mineralisation
CC proteins (LMP) HLMP-2 and HLMP-3. LMPs have osteopathic activity and can
CC be used in gene therapy. LMP nucleic acids can be used to induce or
CC inhibit bone formation, fuse a spine, stimulate production of an
CC osteogenic cell, or inhibit the expression of HLMP-2 or HLMP-3. They can
CC be used to treat bone conditions, such as, osteoporosis and other
CC metabolic bone diseases. Antibodies to the LMP proteins encoded by the
CC nucleic acids are used in marker assays to identify risk factors in bone
CC degenerative diseases, such as osteoporosis. The nucleic acids are used
CC in gene therapy for bone formation which leads to the advantages of: (1)
CC lower production costs; (2) greater efficacy compared to extracellular
CC treatment regiments due to the ability to achieve prolonged expression of
CC the intracellular signal; (3) by-passing the possibility that treatment
CC with extracellular signals might be hampered due to the presence of
CC limiting numbers or receptors for those signals; (4) permitting the
CC delivery of transfected potential osteoprogenitor cells directly to the
CC site where localised bone formation is required; and (5) permitting
CC systemic bone formation, which provides a treatment regimen for
CC osteoporosis and other metabolic bone diseases. The present sequence
CC represents a reverse transcriptase PCR primer which is used in an example
CC from the present invention
XX
SQ Sequence 16 BP; 2 A; 1 C; 2 G; 11 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1767 AAGCTTTTTTTTTTTG 1782
              ||||||||||||||||
Db          1 AAGCTTTTTTTTTTTG 16
```

RESULT 2507
AAA94101
ID AAA94101 standard; DNA; 16 BP.
XX
AC AAA94101;
XX
DT 30-JAN-2001 (first entry)
XX
DE Fruit-associated banana TRX gene PCR primer H-T11G.
XX
KW Banana; fruit-associated TRX gene; promoter; G1A; transgenic plant;
KW fruit ripening; nutrition; PCR primer; ss.
XX
OS Musa acuminata.
XX
PN WO200056863-A1.
XX
PD 28-SEP-2000.
XX
PF 17-MAR-2000; 2000WO-US007293.
XX
PR 19-MAR-1999; 99US-0125310P.
XX
PA (AGRI-) AGRITOPE INC.
XX
PI Clendennen SK, Kellogg JA, Phan CB, Mathews HV, Webb NM;
XX
DR WPI; 2000-628259/60.
XX
PT Nucleic acid molecule encoding banana fruit associated promoter and melon
PT actin promoter, useful for producing transgenic fruit-bearing plants.
XX
PS Example 1; Page 35; 72pp; English.
XX
CC The present sequence is a PCR primer which was used to isolate and
CC amplify the promoter of the banana fruit-associated TRX (also known as
CC the G1A) gene. This was isolated from a banana library using differential
CC display analysis for banana-specific transcripts. The promoters of the
CC invention can be used to produce transgenic fruit, with altered or
CC improved characteristics, in particular their ripening, their nutritional
CC content and the expression of useful proteins
XX
SQ Sequence 16 BP; 2 A; 1 C; 2 G; 11 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1767 AAGCTTTTTTTTTTTG 1782
              ||||||||||||||||
Db          1 AAGCTTTTTTTTTTTG 16
```

RESULT 2508
ABA04585
ID ABA04585 standard; DNA; 16 BP.
XX
AC ABA04585;
XX
DT 15-FEB-2002 (first entry)
XX
DE Oligonucleotide #5.
XX
KW Analytical support; genomic sequencing; mutation detection;
KW pharmaceutical development; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER = Fl(CH2)6-PO-thymine, where Fl is flavine
FT and PO is a phosphate group"
XX
PN FR2805348-A1.
XX
PD 24-AUG-2001.
XX
PF 23-FEB-2000; 2000FR-00002236.
XX
PR 23-FEB-2000; 2000FR-00002236.
XX
PA (COMS) COMMISSARIAT ENERGIE ATOMIQUE.
XX

```
PI   Cuzin M,  Peltie P,  Fontecave M,  Decout JL,  Dueymes C;
XX
DR   WPI; 2001-628265/73.
XX
PT   Support for hybridization analysis of nucleic acids for sequencing
PT   techniques, comprises an array of oligonucleotides having a label where
PT   the fluorescence changes follow hybridization.
XX
PS   Example 1; Page 12; 33pp; French.
XX
CC   The present invention relates to an analytical support, to which a number
CC   of oligonucleotides are fixed. The oligonucleotides are labelled with a
CC   fluorescent compound, the fluorescence of which varies when the
CC   oligonucleotide hybridises to its complement. The analytical support is
CC   useful in hybridisation testing for identification of specific nucleic
CC   acids, such as genomic sequencing, detecting mutations or pharmaceutical
CC   development. The present oligonucleotide was used to illustrate the
CC   invention
XX
SQ   Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 16


RESULT 2509
ABA04585/c
ID   ABA04585 standard; DNA; 16 BP.
XX
AC   ABA04585;
XX
DT   15-FEB-2002  (first entry)
XX
DE   Oligonucleotide #5.
XX
KW   Analytical support; genomic sequencing; mutation detection;
KW   pharmaceutical development; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER = Fl(CH2)6-PO-thymine, where Fl is flavine
FT                   and PO is a phosphate group"
XX
PN   FR2805348-A1.
XX
PD   24-AUG-2001.
XX
PF   23-FEB-2000; 2000FR-00002236.
XX
PR   23-FEB-2000; 2000FR-00002236.
XX
PA   (COMS ) COMMISSARIAT ENERGIE ATOMIQUE.
XX
PI   Cuzin M,  Peltie P,  Fontecave M,  Decout JL,  Dueymes C;
XX
DR   WPI; 2001-628265/73.
XX
PT   Support for hybridization analysis of nucleic acids for sequencing
PT   techniques, comprises an array of oligonucleotides having a label where
PT   the fluorescence changes follow hybridization.
XX
PS   Example 1; Page 12; 33pp; French.
XX
CC   The present invention relates to an analytical support, to which a number
CC   of oligonucleotides are fixed. The oligonucleotides are labelled with a
CC   fluorescent compound, the fluorescence of which varies when the
CC   oligonucleotide hybridises to its complement. The analytical support is
CC   useful in hybridisation testing for identification of specific nucleic
CC   acids, such as genomic sequencing, detecting mutations or pharmaceutical
CC   development. The present oligonucleotide was used to illustrate the
CC   invention
XX
SQ   Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         16 AAAAAAAAAAAAAAAA 1


RESULT 2510
AAF83580
ID   AAF83580 standard; DNA; 16 BP.
XX
AC   AAF83580;
XX
DT   23-JUL-2001  (first entry)
XX
DE   B. gymnorrhiza salt-tolerance cDNA amplifying primer H-T11G.
XX
KW   Salt-stress; genetic modification; salt tolerance; PCR primer; ss.
XX
OS   Bruguiera gymnorrhiza.
XX
PN   WO200130999-A1.
XX
PD   03-MAY-2001.
XX
PF   28-JUL-2000; 2000WO-JP005102.
XX
PR   22-OCT-1999;   99JP-00301621.
PR   20-DEC-1999;   99JP-00361107.
XX
PA   (EBAR ) EBARA CORP.
XX
PI   Karube I,  Hanagata N;
XX
DR   WPI; 2001-308636/32.
XX
PT   Nucleotide sequences, useful for generating salt-tolerant transgenic
PT   plants, obtained from the leaves of Bruguiera gymnorrhiza subjected to
PT   500 mM NaCl.
XX
PS   Example 2; Page 15; 49pp; English.
XX
CC   The invention provides nucleotide sequences highly expressed in salt-
CC   stressed leaves of Bruguiera gymnorrhiza. The invention is useful to
CC   provide salt tolerant plants by genetic modification. Plants transformed
CC   with the DNA sequences have improved salt tolerance. Sequences AAF83580 -
CC   592 represent PCR primers for amplifying B. gymnorrhiza salt tolerance
CC   gene associated cDNA fragments
XX
SQ   Sequence 16 BP; 2 A; 1 C; 2 G; 11 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTG 1782
              ||||||||||||||||
Db          1 AAGCTTTTTTTTTTTG 16


RESULT 2511
```

```
AAS06651
ID   AAS06651 standard; DNA; 16 BP.
XX
AC   AAS06651;
XX
DT   12-SEP-2001  (first entry)
XX
DE   Human cDNA synthesis and differential display primer, HT11G.
XX
KW   Human; Estrogen response element; ERE; DDRT-PCR; ss; PCR primer;
KW   differential display of reverse transcribed mRNAs by PCR;
KW   testicular cancer; breast cancer; prostate cancer; endometrial cancer;
KW   asthma; hypospadia; cryptorchism; allergy; hormone replacement therapy;
KW   HRT; endocrine system; HT11G.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200134834-A2.
XX
PD   17-MAY-2001.
XX
PF   10-NOV-2000; 2000WO-DK000628.
XX
PR   11-NOV-1999;   99DK-00001626.
XX
PA   (RIGS-) RIGSHOSPITALET.
XX
PI   Leffers H,  Jorgensen M,  Skakkebaek NE;
XX
DR   WPI; 2001-335941/35.
XX
PT   Evaluating a cellular response to an environmental compound, for use in
PT   toxicological analysis, involves determining or comparing the expression
PT   levels of at least one endogenous gene.
XX
PS   Example 3; Page 27; 77pp; English.
XX
CC   The sequence represents a downstream PCR primer used in a DDRT-PCR
CC   experiment (and in cDNA synthesis), demonstrating the method of the
CC   invention. The method relates to evaluating a cellular response to an
CC   environmental compound, comprising determining or comparing the
CC   expression levels of at least one endogenous gene e.g by differential
CC   display of reverse transcribed mRNAs by PCR (DDRT-PCR). The method can be
CC   adapted to identify compounds that act on the level of endogenous gene
CC   expression through activating nuclear receptors. The method is useful in
CC   toxicological analysis, diagnostics, for diagnosing cancer (e.g.
CC   testicular, breast, prostate and endometrium), asthma, hypospadia,
CC   cryptorchism and/or allergy, and for evaluating the efficiency of a
CC   treatment for hormonal deficiency or hormonal replacement therapy, in a
CC   human such as a post-menopausal female. The method is also useful for
CC   identifying environmental chemicals or pharmaceutical compositions that
CC   interact with endocrine systems, and for detecting chemicals that pose a
CC   health threat. Expression levels of endogenous genes are determined
CC   rapidly using a sensitive technique, and the expression of any gene can
CC   be monitored. The assays are far more informative than the currently used
CC   assays, and significantly reduces the number of animals required for the
CC   testing, as it is expected that essentially all the animals in a test
CC   group will respond to the compound
XX
SQ   Sequence 16 BP; 2 A; 1 C; 2 G; 11 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTG 1782
              ||||||||||||||||
Db          1 AAGCTTTTTTTTTTTG 16


RESULT 2512
AAF30895
ID   AAF30895 standard; DNA; 16 BP.
XX
AC   AAF30895;
XX
DT   09-JUL-2001  (first entry)
XX
DE   Oligonucleotide-minor groove binder complex.
XX
KW   ODN-MGB-LF; oligonucleotide; minor groove binder; latent fluorophore;
KW   hybridisation; detection; fluorescence; probe; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /note= "thymine modified by a minor groove binder (2-
FT                   dimethylaminonaphthalene-6- sulfonamide"
XX
PN   WO200131063-A1.
XX
PD   03-MAY-2001.
XX
PF   26-OCT-2000; 2000WO-US029786.
XX
PR   26-OCT-1999;   99US-00428236.
XX
PA   (EPOC-) EPOCH BIOSCIENCES INC.
XX
PI   Dempcy RO,  Afonina IA,  Vermeulen NMJ;
XX
DR   WPI; 2001-328656/34.
XX
PT   Conjugate of oligonucleotide, minor groove binder and latent fluorophore,
PT   useful for detecting specific nucleic acids, e.g. for single-nucleotide
PT   mismatch discrimination.
XX
PS   Disclosure; Page 101; 105pp; English.
XX
CC   The present sequence is that of an oligonucleotide (ODN)-minor groove
CC   binder (MGF) complex. MGBs bind in a non-intercalating manner to the
CC   minor groove of non-single-stranded DNA, RNA or their hybrids. ODN-MGB-LF
CC   conjugates of the invention also comprise a latent fluorophore (LF),
CC   which binds similarly to the MGB but in an intercalating manner, or lies
CC   in the minor groove, or is oriented in some other way to the DNA molecule
CC   by MGB, such that it becomes fluorescent (or its fluorescent properties
CC   change detectably). The conjugates are used as hybridisation probes and
CC   amplification primers for fluorescent detection of specifically
CC   hybridising sequences, for analysis or diagnosis, especially (real-time)
CC   PCR, for single-nucleotide mismatch discrimination, target or signal
CC   amplification, array-based assays and sequencing, including detection of
CC   double-stranded DNA by triplex formation
XX
SQ   Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 16


RESULT 2513
AAF30895/c
ID   AAF30895 standard; DNA; 16 BP.
XX
AC   AAF30895;
XX
DT   09-JUL-2001  (first entry)
XX
DE   Oligonucleotide-minor groove binder complex.
```

```
XX
KW   ODN-MGB-LF; oligonucleotide; minor groove binder; latent fluorophore;
KW   hybridisation; detection; fluorescence; probe; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /note= "thymine modified by a minor groove binder (2-
FT                   dimethylaminonaphthalene-6- sulfonamide"
XX
PN   WO200131063-A1.
XX
PD   03-MAY-2001.
XX
PF   26-OCT-2000; 2000WO-US029786.
XX
PR   26-OCT-1999;   99US-00428236.
XX
PA   (EPOC-) EPOCH BIOSCIENCES INC.
XX
PI   Dempcy RO,  Afonina IA,  Vermeulen NMJ;
XX
DR   WPI; 2001-328656/34.
XX
PT   Conjugate of oligonucleotide, minor groove binder and latent fluorophore,
PT   useful for detecting specific nucleic acids, e.g. for single-nucleotide
PT   mismatch discrimination.
XX
PS   Disclosure; Page 101; 105pp; English.
XX
CC   The present sequence is that of an oligonucleotide (ODN)-minor groove
CC   binder (MGF) complex. MGBs bind in a non-intercalating manner to the
CC   minor groove of non-single-stranded DNA, RNA or their hybrids. ODN-MGB-LF
CC   conjugates of the invention also comprise a latent fluorophore (LF),
CC   which binds similarly to the MGB but in an intercalating manner, or lies
CC   in the minor groove, or is oriented in some other way to the DNA molecule
CC   by MGB, such that it becomes fluorescent (or its fluorescent properties
CC   change detectably). The conjugates are used as hybridisation probes and
CC   amplification primers for fluorescent detection of specifically
CC   hybridising sequences, for analysis or diagnosis, especially (real-time)
CC   PCR, for single-nucleotide mismatch discrimination, target or signal
CC   amplification, array-based assays and sequencing, including detection of
CC   double-stranded DNA by triplex formation
XX
SQ   Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         16 AAAAAAAAAAAAAAAA 1


RESULT 2514
AAF30880
ID   AAF30880 standard; DNA; 16 BP.
XX
AC   AAF30880;
XX
DT   09-JUL-2001  (first entry)
XX
DE   Oligonucleotide portion of ODN-MGB-LF conjugate.
XX
KW   ODN-MGB-LF; oligonucleotide; minor groove binder; latent fluorophore;
KW   hybridisation; detection; fluorescence; probe; ss.
XX
OS   Synthetic.
XX
PN   WO200131063-A1.
XX
PD   03-MAY-2001.
XX
PF   26-OCT-2000; 2000WO-US029786.
XX
PR   26-OCT-1999;   99US-00428236.
XX
PA   (EPOC-) EPOCH BIOSCIENCES INC.
XX
PI   Dempcy RO,  Afonina IA,  Vermeulen NMJ;
XX
DR   WPI; 2001-328656/34.
XX
PT   Conjugate of oligonucleotide, minor groove binder and latent fluorophore,
PT   useful for detecting specific nucleic acids, e.g. for single-nucleotide
PT   mismatch discrimination.
XX
PS   Disclosure; Page 58; 105pp; English.
XX
CC   The present sequence is that of the oligonucleotide (ODN) component of an
CC   ODN-MGB (minor groove binder)-LF (latent fluorophore) conjugate of the
CC   invention. MGBs bind in a non-intercalating manner to the minor groove of
CC   non-single-stranded DNA, RNA or their hybrids, while a LF binds similarly
CC   but in an intercalating manner, or lies in the minor groove, or is
CC   oriented in some other way to the DNA molecule by MGB, such that it
CC   becomes fluorescent (or its fluorescent properties change detectably).
CC   The conjugates are used as hybridisation probes and amplification primers
CC   for fluorescent detection of specifically hybridising sequences, for
CC   analysis or diagnosis, especially (real-time) PCR, for single-nucleotide
CC   mismatch discrimination, target or signal amplification, array-based
CC   assays and sequencing, including detection of double-stranded DNA by
CC   triplex formation. Many different targets can be detected a single
CC   reaction vessel. The present ODN-MGB-LF conjugate was used to demonstrate
CC   hybridisation-triggered fluorescence. Upon hybridisation to the
CC   complementary target sequence there was an increase in fluorescence
CC   yield, measured as the ratio of the fluorescence emitted by the hybrid
CC   between the ODN-MGB-LF conjugate and its target sequence to the
CC   fluorescence emitted by unhybridised (i.e. single-stranded) ODN-MGB-LF,
CC   of 8.3
XX
SQ   Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 16


RESULT 2515
AAF30880/c
ID   AAF30880 standard; DNA; 16 BP.
XX
AC   AAF30880;
XX
DT   09-JUL-2001  (first entry)
XX
DE   Oligonucleotide portion of ODN-MGB-LF conjugate.
XX
KW   ODN-MGB-LF; oligonucleotide; minor groove binder; latent fluorophore;
KW   hybridisation; detection; fluorescence; probe; ss.
XX
OS   Synthetic.
XX
PN   WO200131063-A1.
XX
PD   03-MAY-2001.
XX
PF   26-OCT-2000; 2000WO-US029786.
XX
PR   26-OCT-1999;   99US-00428236.
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```
XX
PA   (EPOC-) EPOCH BIOSCIENCES INC.
XX
PI   Dempcy RO,  Afonina IA,  Vermeulen NMJ;
XX
DR   WPI; 2001-328656/34.
XX
PT   Conjugate of oligonucleotide, minor groove binder and latent fluorophore,
PT   useful for detecting specific nucleic acids, e.g. for single-nucleotide
PT   mismatch discrimination.
XX
PS   Disclosure; Page 58; 105pp; English.
XX
CC   The present sequence is that of the oligonucleotide (ODN) component of an
CC   ODN-MGB (minor groove binder)-LF (latent fluorophore) conjugate of the
CC   invention. MGBs bind in a non-intercalating manner to the minor groove of
CC   non-single-stranded DNA, RNA or their hybrids, while a LF binds similarly
CC   but in an intercalating manner, or lies in the minor groove, or is
CC   oriented in some other way to the DNA molecule by MGB, such that it
CC   becomes fluorescent (or its fluorescent properties change detectably).
CC   The conjugates are used as hybridisation probes and amplification primers
CC   for fluorescent detection of specifically hybridising sequences, for
CC   analysis or diagnosis, especially (real-time) PCR, for single-nucleotide
CC   mismatch discrimination, target or signal amplification, array-based
CC   assays and sequencing, including detection of double-stranded DNA by
CC   triplex formation. Many different targets can be detected a single
CC   reaction vessel. The present ODN-MGB-LF conjugate was used to demonstrate
CC   hybridisation-triggered fluorescence. Upon hybridisation to the
CC   complementary target sequence there was an increase in fluorescence
CC   yield, measured as the ratio of the fluorescence emitted by the hybrid
CC   between the ODN-MGB-LF conjugate and its target sequence to the
CC   fluorescence emitted by unhybridised (i.e. single-stranded) ODN-MGB-LF,
CC   of 8.3
XX
SQ   Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         16 AAAAAAAAAAAAAAAA 1


RESULT 2516
AAH42481
ID   AAH42481 standard; DNA; 16 BP.
XX
AC   AAH42481;
XX
DT   01-OCT-2001  (first entry)
XX
DE   Oligonucleotide used to produce branched chain compounds.
XX
KW   Branched chain compound; nucleic acid synthesis; primer extension;
KW   reverse transcription; nucleic acid hybridization;
KW   nucleic acid amplification; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /note= "COOH attached"
FT   misc_feature    2. .3
FT                   /*tag=  c
FT                   /note= "branch present"
FT   modified_base   2
FT                   /*tag=  b
FT                   /note= "COOH attached"
XX
PN   EP1111068-A1.
XX
PD   27-JUN-2001.
XX
PF   21-DEC-1999;   99EP-00125484.
XX
PR   21-DEC-1999;   99EP-00125484.
XX
PA   (LION-) LION BIOSCIENCE AG.
PA   (VBCG-) VBC GENOMICS GMBH.
XX
PI   Schmidt W,  Hiller R,  Huber M,  Mueller M;
XX
DR   WPI; 2001-466959/51.
XX
PT   Branched compounds useful in e.g. nucleic acid synthesis reaction
PT   comprises nucleic acid moieties optionally extended by a polymerase.
XX
PS   Example 1; Page 10; 31pp; English.
XX
CC   The specification describes branched compounds containing nucleic acid
CC   moieties optionally extended by a polymerase. The branched chain
CC   compounds of the invention are used in nucleic acid synthesis reaction,
CC   primer extension reaction, reverse transcription reaction of RNA into
CC   DNA, nucleic acid hybridization experiment (for identifying sequence of a
CC   nucleic acid), and nucleic acid amplification experiment (for analysing
CC   the expression pattern of genes). The compounds are also used in solid-
CC   phase enzymatic reactions. The present sequence was used in the course of
CC   the invention to produce branched chain compounds
XX
SQ   Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 16


RESULT 2517
AAH42481/c
ID   AAH42481 standard; DNA; 16 BP.
XX
AC   AAH42481;
XX
DT   01-OCT-2001  (first entry)
XX
DE   Oligonucleotide used to produce branched chain compounds.
XX
KW   Branched chain compound; nucleic acid synthesis; primer extension;
KW   reverse transcription; nucleic acid hybridization;
KW   nucleic acid amplification; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /note= "COOH attached"
FT   misc_feature    2. .3
FT                   /*tag=  c
FT                   /note= "branch present"
FT   modified_base   2
FT                   /*tag=  b
FT                   /note= "COOH attached"
XX
PN   EP1111068-A1.
XX
PD   27-JUN-2001.
XX
PF   21-DEC-1999;   99EP-00125484.
XX
```

```
PR   21-DEC-1999;   99EP-00125484.
XX
PA   (LION-) LION BIOSCIENCE AG.
PA   (VBCG-) VBC GENOMICS GMBH.
XX
PI   Schmidt W,  Hiller R,  Huber M,  Mueller M;
XX
DR   WPI; 2001-466959/51.
XX
PT   Branched compounds useful in e.g. nucleic acid synthesis reaction
PT   comprises nucleic acid moieties optionally extended by a polymerase.
XX
PS   Example 1; Page 10; 31pp; English.
XX
CC   The specification describes branched compounds containing nucleic acid
CC   moieties optionally extended by a polymerase. The branched chain
CC   compounds of the invention are used in nucleic acid synthesis reaction,
CC   primer extension reaction, reverse transcription reaction of RNA into
CC   DNA, nucleic acid hybridization experiment (for identifying sequence of a
CC   nucleic acid), and nucleic acid amplification experiment (for analysing
CC   the expression pattern of genes). The compounds are also used in solid-
CC   phase enzymatic reactions. The present sequence was used in the course of
CC   the invention to produce branched chain compounds
XX
SQ   Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         16 AAAAAAAAAAAAAAAA 1


RESULT 2518
ABA02556
ID   ABA02556 standard; DNA; 16 BP.
XX
AC   ABA02556;
XX
DT   18-JUN-2002  (first entry)
XX
DE   HCCS-1 differential display primer H-T_11_A.
XX
KW   Human cervical cancer suppressor protein; HCCS-1; tumour suppressor;
KW   apoptosis; cancer; cytostatic; proliferation; differential display; ss;
KW   normal exocervical tissue; primer.
XX
OS   Homo sapiens.
XX
PN   WO200181387-A1.
XX
PD   01-NOV-2001.
XX
PF   04-DEC-2000; 2000WO-KR001406.
XX
PR   25-APR-2000; 2000KR-00021897.
XX
PA   (KIMJ/) KIM J W.
XX
PI   Kim JW;
XX
DR   WPI; 2002-075106/10.
XX
PT   Human tumor suppressor protein and the encoding polynucleotide useful for
PT   treating cancer, and vector comprising the polynucleotide useful for
PT   suppressing proliferation of cancer cells.
XX
PS   Example 1; Page 34; 37pp; English.
XX
CC   The present sequence is that of a primer used for the differential
CC   display of a human cervical cancer suppressor 1 (HCCS-1) gene fragment
CC   (see ABA02555 and ABA02558) from normal exocervical tissue. The gene
CC   encodes the HCCS-1 protein (see ABB04180). The specification describes a
CC   tumour suppressor protein, HCCS-1, and the polynucleotide that encodes
CC   it. The invention has cytostatic activity. HCCS-1 acts as a tumour
CC   suppressor by inducing apoptosis of the cancer cell. An expression vector
CC   containing the inventive HCCS-1 gene may be used to suppress the
CC   proliferation of cancer cells by inducing apoptosis. The invention also
CC   provides a pharmaceutical composition for treating or preventing cancer
CC   which comprises the inventive tumour suppressor gene
XX
SQ   Sequence 16 BP; 2 A; 1 C; 2 G; 11 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTG 1782
              ||||||||||||||||
Db          1 AAGCTTTTTTTTTTTG 16


RESULT 2519
ABK87148
ID   ABK87148 standard; DNA; 16 BP.
XX
AC   ABK87148;
XX
DT   07-OCT-2002  (first entry)
XX
DE   Scarlet runner bean anchor/reverse RT-PCR primer G.
XX
KW   Expression cassette; promoter activity; suspensor cell; plant embryo;
KW   modulation of gene transcription; Scarlet runner bean; RT-PCR;
KW   reverse transcriptase-PCR; primer; transgenic; ss.
XX
OS   Phaseolus coccineus.
OS   Synthetic.
XX
PN   WO200244333-A2.
XX
PD   06-JUN-2002.
XX
PF   28-NOV-2001; 2001WO-US044737.
XX
PR   28-NOV-2000; 2000US-00724857.
PR   28-NOV-2000; 2000US-0253672P.
XX
PA   (REGC ) UNIV CALIFORNIA.
PA   (CERE-) CERES INC.
XX
PI   Weterings K,  Apuya NR,  Tatarinova T,  Goldberg RB;
XX
DR   WPI; 2002-508506/54.
XX
PT   Expression cassette comprises promoters with basal promoter activity
PT   operably linked to a heterologous polynucleotide, useful for expression
PT   genes in suspensor cells in plants and/or basal region of plant embryo.
XX
PS   Example; Page 54; 114pp; English.
XX
CC   The present invention relates to expression cassettes comprising a
CC   promoter sequence and a promoter polynucleotide with basal promoter
CC   activity, where the promoter sequence is operably linked to a
CC   heterologous polynucleotide, and when the expression cassette is inserted
CC   into a plant, the heterologous polynucleotide is specifically expressed
CC   in a suspensor cell and/or basal region of a plant embryo. The invention
CC   also provides polynucleotide sequences encoding Scarlet runner bean
CC   (Phaseolus coccineus) G564 and C541 proteins for use in the expression
CC   cassettes of the invention. The expression cassettes comprising promoters
CC   and promoter control elements are useful for modulating transcription of
CC   genes in a plant suspensor cell and/or basal region of a plant embryo.
CC   The present sequence represents an anchor/reverse reverse transcriptase
CC   (RT)-PCR primer used in the examples of the present invention
```

```
XX
SQ   Sequence 16 BP; 2 A; 1 C; 2 G; 11 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTG 1782
              ||||||||||||||||
Db          1 AAGCTTTTTTTTTTTG 16


RESULT 2520
AAD34285
ID   AAD34285 standard; DNA; 16 BP.
XX
AC   AAD34285;
XX
DT   16-JUL-2002  (first entry)
XX
DE   Mouse E2 cDNA amplifying PCR primer, H-T11-G.
XX
KW   Mouse; metabolism; E2 gene; insulin resistance syndrome; dyslipidaemia;
KW   therapy; non-insulin dependent diabetes mellitus; NIDDM; antilipaemic;
KW   obesity; atherosclerosis; antiarteriosclerotic; anorectic; PCR; primer;
KW   ss.
XX
OS   Mus sp.
XX
PN   WO200218421-A2.
XX
PD   07-MAR-2002.
XX
PF   23-AUG-2001; 2001WO-GB003807.
XX
PR   28-AUG-2000; 2000US-0228118P.
XX
PA   (ASTR ) ASTRAZENECA AB.
PA   (ASTR ) ASTRAZENECA UK LTD.
XX
PI   Brodin P,  Thelin A;
XX
DR   WPI; 2002-329753/36.
XX
PT   New E2 genes and proteins, useful for identifying or manufacturing agents
PT   for controlling insulin resistance syndrome or related disorders, e.g.
PT   non-insulin dependent diabetes mellitus, dyslipidemia or atherosclerosis.
XX
PS   Example 3; Page 19; 52pp; English.
XX
CC   The invention relates to the regulation of metabolism and in particular
CC   to a gene named E2 involved in insulin resistance syndrome. E2 gene and
CC   protein are useful for identifying therapeutic agents for controlling
CC   insulin resistance syndrome and other related disorders. They are
CC   particularly useful in manufacturing compositions or pharmaceutical for
CC   controlling the disorders. Particularly, the chemical compound or
CC   composition is useful for controlling insulin resistance syndrome and
CC   other related disorders, e.g. non-insulin dependent diabetes mellitus
CC   (NIDDM), dyslipidaemia, obesity or atherosclerosis. The present sequence
CC   is a PCR primer used to amplify mouse E2 cDNA
XX
SQ   Sequence 16 BP; 2 A; 1 C; 2 G; 11 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTG 1782
              ||||||||||||||||
Db          1 AAGCTTTTTTTTTTTG 16


RESULT 2521
ABL57075
ID   ABL57075 standard; DNA; 16 BP.
XX
AC   ABL57075;
XX
DT   22-JUL-2002  (first entry)
XX
DE   Molecular beacon target sequence.
XX
KW   Molecular beacon; fluorophore; nanoparticle; nucleic acid detection; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_binding    1. .16
FT                   /*tag=  a
FT                   /bound_moiety= "Molecular beacon"
FT                   /note= "forms double-stranded region with bases 5-21 of
FT                   sequence in ABL57069"
XX
PN   WO200218951-A2.
XX
PD   07-MAR-2002.
XX
PF   29-AUG-2001; 2001WO-US041941.
XX
PR   29-AUG-2000; 2000US-0228728P.
PR   30-MAR-2001; 2001US-0280350P.
XX
PA   (UYRQ ) UNIV ROCKEFELLER.
XX
PI   Dubertret B,  Calame M,  Libchaber A;
XX
DR   WPI; 2002-404569/43.
XX
PT   Sensitively detecting proximity changes in a system that utilizes an
PT   interacting fluorophore and quencher, for high sensitivity applications,
PT   involves utilizing a metal surface as quencher.
XX
PS   Example 3; Page 30; 62pp; English.
XX
CC   The present sequence is that of a perfectly matched target sequence for a
CC   molecular beacon comprising an oligonucleotide probe (see ABL57069)
CC   covalently attached at the 3' end to fluorescent dye and at the 5' end to
CC   a nanoparticle. In the native state, the probe forms a hairpin
CC   conformation with hybridised termini. The proximity of the fluorophore
CC   and quencher (gold nanoparticle) in the molecular beacon results in
CC   little or no detectable fluorescence. Upon hybridisation of the central
CC   complementary stretch of the probe to a target sequence, such as the
CC   present sequence, the hairpin undergoes a conformational change resulting
CC   in an increase in fluorescence, the extent of which is proportional to
CC   the amount of target sequence present. Single mismatches can be detected.
CC   The invention relates generally to the use of metal surface quenchers
CC   such as particles or films for high sensitivity applications in, for
CC   example, detection and diagnostic systems
XX
SQ   Sequence 16 BP; 15 A; 0 C; 1 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db          1 GAAAAAAAAAAAAAAA 16


RESULT 2522
ABA97402
ID   ABA97402 standard; DNA; 16 BP.
XX
AC   ABA97402;
XX
```

```
DT   18-JUN-2002  (first entry)
XX
DE   Nucleotide sequence of oligomer # 1 used to test thermal stability.
XX
KW   Protein nucleic acid molecule; PNA; ds.
XX
OS   Synthetic.
XX
PN   WO200168673-A1.
XX
PD   20-SEP-2001.
XX
PF   13-MAR-2001; 2001WO-US008111.
XX
PR   14-MAR-2000; 2000US-0189190P.
PR   30-NOV-2000; 2000US-0250334P.
XX
PA   (ACTI-) ACTIVE MOTIF.
XX
PI   Efimov V,  Fernandez J,  Archdeacon D,  Archdeacon J;
PI   Chakhmakhcheau O,  Buryakova A,  Choob M,  Hondorp K;
XX
DR   WPI; 2002-041177/05.
XX
PT   Oligonucleotides analogs useful in detection, separation and purification
PT   of nucleic acid molecules, comprise monomers, dimers and oligomers.
XX
PS   Example 17; Page 118; 197pp; English.
XX
CC   This invention relates to oligonucleotide analogues comprising a protein
CC   nucleic acid molecule (PNA) monomer. They are used in the detection and
CC   separation of nucleic acid molecules and as probes, primers, linkers,
CC   adapters and antisense agents on solid supports. Modifications enhance
CC   their use as capture and detection probes e.g. by the incorporation of
CC   biotin, digoxigenen, radioisotopes, fluorescent labels such as
CC   fluorescein and reporter molecules such as alkaline phosphatase. They are
CC   also used for enhancing or inhibiting the activity of an enzyme or
CC   cellular activity. The compounds are stable to nucleases and proteases,
CC   have high affinity, binding specificity and solubility. The polyamide
CC   backbone of PNAs is resistant to both nucleases and proteases. PNAs bind
CC   nucleic acid molecules with greater affinity than DNA or RNA
CC   concentration. The compounds are relatively simple to synthesize and are
CC   used in a wide variety of applications. This sequence represents a DNA
CC   oligomer which is used to represent the thermal stability of the
CC   oligomers of the invention
XX
SQ   Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
             ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 16


RESULT 2523
ABA97402/c
ID   ABA97402 standard; DNA; 16 BP.
XX
AC   ABA97402;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Nucleotide sequence of oligomer # 1 used to test thermal stability.
XX
KW   Protein nucleic acid molecule; PNA; ds.
XX
OS   Synthetic.
XX
PN   WO200168673-A1.
XX
PD   20-SEP-2001.
XX
PF   13-MAR-2001; 2001WO-US008111.
XX
PR   14-MAR-2000; 2000US-0189190P.
PR   30-NOV-2000; 2000US-0250334P.
XX
PA   (ACTI-) ACTIVE MOTIF.
XX
PI   Efimov V,  Fernandez J,  Archdeacon D,  Archdeacon J;
PI   Chakhmakhcheau O,  Buryakova A,  Choob M,  Hondorp K;
XX
DR   WPI; 2002-041177/05.
XX
PT   Oligonucleotides analogs useful in detection, separation and purification
PT   of nucleic acid molecules, comprise monomers, dimers and oligomers.
XX
PS   Example 17; Page 118; 197pp; English.
XX
CC   This invention relates to oligonucleotide analogues comprising a protein
CC   nucleic acid molecule (PNA) monomer. They are used in the detection and
CC   separation of nucleic acid molecules and as probes, primers, linkers,
CC   adapters and antisense agents on solid supports. Modifications enhance
CC   their use as capture and detection probes e.g. by the incorporation of
CC   biotin, digoxigenen, radioisotopes, fluorescent labels such as
CC   fluorescein and reporter molecules such as alkaline phosphatase. They are
CC   also used for enhancing or inhibiting the activity of an enzyme or
CC   cellular activity. The compounds are stable to nucleases and proteases,
CC   have high affinity, binding specificity and solubility. The polyamide
CC   backbone of PNAs is resistant to both nucleases and proteases. PNAs bind
CC   nucleic acid molecules with greater affinity than DNA or RNA
CC   concentration. The compounds are relatively simple to synthesize and are
CC   used in a wide variety of applications. This sequence represents a DNA
CC   oligomer which is used to represent the thermal stability of the
CC   oligomers of the invention
XX
SQ   Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
             ||||||||||||||||
Db         16 AAAAAAAAAAAAAAAA 1


RESULT 2524
ABK90584
ID   ABK90584 standard; DNA; 16 BP.
XX
AC   ABK90584;
XX
DT   15-NOV-2002  (first entry)
XX
DE   Target cDNA PCR primer #2.
XX
KW   Cancer; somatic cell; embryonic cell; cancer; pre-implantation embryo;
KW   germ cell; embryonal carcinoma cell; embryonic stem cell; oocyte; ss;
KW   PCR; primer.
XX
OS   Unidentified.
XX
PN   WO200264828-A1.
XX
PD   22-AUG-2002.
XX
PF   09-FEB-2001; 2001WO-GB000538.
XX
PR   09-FEB-2001; 2001WO-GB000538.
XX
PA   (UNLO ) UNIV COLLEGE LONDON.
XX
```

PI Monk M;
XX
DR WPI; 2002-643493/69.
XX
PT New targets expressed in embryonic cell but not in non-diseased somatic
PT cell, useful in medicine for diagnosis and/or therapy, and for
PT identifying an agent capable of inhibiting the action of the target.
XX
PS Example 1; Page 54; 77pp; English.
XX
CC The invention relates to a new target for use in medicine which is
CC expressed and/or present at a high level in an embryonic cell, is not
CC expressed or is expressed and/or present at low level in a non-diseased
CC somatic cell and is not expressed in or is expressed and/or present at a
CC low level in a diseased somatic cell. The target is useful in the
CC preparation of a medicament for treating a disease, particularly cancer.
CC The human embryonic cells (oocytes, pre-implantation embryos, germ cells,
CC embryonal carcinoma cells and/or embryonic stem cells) are useful in
CC identifying targets re-expressed in cancer cells for preventing, treating
CC or curing cancer. The target may be used in medicine for diagnosis and/or
CC therapy, and to identify an agent capable of inhibiting the action of the
CC target. This sequence represents a PCR primer used to amplify target cDNA
CC of the invention
XX
SQ Sequence 16 BP; 2 A; 1 C; 2 G; 11 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1767 AAGCTTTTTTTTTTTG 1782
||||||||||||||||
Db 1 AAGCTTTTTTTTTTTG 16

RESULT 2525
AAD32157
ID AAD32157 standard; DNA; 16 BP.
XX
AC AAD32157;
XX
DT 18-JUN-2002 (first entry)
XX
DE H-T11-G PCR primer, to determine ADAMTS-1 role in IRS and obesity.
XX
KW A disintegrin and metalloproteinase with thrombospondin type 1 motif;
KW ADAMTS-1; non-insulin dependent diabetes mellitus; ADAM; obesity; IRS;
KW insulin resistance syndrome; NIDDM; atherosclerosis; PCR; primer; ss.
XX
OS Unidentified.
XX
PN WO200216632-A1.
XX
PD 28-FEB-2002.
XX
PF 16-AUG-2001; 2001WO-GB003650.
XX
PR 22-AUG-2000; 2000SE-00002973.
XX
PA (ASTR) ASTRAZENECA AB.
PA (ASTR) ASTRAZENECA UK LTD.
XX
PI Brodin P, Thelin A;
XX
DR WPI; 2002-269365/31.
XX
PT Use of a modulator of ADAMTS-1 (a disintegrin and metalloproteinase) for
PT the treatment of obesity, insulin resistance syndrome (IRS), non-insulin
PT dependent diabetes mellitus (NIDDM) or atherosclerosis.
XX
PS Example 1; Page 39; 47pp; English.
XX
CC The invention relates to the use of modulators of A Disintegrin And
CC Metalloproteinase (ADAM) with Thrombospondin type 1 motif (ADAMTS-1)
CC which are used in the preparation of a medicament for the treatment of
CC obesity, insulin resistance syndrome (IRS), non-insulin dependent
CC diabetes mellitus (NIDDM) and atherosclerosis. The invention also relates
CC to methods for screening specific modulators of ADAMTS-1 activity. The
CC present sequence is a PCR primer used to determine the role of ADAMTS-1
CC in IRS, obesity, NIDDM and atherosclerosis
XX
SQ Sequence 16 BP; 2 A; 1 C; 2 G; 11 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1767 AAGCTTTTTTTTTTTG 1782
||||||||||||||||
Db 1 AAGCTTTTTTTTTTTG 16

RESULT 2526
ABK12623
ID ABK12623 standard; DNA; 16 BP.
XX
AC ABK12623;
XX
DT 18-JUN-2002 (first entry)
XX
DE Mouse E4 protein, PCR primer H-T11-G.
XX
KW Mouse; E4; insulin resistance syndrome; NIDDM; dyslipidaemia; obesity;
KW non-insulin dependent diabetes mellitus; atherosclerosis; primer; ss.
XX
OS Mus sp.
OS Synthetic.
XX
PN WO200218568-A2.
XX
PD 07-MAR-2002.
XX
PF 23-AUG-2001; 2001WO-GB003828.
XX
PR 28-AUG-2000; 2000US-0228117P.
PR 10-APR-2001; 2001US-0282496P.
XX
PA (ASTR) ASTRAZENECA AB.
PA (ASTR) ASTRAZENECA UK LTD.
XX
PI Brodin P, Thelin A;
XX
DR WPI; 2002-304254/34.
XX
PT New isolated polynucleotide encoding E4 gene involved in insulin
PT resistance syndrome, useful for identifying chemical compound useful for
PT controlling e.g. non-insulin dependent diabetes mellitus.
XX
PS Example 3; Page 19; 46pp; English.
XX
CC The invention relates to an isolated polynucleotide (I) molecule
CC comprising a nucleotide sequence which encodes an E4 polypeptide (II) or
CC its fragment of at least 10 amino acids. (II) is useful for identifying a
CC chemical compound capable of modulating the activity of E4 by contacting
CC the chemical compound with (II) or a transgenic non-human mammal and
CC measuring any effect of chemical compound on the activity of (II) or
CC transgenic non-human mammal, where the identifying method is useful for
CC making a pharmaceutical composition, which comprises mixing the compound
CC thus identified with a carrier, and the compound is preferably an
CC antibody that is useful for controlling insulin resistance syndrome and
CC other related disorders such as non-insulin dependent diabetes mellitus
CC (NIDDM), dyslipidaemia, obesity, and atherosclerosis. The present
CC sequence represents a PCR primer used to isolate the coding sequence of
CC mouse E4 protein
XX
SQ Sequence 16 BP; 2 A; 1 C; 2 G; 11 T; 0 U; 0 Other;

```
  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTG 1782
              ||||||||||||||||
Db          1 AAGCTTTTTTTTTTTG 16


RESULT 2527
AAD30090
ID   AAD30090 standard; DNA; 16 BP.
XX
AC   AAD30090;
XX
DT   17-MAY-2002  (first entry)
XX
DE   PTTG cDNA isolating anchored PCR primer #1.
XX
KW   Pituitary tumour transforming gene; PTTG1; vulnerary; cytostatic;
KW   ophthalmological; antiangiogenic; antisense gene therapy; angiogenesis;
KW   wound healing; tissue regeneration; scar formation; malignant tumour;
KW   retinopathy; PCR primer; ss.
XX
OS   Unidentified.
XX
PN   WO200187935-A2.
XX
PD   22-NOV-2001.
XX
PF   12-MAY-2001; 2001WO-US015437.
XX
PR   12-MAY-2000; 2000US-00569956.
PR   13-OCT-2000; 2000US-00687911.
PR   04-DEC-2000; 2000US-00730469.
PR   05-FEB-2001; 2001US-00777422.
PR   11-MAY-2001; 2001US-00854326.
XX
PA   (CEDA-) CEDARS SINAI MEDICAL CENT.
XX
PI   Heaney AP,  Ishikawa H,  Yu R,  Horwitz GA,  Zhang X,  Melmed S;
XX
DR   WPI; 2002-188148/24.
XX
PT   Modulating angiogenesis in a tissue comprising mammalian cells by
PT   modulating pituitary tumor transforming gene (PTTG1) expression and/or
PT   endogenous PTTG1 protein function.
XX
PS   Example 1; Page 63; 183pp; English.
XX
CC   The invention relates to a method of modulating angiogenesis in a tissue
CC   comprising mammalian cells by modulating pituitary tumour transforming
CC   gene (PTTG) expression and/or endogenous PTTG1 protein function in at
CC   least one of the cells. The method is useful for enhancing or inhibiting
CC   angiogenesis. Specifically, enhancing wound healing and/or tissue
CC   regeneration and limiting scar formation. The method is also useful in
CC   treating malignant tumours and retinopathy. The present sequence is a PCR
CC   primer used for isolating PTTG1 cDNA
XX
SQ   Sequence 16 BP; 2 A; 1 C; 2 G; 11 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTG 1782
              ||||||||||||||||
Db          1 AAGCTTTTTTTTTTTG 16


RESULT 2528
AAD30914
ID   AAD30914 standard; DNA; 16 BP.
XX
AC   AAD30914;
XX
DT   31-MAY-2002  (first entry)
XX
DE   Rat PTTG1 cDNA amplifying PCR primer #1.
XX
KW   Rat; pituitary tumour transforming gene 1; cellular transformation;
KW   PTTG1; inhibition; immunogen; neoplastic cellular proliferation;
KW   T-lymphocyte; PCR primer; ss.
XX
OS   Rattus rattus.
XX
PN   WO200187934-A2.
XX
PD   22-NOV-2001.
XX
PF   12-MAY-2001; 2001WO-US015254.
XX
PR   12-MAY-2000; 2000US-00569956.
PR   13-OCT-2000; 2000US-00687911.
PR   04-DEC-2000; 2000US-00730469.
PR   05-FEB-2001; 2001US-00777422.
XX
PA   (CEDA-) CEDARS SINAI MEDICAL CENT.
XX
PI   Horwitz GA,  Zhang X,  Heaney AP,  Melmed S;
XX
DR   WPI; 2002-226703/28.
XX
PT   Inhibiting neoplastic cellular proliferation and/or transformation of a
PT   mammalian cell, by using Pituitary tumor transforming gene carboxy-
PT   terminal peptides.
XX
PS   Example 1; Page 65; 190pp; English.
XX
CC   The patent discloses pituitary tumour transforming gene (PTTG) carboxy
CC   terminal peptides. The invention also relates to methods for inhibiting
CC   neoplastic cellular proliferation and transformation (NP/T) of mammalian
CC   cells. The method involves delivering a composition comprising a PTTG
CC   carboxy-terminal-related polynucleotide, an expression vector comprising
CC   a polynucleotide encoding PTTG C-terminal (PTTG-C) peptide, PTTG-C
CC   peptide to a mammalian cell that overexpresses PTTG. The compositions
CC   comprising PTTG-C peptides are useful for inhibiting neoplastic cellular
CC   proliferation and/or transformation of a mammalian cell. PTTG-C peptides
CC   are useful in bioassays, as immunogens to produce anti-PTTG-C antibodies
CC   and in therapeutic compositions. PTTG antibodies are also useful for
CC   inhibiting the activation of mammalian T-lymphocytes. Sequences of the
CC   invention are used as vaccines and in gene therapy. The present sequence
CC   is a PCR primer which is used for amplifying rat PTTG1 cDNA
XX
SQ   Sequence 16 BP; 2 A; 1 C; 2 G; 11 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTG 1782
              ||||||||||||||||
Db          1 AAGCTTTTTTTTTTTG 16


RESULT 2529
ABZ21814
ID   ABZ21814 standard; DNA; 16 BP.
XX
AC   ABZ21814;
XX
DT   03-MAR-2003  (first entry)
XX
DE   Anti-cancer drug resistance related oligonucleotide #1.
XX
```

KW Anti-cancer; drug resistance; lung cancer; head and neck cancer; ss.
XX
OS Synthetic.
XX
PN KR2002031530-A.
XX
PD 02-MAY-2002.
XX
PF 20-OCT-2000; 2000KR-00062030.
XX
PR 20-OCT-2000; 2000KR-00062030.
XX
PA (PHAR-) PHARMGENIA CO LTD.
XX
PI Jun SH;
XX
DR WPI; 2002-737801/80.
XX
PT DNA sequences relating to anti-cancer drug resistance and the use
PT thereof.
XX
PS Disclosure; Page 4; 34pp; Korean.
XX
CC The present invention describes DNA sequences relating to anti-cancer
CC drug resistance. The DNA sequences can be used as a component of a kit or
CC a DNA chip for detecting the presence of anti-cancer resistance. The
CC method for identifying and sequencing the DNA sequences comprises
CC obtaining an anti-cancer sensitive cancer tissue and an anti-cancer drug
CC resistant cancer tissue from patients suffering from lung cancer and head
CC and neck cancer, isolating mRNAs from the tissues, preparing cDNAs of the
CC tissues from mRNAs using reverse transcriptase; finding genes showing the
CC increase or decrease of gene expression in the cancer tissues before and
CC after the anti-cancer drug treatment using differential display of
CC polymerase chain reaction (PCR), subjecting the genes to electrophoresis,
CC amplifying the cDNAs by using PCR, sub-cloning the amplified cDNAs into
CC pGEM-Teasy plasmid, and sequencing the cDNA using an auto-sequencing
CC machine. The present sequence represents an oligonucleotide which is used
CC in the exemplification of the present invention
XX
SQ Sequence 16 BP; 2 A; 1 C; 2 G; 11 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1767 AAGCTTTTTTTTTTTG 1782
||||||||||||||||
Db 1 AAGCTTTTTTTTTTTG 16

RESULT 2530
ABN87395
ID ABN87395 standard; DNA; 16 BP.
XX
AC ABN87395;
XX
DT 05-AUG-2002 (first entry)
XX
DE PTTG isolation related anchor primer SEQ ID NO:11.
XX
KW Pituitary tumour-specific gene; PTTG1; PTTG2; transformation;
KW pituitary tumour transforming gene; malignant tumour; cytostatic;
KW neoplastic cellular proliferation inhibition; primer; ss.
XX
OS Synthetic.
XX
PN WO200187039-A2.
XX
PD 22-NOV-2001.
XX
PF 12-MAY-2001; 2001WO-US015255.
XX
PR 12-MAY-2000; 2000US-00569956.
PR 13-OCT-2000; 2000US-00687911.
PR 04-DEC-2000; 2000US-00730469.
PR 05-FEB-2001; 2001US-00777422.
XX
PA (CEDA-) CEDARS SINAI MEDICAL CENT.
XX
PI Prezant TR, Heaney AP, Melmed S;
XX
DR WPI; 2002-195496/25.
XX
PT Novel method of inhibiting neoplastic cellular proliferation and/or
PT transformation of a mammalian cell used for treating e.g. malignant
PT tumours.
XX
PS Example 1; Page 61; 175pp; English.
XX
CC The present invention describes a method for inhibiting neoplastic
CC cellular proliferation and/or transformation of a mammalian cell. The
CC method comprises delivering to a mammalian cell that endogenously over
CC expresses pituitary tumour transforming gene (PTTG1), a composition
CC comprising, an expression vector comprising a promoter and a
CC polynucleotide, where the polynucleotide comprises a first DNA segment
CC encoding a mammalian PTTG2 peptide the polynucleotide being operatively
CC linked to the promoter in a transcriptional unit, where PTTG2 is selected
CC from: (a) a peptide (I) consisting essentially of a 191 amino acid
CC sequence (see ABB79058) or a functional fragment comprising at least
CC amino acid residues 1-180; or (b) a mammalian PTTG2 peptide having at
CC least 95% sequence homology with (I). The expression vector is complexed
CC with a cellular uptake-enhancing agent such that the PTTG2 peptide is
CC expressed in the cell where neoplastic cellular proliferation and/or
CC transformation of the cell is inhibited. PTTG2 protein regulates
CC transactivating activity by PTTG1 and that PTTG2 peptide molecules have
CC the ability to down regulate PTTG1 gene expression and/or PTTG1 protein
CC function in a negative manner. The method is useful in inhibiting
CC neoplastic cellular proliferation and/or transformation of mammalian
CC cells both in vivo and in vitro. The method is also useful in treating
CC malignant tumours. The present sequence represents an anchor primer used
CC in the isolation of PTTG cDNA, which is used in an example from the
CC present invention
XX
SQ Sequence 16 BP; 2 A; 1 C; 2 G; 11 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1767 AAGCTTTTTTTTTTTG 1782
||||||||||||||||
Db 1 AAGCTTTTTTTTTTTG 16

RESULT 2531
ABA98029
ID ABA98029 standard; cDNA; 16 BP.
XX
AC ABA98029;
XX
DT 03-MAY-2002 (first entry)
XX
DE Human PTTG2 cDNA coding sequence SEQ ID NO 63.
XX
KW Human; mouse; rat; gene; cytostatic; immunosuppressive; antiasthmatic;
KW dermatalogical; antirheumatic; antiarthritic; neuroprotective;
KW antiinflammatory; antipsoriatic; antiatherosclerotic; antiallergic;
KW T-lymphocyte cell; pituitary tumour transforming gene; PTTG; bFGF;
KW transcription; cell proliferation; lymphocyte; graft rejection; allergic;
KW asthmatic; autoimmune disease; rheumatoid arthritis; leukaemia; cancer;
KW tumour; Hodgkin's disease; ss.
XX
OS Homo sapiens.
XX
PN WO200188116-A2.
XX

```
PD   22-NOV-2001.
XX
PF   12-MAY-2001; 2001WO-US015438.
XX
PR   12-MAY-2000; 2000US-00569956.
PR   13-OCT-2000; 2000US-00687911.
PR   04-DEC-2000; 2000US-00730469.
PR   05-FEB-2001; 2001US-00777422.
PR   11-MAY-2001; 2001US-00854326.
XX
PA   (CEDA-) CEDARS SINAI MEDICAL CENT.
XX
PI   Stoika R,  Horwitz GA,  Zhang X,  Melmed S;
XX
DR   WPI; 2002-188151/24.
DR   P-PSDB; ABB08709.
XX
PT   Inhibiting the activation of a mammalian T-lymphocyte cell useful for
PT   treating immune-related disorders by inhibiting PTTG1 gene expression.
XX
PS   Example 21; Page 182; 185pp; English.
XX
CC   The invention relates to inhibiting the activation of a mammalian T-
CC   lymphocyte cell comprising inhibiting pituitary tumour transforming gene
CC   (PTTG1) expression and/or endogenous PTTG1 protein function in the T-
CC   lymphocyte cell, whereby activation of the T-lymphocyte cell is
CC   inhibited. PTTG upregulates bFGF secretion and transactivates DNA
CC   transcription. Compositions and methods of the invention are useful for
CC   inhibiting neoplastic and non-neoplastic proliferation of mammalian T-
CC   lymphocyte cells, including activated normal lymphocytes and transformed
CC   lymphocytes. The compositions and methods are useful in the prevention or
CC   inhibition of xenograft or allograft rejection and in the treatment of
CC   allergic, asthmatic and/or autoimmune conditions such as systemic lupus
CC   erythematosus (SLE), autoimmune myasthenia gravis, rheumatoid arthritis,
CC   autoimmune encephalomyelitis, psoriasis, atherosclerosis and other
CC   autoimmune diseases. The inventive methods and compositions are also
CC   useful in the treatment of T-cell neoplasias, such as leukaemia, or any
CC   haematologic or lymphopoietic neoplasm e.g. Hodgkin's disease. The
CC   present sequence is that of a PTTG encoding polynucleotide sequence
XX
SQ   Sequence 16 BP; 2 A; 1 C; 2 G; 11 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTG 1782
              ||||||||||||||||
Db          1 AAGCTTTTTTTTTTTG 16


RESULT 2532
ACC58340
ID   ACC58340 standard; DNA; 16 BP.
XX
AC   ACC58340;
XX
DT   26-AUG-2003  (first entry)
XX
DE   MMLV-RT PCR; primer H-T11G.
XX
KW   MMLV; reverse transcriptase; enzyme; LIM mineralization protein; LMP;
KW   osteopathic; cytokine; gene therapy; PCR; primer; ss.
XX
OS   Moloney murine leukemia virus.
XX
PN   WO2003042368-A2.
XX
PD   22-MAY-2003.
XX
PF   14-NOV-2002; 2002WO-US036465.
XX
PR   14-NOV-2001; 2001US-0331321P.
PR   13-NOV-2002; 2002US-00331321.
XX
PA   (MEDT ) MEDTRONIC SOFAMOR DANEK INC.
XX
PI   Mckay WF,  Boden SD,  Yoon ST;
XX
DR   WPI; 2003-505113/47.
XX
PT   Expressing LIM mineralization protein in non-osseous mammalian cell for
PT   treating intervertebral disc injury, by transfecting cell with nucleic
PT   acid encoding LIM mineralization protein operably linked to promoter.
XX
PS   Example 9; Page 74; 94pp; English.
XX
CC   The present sequence is that of H-T11G, an MMLV-RT primer that was used
CC   in differential display PCR of RNA extracted from glucocorticoid-
CC   stimulated rat osteoblasts. cDNA (see ACC58339) encoding rat LIM
CC   mineralization protein (RLMP), a cytokine involved in mineralization of
CC   the bone matrix and in the differentiation of cells into the osteoblast
CC   lineage was subsequently isolated. The invention provides methods of
CC   expressing LIM mineralization protein in non-osseous mammalian cells,
CC   such as stem cells or intervertebral disc cells. The methods involved
CC   transfecting the cells with a nucleic acid encoding LIM mineralization
CC   protein operably linked to a promoter. Expression of the LIM
CC   mineralization protein can stimulate proteoglycan and/or collagen
CC   production for treatment of disc disease associated with trauma or disc
CC   degeneration, e.g. for enhancement of bone repair in fractures and bone
CC   defects, in bone grafting, and in the treatment of osteoporosis
XX
SQ   Sequence 16 BP; 2 A; 1 C; 2 G; 11 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTG 1782
              ||||||||||||||||
Db          1 AAGCTTTTTTTTTTTG 16


RESULT 2533
ABX16054
ID   ABX16054 standard; DNA; 16 BP.
XX
AC   ABX16054;
XX
DT   02-APR-2003  (first entry)
XX
DE   RNA differential display 3' anchor primer.
XX
KW   PCR; primer; ss; SPAF; spermatogenesis associated factor; cytostatic;
KW   AAA-protein; ATPase associated with diverse cellular activities;
KW   squamous cell carcinoma; cancer; infertility; fertility; contraception;
KW   spermatogonia; primary spermatocyte; early pachytene stage;
KW   chemotherapeutic agent; tumour; carcinogenesis; differentiation; RT-PCR;
KW   reverse transcriptase PCR; RNA differential display.
XX
OS   Synthetic.
XX
PN   US2002143169-A1.
XX
PD   03-OCT-2002.
XX
PF   08-MAY-2001; 2001US-00850697.
XX
PR   27-SEP-1997;   97US-00938308.
PR   06-FEB-2001; 2001US-00777753.
XX
PA   (KULE/) KULESZ-MARTIN M F.
PA   (LIUY/) LIU Y.
XX
PI   Kulesz-Martin MF,  Liu Y;
XX
```

```
DR   WPI; 2003-174143/17.
XX
PT   New spermatogenesis associated factor DNA, useful in diagnosing cancer,
PT   in designing selective cancer therapy by targeting this gene product, and
PT   in basic research on carcinogenesis and differentiation.
XX
PS   Example; Page 3; 42pp; English.
XX
CC   The invention relates to a purified spermatogenesis associated factor
CC   (SPAF, an AAA-protein family member (ATPase associated with diverse
CC   cellular activities)) DNA molecule designated SPAF DNA, which is a gene
CC   that is altered and overexpressed in poorly differentiated squamous cell
CC   carcinoma as compared with normal parental epidermal cells. The gene is
CC   naturally expressed in testes, and expresses a spermatogenesis associated
CC   protein by translation of the SPAF DNA molecule. The protein is an SPAF
CC   protein, which is naturally localised in spermatogonia and primary
CC   spermatocyte up to early pachytene stage. Also included are a SPAF cDNA
CC   molecule having a DNA sequence which is complementary DNA sequence to the
CC   novel SPAF DNA, an anti-SPAF antibody, diagnosing cancer (comprising: (a)
CC   contacting a cell with a specific probe comprising SPAF cDNA and
CC   detecting a reaction; or (b) contacting a cancer cell with an anti-SPAF
CC   antibody, and detecting reaction to the antibody), isolating the SPAF
CC   gene by contacting the gene with SPAF cDNA or with anti-SPAF antibody,
CC   diagnosing infertility by contacting a testes generated cellular material
CC   with an anti-SPAF antibody, a chemotherapeutic agent comprising an
CC   antibody to SPAF protein conjugated with a tumour binding inhibiting
CC   material and a vector containing a testes specific nucleic acid
CC   comprising at least a portion of the novel SPAF DNA. SPAF is useful in
CC   diagnosing cancer, in designing selective cancer therapy by targeting
CC   this gene product, and in basic research on carcinogenesis and
CC   differentiation. The SPAF protein, peptide, mRNA and cDNA may be used in
CC   designing drugs for treatment and prevention of abnormal development and
CC   tumours, and for fertility and/infertility/contraception. The present
CC   sequence is a reverse transcriptase (RT)-PCR primer used in an RNA
CC   differential display experiment for mouse SPAF mRNA
XX
SQ   Sequence 16 BP; 2 A; 1 C; 2 G; 11 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTG 1782
              ||||||||||||||||
Db          1 AAGCTTTTTTTTTTTG 16


RESULT 2534
ABZ58394
ID   ABZ58394 standard; DNA; 16 BP.
XX
AC   ABZ58394;
XX
DT   28-APR-2003  (first entry)
XX
DE   H-T11G anchored oligo-dT primer.
XX
KW   Human cervical cancer 2; HCC-2; human; cervix cancer; oncogene;
KW   diagnosis; cytostatic; gene therapy; PCR; primer; ss.
XX
OS   Synthetic.
XX
PN   WO2003002744-A1.
XX
PD   09-JAN-2003.
XX
PF   27-JUN-2002; 2002WO-KR001227.
XX
PR   28-JUN-2001; 2001KR-00037589.
XX
PA   (KIMJ/) KIM J.
XX
PI   Kim J;
XX
DR   WPI; 2003-210277/20.
XX
PT   Human cervical cancer 2 proto-oncogene for diagnosing cancer.
XX
PS   Example 2; Page 24; 26pp; English.
XX
CC   The present sequence is that of H-T11G-anchored oligo-dT primer, which
CC   was used in an example from the invention in the RT-PCR amplification of
CC   RNA obtained from healthy cervical, primary cervical cancer and
CC   metastatic common iliac lymph node tissues, and from a human cervical
CC   cancer cell line. A partial clone (CG401) was obtained, which was used to
CC   identify a full-length cDNA (see ABZ58393) for novel human cervical
CC   cancer 2 (HCC-2) proto-oncogene. Differential display RT-PCR using the
CC   oligo-dT primer showed that CG401 was expressed in cervical cancer
CC   tissue, metastatic lymph node tissues and CUMC-6 cells, but not in normal
CC   tissues. HCC-2 proto-oncogene can be used in the diagnosis of various
CC   cancers, in the production of transgenic animals useful for drug
CC   screening, in the production of HCC-2 protein, and in the construction of
CC   an antisense gene (claimed) useful in antisense gene therapy
XX
SQ   Sequence 16 BP; 2 A; 1 C; 2 G; 11 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTG 1782
              ||||||||||||||||
Db          1 AAGCTTTTTTTTTTTG 16


RESULT 2535
AAD56451
ID   AAD56451 standard; DNA; 16 BP.
XX
AC   AAD56451;
XX
DT   07-AUG-2003  (first entry)
XX
DE   2'F-ANA antisense oligo #6, to elicit RNase H degradation of target RNA.
XX
KW   Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
KW   antisense; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .16
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "2'-deoxy-2'-fluoroarabinothymidine"
FT   misc_feature     8. .9
FT                    /*tag=  b
FT                    /note= "Bases 8 and 9 are linked by two secouridine
FT                    linkers which is represented as S in page 49 and X in
FT                    page 57 and Fig 7 and 8 of the specification"
XX
PN   WO2003037909-A1.
XX
PD   08-MAY-2003.
XX
PF   29-OCT-2002; 2002WO-CA001628.
XX
PR   29-OCT-2001; 2001US-0330719P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Viazovkina E,  Mangos MM,  Parniak MA,  Min K;
XX
DR   WPI; 2003-421516/39.
XX
PT   Novel acyclic linker-containing oligonucleotide useful for preventing or
```

```
PT   decreasing translation, reverse transcription and/or replication of a
PT   target RNA in a system, comprises a modified deoxyribonucleotide.
XX
PS   Example 2; Fig 7; 104pp; English.
XX
CC   The invention relates to an acyclic linker-containing oligonucleotide
CC   comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC   the invention are useful for preventing or decreasing translation,
CC   reverse transcription and/or replication of a target RNA in a system.
CC   They are useful for selectively preventing gene expression in a sequence-
CC   specific manner, for hybridising to complementary RNA such as cellular
CC   mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC   RNA. They are also useful therapeutically in formulations or medicaments
CC   to prevent or treat a disease characterised by the expression of a
CC   particular target RNA. The invention is used in gene therapy. The present
CC   sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC   H degradation of target RNA. This sequence is used in the exemplification
CC   of the invention
XX
SQ   Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 16


RESULT 2536
AAD56451/c
ID   AAD56451 standard; DNA; 16 BP.
XX
AC   AAD56451;
XX
DT   07-AUG-2003  (first entry)
XX
DE   2'F-ANA antisense oligo #6, to elicit RNase H degradation of target RNA.
XX
KW   Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
KW   antisense; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .16
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-deoxy-2'-fluoroarabinothymidine"
FT   misc_feature    8. .9
FT                   /*tag=  b
FT                   /note= "Bases 8 and 9 are linked by two secouridine
FT                   linkers which is represented as S in page 49 and X in
FT                   page 57 and Fig 7 and 8 of the specification"
XX
PN   WO2003037909-A1.
XX
PD   08-MAY-2003.
XX
PF   29-OCT-2002; 2002WO-CA001628.
XX
PR   29-OCT-2001; 2001US-0330719P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Viazovkina E,  Mangos MM,  Parniak MA,  Min K;
XX
DR   WPI; 2003-421516/39.
XX
PT   Novel acyclic linker-containing oligonucleotide useful for preventing or
PT   decreasing translation, reverse transcription and/or replication of a
PT   target RNA in a system, comprises a modified deoxyribonucleotide.
XX
PS   Example 2; Fig 7; 104pp; English.
XX
CC   The invention relates to an acyclic linker-containing oligonucleotide
CC   comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC   the invention are useful for preventing or decreasing translation,
CC   reverse transcription and/or replication of a target RNA in a system.
CC   They are useful for selectively preventing gene expression in a sequence-
CC   specific manner, for hybridising to complementary RNA such as cellular
CC   mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC   RNA. They are also useful therapeutically in formulations or medicaments
CC   to prevent or treat a disease characterised by the expression of a
CC   particular target RNA. The invention is used in gene therapy. The present
CC   sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC   H degradation of target RNA. This sequence is used in the exemplification
CC   of the invention
XX
SQ   Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         16 AAAAAAAAAAAAAAAA 1


RESULT 2537
AAL54078
ID   AAL54078 standard; DNA; 16 BP.
XX
AC   AAL54078;
XX
DT   06-MAR-2003  (first entry)
XX
DE   Oligo-homodeoxyribonucleotide sequence, oligo dT.
XX
KW   Detection; single-stranded sensor; detectable fluorescence emission;
KW   forensic testing; paternity testing; tissue typing; hereditary disorder;
KW   human population genetics; human evolutionary history; cystic fibrosis;
KW   human haplotype diversity; Tay-Sachs; sickle-cell anaemia; ss.
XX
OS   Unidentified.
XX
PN   WO200284271-A2.
XX
PD   24-OCT-2002.
XX
PF   16-APR-2002; 2002WO-US012176.
XX
PR   16-APR-2001; 2001US-00836579.
XX
PA   (REGC ) UNIV CALIFORNIA.
PA   (CHAJ/) CHA J N.
XX
PI   Cha JN,  Morse DE,  Stucky GD;
XX
DR   WPI; 2003-103378/09.
XX
PT   Detecting polynucleotides, for pharmacogenetic testing, comprises
PT   contacting a target polynucleotide with a complementary single-stranded
PT   sensor polynucleotide and an agent that allows the sensor to fluoresce
PT   upon excitation.
XX
PS   Example 1; Page 25; 41pp; English.
XX
CC   The invention relates to a novel assay for detecting a polynucleotide in
CC   a sample, which comprises: contacting a sample suspected of containing a
CC   target polynucleotide with a predetermined single-stranded sensor
CC   polynucleotide complementary to the target polynucleotide, in a solution
CC   comprising an agent that is a nonaqueous solvent that allows the sensor
CC   polynucleotide to produce a detectable fluorescence emission; exciting
```

CC the sensor polynucleotide; and determining fluorescence emission. The
CC assay is useful for detecting a single or double-stranded target
CC polynucleotide, such as, DNA or RNA in a sample. The assay finds use in a
CC wide variety of different applications including pharmacogenetic testing,
CC forensic testing to identify the species or individual which was the
CC source of a forensic specimen, in anthropological setting, paternity
CC testing, testing for compatibility between prospective tissue or blood
CC donors and patients and in screening for hereditary disorders. The method
CC is also useful to study alterations of gene expression in response to a
CC stimulus, disease, drug or medication, and other applications include
CC human population genetics, analyses of human evolutionary history and
CC characterisation of human haplotype diversity. The method is useful for
CC detecting polynucleotide sequences from contaminants or pathogens
CC including bacteria, yeast, and viruses to detect single nucleotide
CC polymorphisms, which may be associated with particular alleles or subsets
CC of alleles. The method is useful for detection of mutations and to detect
CC nucleotide sequences associated with increased risk of diseases or
CC disorders including cystic fibrosis, Tay-Sachs, and sickle-cell anaemia.
CC This polynucleotide sequence represents an oligonucleotide sequence used
CC in a fluorescence technique of the invention
XX
SQ Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTT 2181
||||||||||||||||
Db 1 TTTTTTTTTTTTTTTT 16

RESULT 2538
AAL54078/c
ID AAL54078 standard; DNA; 16 BP.
XX
AC AAL54078;
XX
DT 06-MAR-2003 (first entry)
XX
DE Oligo-homodeoxyribonucleotide sequence, oligo dT.
XX
KW Detection; single-stranded sensor; detectable fluorescence emission;
KW forensic testing; paternity testing; tissue typing; hereditary disorder;
KW human population genetics; human evolutionary history; cystic fibrosis;
KW human haplotype diversity; Tay-Sachs; sickle-cell anaemia; ss.
XX
OS Unidentified.
XX
PN WO200284271-A2.
XX
PD 24-OCT-2002.
XX
PF 16-APR-2002; 2002WO-US012176.
XX
PR 16-APR-2001; 2001US-00836579.
XX
PA (REGC) UNIV CALIFORNIA.
PA (CHAJ/) CHA J N.
XX
PI Cha JN, Morse DE, Stucky GD;
XX
DR WPI; 2003-103378/09.
XX
PT Detecting polynucleotides, for pharmacogenetic testing, comprises
PT contacting a target polynucleotide with a complementary single-stranded
PT sensor polynucleotide and an agent that allows the sensor to fluoresce
PT upon excitation.
XX
PS Example 1; Page 25; 41pp; English.
XX
CC The invention relates to a novel assay for detecting a polynucleotide in
CC a sample, which comprises: contacting a sample suspected of containing a
CC target polynucleotide with a predetermined single-stranded sensor
CC polynucleotide complementary to the target polynucleotide, in a solution
CC comprising an agent that is a nonaqueous solvent that allows the sensor
CC polynucleotide to produce a detectable fluorescence emission; exciting
CC the sensor polynucleotide; and determining fluorescence emission. The
CC assay is useful for detecting a single or double-stranded target
CC polynucleotide, such as, DNA or RNA in a sample. The assay finds use in a
CC wide variety of different applications including pharmacogenetic testing,
CC forensic testing to identify the species or individual which was the
CC source of a forensic specimen, in anthropological setting, paternity
CC testing, testing for compatibility between prospective tissue or blood
CC donors and patients and in screening for hereditary disorders. The method
CC is also useful to study alterations of gene expression in response to a
CC stimulus, disease, drug or medication, and other applications include
CC human population genetics, analyses of human evolutionary history and
CC characterisation of human haplotype diversity. The method is useful for
CC detecting polynucleotide sequences from contaminants or pathogens
CC including bacteria, yeast, and viruses to detect single nucleotide
CC polymorphisms, which may be associated with particular alleles or subsets
CC of alleles. The method is useful for detection of mutations and to detect
CC nucleotide sequences associated with increased risk of diseases or
CC disorders including cystic fibrosis, Tay-Sachs, and sickle-cell anaemia.
CC This polynucleotide sequence represents an oligonucleotide sequence used
CC in a fluorescence technique of the invention
XX
SQ Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAA 2801
||||||||||||||||
Db 16 AAAAAAAAAAAAAAAA 1

RESULT 2539
AAD57845
ID AAD57845 standard; DNA; 16 BP.
XX
AC AAD57845;
XX
DT 20-NOV-2003 (first entry)
XX
DE Target oligonucleotide #2 used in nonlinear optical technique.
XX
KW Nonlinear optical technique; screening; ss.
XX
OS Unidentified.
XX
PN WO2003064991-A2.
XX
PD 07-AUG-2003.
XX
PF 17-JUL-2002; 2002WO-US022681.
XX
PR 17-JUL-2001; 2001US-0306040P.
PR 23-OCT-2001; 2001US-0347821P.
PR 06-FEB-2002; 2002US-0354668P.
XX
PA (SALA/) SALAFSKY J S.
XX
PI Salafsky JS;
XX
DR WPI; 2003-646172/61.
XX
PT Screening candidate binding partner(s) for binding to test molecule by
PT applying external force field to sample in homogeneous phase,
PT illuminating sample with light beam(s) at fundamental frequencies, and
PT measuring physical properties.
XX
PS Disclosure; Fig 20-B; 146pp; English.
XX

```
CC   The present invention relates to a method for detecting interactions
CC   between biological components using a nonlinear optical technique. The
CC   invention is used for screening candidate binding partner(s) for binding
CC   to test molecule. It can also be used to detect changes in orientation or
CC   conformation of the probe and/or target. The present sequence is a target
CC   oligonucleotide used in nonlinear optical technique
XX
SQ   Sequence 16 BP; 15 A; 0 C; 1 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db          1 GAAAAAAAAAAAAAAA 16


RESULT 2540
ADB68519
ID   ADB68519 standard; DNA; 16 BP.
XX
AC   ADB68519;
XX
DT   04-DEC-2003  (first entry)
XX
DE   DNA hybridisation oligomer SEQ ID 9.
XX
KW   hydroxyproline nucleic acid; HypNA; PNA; peptide nucleic acid;
KW   gene expression; respiration; secretion; signalling;
KW   ion-channel activity; cell motility; developmental phenotype;
KW   tumour regression; hybridisation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1
FT                   /*tag=  a
FT                   /note= "Optional N-terminal acetyl"
XX
PN   WO2003068798-A2.
XX
PD   21-AUG-2003.
XX
PF   07-FEB-2003; 2003WO-US003904.
XX
PR   09-FEB-2002; 2002US-00072975.
XX
PA   (ACTI-) ACTIVE MOTIF.
XX
PI   Efimov V,  Fernandez J,  Archdeacon D,  Archdeachon J,  Choob M;
XX
DR   WPI; 2003-689653/65.
XX
PT   Method of inhibiting expression of genes or RNA transcripts, useful for
PT   therapy and determining effects of genes, by administering oligomers
PT   containing hydroxyproline nucleic acid.
XX
PS   Example 17; Page 233; 240pp; English.
XX
CC   The invention relates to a novel method of inhibiting the expression of
CC   one or more genes or RNA transcripts by administering at least one
CC   oligonucleotide analogue that includes at least one hydroxyproline
CC   nucleic acid (HypNA) monomer to a cell or organism or their extracts. Thr
CC   oligonucleotides of the invention may be used to monitor properties
CC   including gene expression, respiration, secretion, signalling, ion-
CC   channel activity, cell motility, developmental phenotype and tumour
CC   regression. Furthermore, they may be utilised to determine the effects of
CC   particular genes, as antisense or homologous recombination constructs
CC   e.g. for creating animal models of disease and finally, for increasing
CC   the activity of some enzymes, such as polymerases. The current sequence
CC   is that of the DNA hybridisation oligomer SEQ ID 9 of the invention. This
CC   sequence may also comprise a peptide nucleic acid (PNA).
XX
SQ   Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 16


RESULT 2541
ADB68519/c
ID   ADB68519 standard; DNA; 16 BP.
XX
AC   ADB68519;
XX
DT   04-DEC-2003  (first entry)
XX
DE   DNA hybridisation oligomer SEQ ID 9.
XX
KW   hydroxyproline nucleic acid; HypNA; PNA; peptide nucleic acid;
KW   gene expression; respiration; secretion; signalling;
KW   ion-channel activity; cell motility; developmental phenotype;
KW   tumour regression; hybridisation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1
FT                   /*tag=  a
FT                   /note= "Optional N-terminal acetyl"
XX
PN   WO2003068798-A2.
XX
PD   21-AUG-2003.
XX
PF   07-FEB-2003; 2003WO-US003904.
XX
PR   09-FEB-2002; 2002US-00072975.
XX
PA   (ACTI-) ACTIVE MOTIF.
XX
PI   Efimov V,  Fernandez J,  Archdeacon D,  Archdeachon J,  Choob M;
XX
DR   WPI; 2003-689653/65.
XX
PT   Method of inhibiting expression of genes or RNA transcripts, useful for
PT   therapy and determining effects of genes, by administering oligomers
PT   containing hydroxyproline nucleic acid.
XX
PS   Example 17; Page 233; 240pp; English.
XX
CC   The invention relates to a novel method of inhibiting the expression of
CC   one or more genes or RNA transcripts by administering at least one
CC   oligonucleotide analogue that includes at least one hydroxyproline
CC   nucleic acid (HypNA) monomer to a cell or organism or their extracts. Thr
CC   oligonucleotides of the invention may be used to monitor properties
CC   including gene expression, respiration, secretion, signalling, ion-
CC   channel activity, cell motility, developmental phenotype and tumour
CC   regression. Furthermore, they may be utilised to determine the effects of
CC   particular genes, as antisense or homologous recombination constructs
CC   e.g. for creating animal models of disease and finally, for increasing
CC   the activity of some enzymes, such as polymerases. The current sequence
CC   is that of the DNA hybridisation oligomer SEQ ID 9 of the invention. This
CC   sequence may also comprise a peptide nucleic acid (PNA).
XX
SQ   Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         16 AAAAAAAAAAAAAAAA 1


RESULT 2542
AAX69800/c
ID   AAX69800 standard; RNA; 17 BP.
XX
AC   AAX69800;
XX
DT   28-JUL-1999  (first entry)
XX
DE   Human flt1 VEGF receptor hammerhead ribozyme substrate #1095.
XX
KW   Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW   KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW   tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW   fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW   foetal liver kinase 1; ss.
XX
OS   Homo sapiens.
XX
PN   WO9715662-A2.
XX
PD   01-MAY-1997.
XX
PF   25-OCT-1996;   96WO-US017480.
XX
PR   26-OCT-1995;   95US-0005974P.
PR   11-JAN-1996;   96US-00584040.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (CHIR ) CHIRON CORP.
XX
PI   Pavco P,  Mcswiggen J,  Stinchcomb D,  Escobedo J;
XX
DR   WPI; 1997-259017/23.
XX
PT   Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT   stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT   rheumatoid arthritis, etc., in a human patient.
XX
PS   Claim 4; Page 79; 218pp; English.
XX
CC   The present invention describes nucleic acid molecules which modulate the
CC   synthesis, expression and/or stability of a mRNA encoding 1 or more
CC   receptors of vascular endothelial growth factor (VEGF). A patient
CC   (preferably human) having a condition associated with the level of the
CC   fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC   receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC   angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC   treated by administering the nucleic acid molecule or the expression
CC   vector to the patient. AAX67275 to AAX75752 represent specific examples
CC   of nucleic acid molecules from the present invention
XX
SQ   Sequence 17 BP; 0 A; 1 C; 0 G; 0 T; 16 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         17 AAAAAAAAAAAAAAAA 2


RESULT 2543
AAX69801
ID   AAX69801 standard; RNA; 17 BP.
XX
AC   AAX69801;
XX
DT   28-JUL-1999  (first entry)
XX
DE   Human flt1 VEGF receptor hammerhead ribozyme substrate #1096.
XX
KW   Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW   KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW   tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW   fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW   foetal liver kinase 1; ss.
XX
OS   Homo sapiens.
XX
PN   WO9715662-A2.
XX
PD   01-MAY-1997.
XX
PF   25-OCT-1996;   96WO-US017480.
XX
PR   26-OCT-1995;   95US-0005974P.
PR   11-JAN-1996;   96US-00584040.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (CHIR ) CHIRON CORP.
XX
PI   Pavco P,  Mcswiggen J,  Stinchcomb D,  Escobedo J;
XX
DR   WPI; 1997-259017/23.
XX
PT   Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT   stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT   rheumatoid arthritis, etc., in a human patient.
XX
PS   Claim 4; Page 79; 218pp; English.
XX
CC   The present invention describes nucleic acid molecules which modulate the
CC   synthesis, expression and/or stability of a mRNA encoding 1 or more
CC   receptors of vascular endothelial growth factor (VEGF). A patient
CC   (preferably human) having a condition associated with the level of the
CC   fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC   receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC   angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC   treated by administering the nucleic acid molecule or the expression
CC   vector to the patient. AAX67275 to AAX75752 represent specific examples
CC   of nucleic acid molecules from the present invention
XX
SQ   Sequence 17 BP; 0 A; 1 C; 0 G; 0 T; 16 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   0.0%;  Pred. No. 1.4e+03;
  Matches    0;  Conservative   16;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ::::::::::::::::
Db          1 UUUUUUUUUUUUUUUU 16


RESULT 2544
ABK13941
ID   ABK13941 standard; DNA; 17 BP.
XX
AC   ABK13941;
XX
DT   21-MAY-2002  (first entry)
XX
DE   5'-PCR primer used to produce single pattern characteristic by FokI.
XX
KW   Identification of transcribed gene; mRNA profile; gene expression;
KW   cellular process; fingerprinting; susceptibility to external factor;
KW   development; disease; PCR; primer; ss.
XX
OS   Synthetic.
XX
```

```
PN   WO200208461-A2.
XX
PD   31-JAN-2002.
XX
PF   23-JUL-2001; 2001WO-IB001539.
XX
PR   21-JUL-2000; 2000GB-00018016.
PR   21-JUL-2000; 2000US-0219925P.
XX
PA   (GLOB-) GLOBAL GENOMICS AB.
XX
PI   Linnarsson S,  Ernfors P,  Bauren G;
XX
DR   WPI; 2002-217065/27.
XX
PT   Providing mRNA profile, by generating two independent patterns
PT   characteristic of sample mRNA population, analyzing patterns, comparing
PT   gene expression by cell types under varied conditions, and identifying
PT   genes.
XX
PS   Disclosure; Fig 2; 67pp; English.
XX
CC   The present invention relates to a method for providing a profile of mRNA
CC   molecules present in a sample. The method comprises generating two
CC   independent patterns characteristic of the population of mRNA molecules
CC   expressed in the sample and analysing the patterns using a combinatorial
CC   algorithm, comparing gene expression by different or same cell types
CC   under different conditions, and identifying genes having a role in
CC   various cellular processes. The method is useful for the analysis and
CC   identification of transcribed genes, and fingerprinting. The method can
CC   be used to identify genes which play a role in determining various
CC   cellular processes, including susceptibility to external factors,
CC   development, and disease. The present sequence for a PCR primer is used
CC   in the production of a single pattern characteristic of a sample,
CC   employing a Type IIS restriction enzyme (i.e. FokI) in the methods of the
CC   present invention
XX
SQ   Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 16


RESULT 2545
ADB04271/c
ID   ADB04271 standard; DNA; 17 BP.
XX
AC   ADB04271;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ7 scanning oligonucleotide SEQ ID 5257.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 5257; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         17 AAAAAAAAAAAAAAAA 2


RESULT 2546
ACF36345
ID   ACF36345 standard; DNA; 17 BP.
XX
AC   ACF36345;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Nucleotide sequence of a double stranded product DNA fragment.
XX
KW   Gene variant identification; restriction enzyme; FokI; ds.
XX
OS   Synthetic.
XX
PN   WO2003064689-A2.
XX
PD   07-AUG-2003.
XX
PF   28-JAN-2003; 2003WO-IB000255.
XX
PR   29-JAN-2002; 2002US-0352245P.
XX
PA   (GLOB-) GLOBAL GENOMICS AB.
XX
PI   Lonnerberg P,  Oldin M,  Linnarsson S,  Ernfors P;
XX
DR   WPI; 2003-627619/59.
XX
PT   Determining polyadenylation sites within transcribed gene sequences
PT   present in a sample comprises assigning to gene fragments gene candidates
PT   within a database by comparing signals in the dataset with the database.
XX
PS   Example; Fig 3; 81pp; English.
```

```
XX
CC   The invention relates to determining the presence of and/or identifying a
CC   polyadenylation site within a sequence of a transcribed gene or variants
CC   present in a sample. The method involves assigning to gene fragments gene
CC   candidates within a database by comparing signals in the dataset with the
CC   database, the database comprising data representing mRNAs with known
CC   polyA sites and/or 'virtual genes' representing a possible
CC   polyadenylation site within an actual gene. The method is useful for
CC   determining the presence of and/or identifying a polyadenylation site or
CC   alternative polyadenylation sites within a sequence of a transcribed gene
CC   or sequences of transcribed gene variants present or potentially present
CC   in a sample, in identifying gene features, particularly in identifying
CC   differences between sequence variants that occur in a population of
CC   nucleic acid molecules, especially in identifying or discovering polyA
CC   site usage or determining polyA site usage in a nucleic acid sample, and
CC   gene variants arising from alternative polyA sites. The present sequence
CC   represents a double stranded product DNA fragment
XX
SQ   Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 16


RESULT 2547
ACF36370
ID   ACF36370 standard; DNA; 17 BP.
XX
AC   ACF36370;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Nucleotide sequence of a double stranded product DNA.
XX
KW   Nucleic acid manipulation; mRNA profiling; polymerase chain reaction;
KW   electrophoresis; type II restriction enzyme; FokI; ds.
XX
OS   Synthetic.
XX
PN   WO2003064691-A2.
XX
PD   07-AUG-2003.
XX
PF   28-JAN-2003; 2003WO-IB000843.
XX
PR   29-JAN-2002; 2002US-0352215P.
XX
PA   (GLOB-) GLOBAL GENOMICS AB.
XX
PI   Linnarsson S,  Ernfors P,  Bauren G,  Metsis A,  Pihlak A;
PI   Montelius A;
XX
DR   WPI; 2003-618365/58.
XX
PT   Producing a population of double-stranded product DNA molecules, useful
PT   for mRNA profiling, comprises amplification by nested polymerase chain
PT   reaction.
XX
PS   Example; Fig 2; 105pp; English.
XX
CC   The invention relates to producing a population of double-stranded
CC   product DNA molecules comprising amplification by a nested PCR method.
CC   The method is useful in profiling mRNA transcribed in a system under
CC   investigation. The oligonucleotides are used as size standards in
CC   electrophoresis, and as internal controls allowing for calculation of
CC   relative amounts of material present. The present sequence represents a
CC   double stranded product DNA, which aids in outlining an approach to
CC   production of a single pattern characteristic of a sample, employing a
CC   type II restriction enzyme (FokI)
XX
SQ   Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 16


RESULT 2548
AAX69799
ID   AAX69799 standard; RNA; 17 BP.
XX
AC   AAX69799;
XX
DT   28-JUL-1999  (first entry)
XX
DE   Human flt1 VEGF receptor hammerhead ribozyme substrate #1094.
XX
KW   Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW   KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW   tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW   fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW   foetal liver kinase 1; ss.
XX
OS   Homo sapiens.
XX
PN   WO9715662-A2.
XX
PD   01-MAY-1997.
XX
PF   25-OCT-1996;   96WO-US017480.
XX
PR   26-OCT-1995;   95US-0005974P.
PR   11-JAN-1996;   96US-00584040.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (CHIR ) CHIRON CORP.
XX
PI   Pavco P,  Mcswiggen J,  Stinchcomb D,  Escobedo J;
XX
DR   WPI; 1997-259017/23.
XX
PT   Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT   stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT   rheumatoid arthritis, etc., in a human patient.
XX
PS   Claim 4; Page 79; 218pp; English.
XX
CC   The present invention describes nucleic acid molecules which modulate the
CC   synthesis, expression and/or stability of a mRNA encoding 1 or more
CC   receptors of vascular endothelial growth factor (VEGF). A patient
CC   (preferably human) having a condition associated with the level of the
CC   fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC   receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC   angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC   treated by administering the nucleic acid molecule or the expression
CC   vector to the patient. AAX67275 to AAX75752 represent specific examples
CC   of nucleic acid molecules from the present invention
XX
SQ   Sequence 17 BP; 1 A; 1 C; 0 G; 0 T; 15 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   6.2%;  Pred. No. 1.4e+03;
  Matches    1;  Conservative   15;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTT 2180
              |:::::::::::::::
Db          2 CUUUUUUUUUUUUUUU 17
```

```
RESULT 2549
AAX69802/c
ID   AAX69802 standard; RNA; 17 BP.
XX
AC   AAX69802;
XX
DT   28-JUL-1999  (first entry)
XX
DE   Human flt1 VEGF receptor hammerhead ribozyme substrate #1097.
XX
KW   Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW   KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW   tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW   fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW   foetal liver kinase 1; ss.
XX
OS   Homo sapiens.
XX
PN   WO9715662-A2.
XX
PD   01-MAY-1997.
XX
PF   25-OCT-1996;   96WO-US017480.
XX
PR   26-OCT-1995;   95US-0005974P.
PR   11-JAN-1996;   96US-00584040.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (CHIR ) CHIRON CORP.
XX
PI   Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX
DR   WPI; 1997-259017/23.
XX
PT   Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT   stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT   rheumatoid arthritis, etc., in a human patient.
XX
PS   Claim 4; Page 79; 218pp; English.
XX
CC   The present invention describes nucleic acid molecules which modulate the
CC   synthesis, expression and/or stability of a mRNA encoding 1 or more
CC   receptors of vascular endothelial growth factor (VEGF). A patient
CC   (preferably human) having a condition associated with the level of the
CC   fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC   receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC   angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC   treated by administering the nucleic acid molecule or the expression
CC   vector to the patient. AAX67275 to AAX75752 represent specific examples
CC   of nucleic acid molecules from the present invention
XX
SQ   Sequence 17 BP; 0 A; 2 C; 0 G; 0 T; 15 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         16 GAAAAAAAAAAAAAAA 1


RESULT 2550
AAV37934/c
ID   AAV37934 standard; cDNA; 17 BP.
XX
AC   AAV37934;
XX
DT   05-OCT-1998  (first entry)
XX
DE   Primer of the specification.
XX
KW   Leukocyte; IgA nephropathy; diagnosis; treatment; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO9824815-A1.
XX
PD   11-JUN-1998.
XX
PF   05-DEC-1997;   97WO-JP004469.
XX
PR   05-DEC-1996;   96JP-00325752.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
PA   (KAZU-) KAZUSA DNA RES INST FOUND.
XX
PI   Ishiwata T,  Sakurada M,  Nishimura A,  Nakagawa S,  Kuga T,  Nishi T;
PI   Nomura N,  Nagase T,  Sawada S,  Takei M;
XX
DR   WPI; 1998-333259/29.
XX
PT   Protein from leukocytes and DNA encoding it - useful as reagents for
PT   diagnosing and treating IgA nephropathy.
XX
PS   Example 2; Page 33; 41pp; Japanese.
XX
CC   PCR primers AAV37933-39 are used in the course of the invention. The
CC   specification descibes a novel protein isolated from leukocytes of
CC   patients with IgA nephropathy. Oligonucleotides based on the DNA sequence
CC   encoding this protein are useful as reagents for diagnosing and treating
CC   IgA nephropathy
XX
SQ   Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 2551
AAV49503
ID   AAV49503 standard; cDNA to mRNA; 17 BP.
XX
AC   AAV49503;
XX
DT   18-NOV-1998  (first entry)
XX
DE   Human eosinophil cell activator HVC002 primer #1.
XX
KW   Eosinophil cell activator; treatment; diagnosis; malignant tumour;
KW   parasitic infection; allergic inflammation; eosinophilic pneumonia;
KW   rapid onset eosinophilia; autoimmune disease; gene therapy; primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9824817-A1.
XX
PD   11-JUN-1998.
XX
PF   05-DEC-1997;   97WO-JP004470.
XX
PR   05-DEC-1996;   96JP-00325762.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Yoshisue H,  Saito A,  Nakagawa S,  Kuga T,  Shinkai A,  Koike M;
PI   Nishi T;
XX
```

```
DR   WPI; 1998-333261/29.
XX
PT   DNA and encoded protein which activates eosinophil cells - for treatment
PT   of cancer, parasite infection, autoimmune disease and allergic
PT   inflammation.
XX
PS   Example 1; Page 64; 92pp; Japanese.
XX
CC   AAV49503-V49507 are primers used in the isolation of a human eosinophil
CC   cell activator. This protein and antibodies generated from the protein
CC   can be used for treatment and diagnosis of malignant tumours, parasitic
CC   infections, allergic inflammation, eosinophilic pneumonia, rapid onset
CC   eosinophilia, and autoimmune diseases. DNA can be used for diagnosis, and
CC   the antisense DNA in gene therapy of these disorders. The protein can be
CC   used for screening of potential agonists or antagonists of its activity
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTA 2187
              ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTA 17


RESULT 2552
AAX18371
ID   AAX18371 standard; DNA; 17 BP.
XX
AC   AAX18371;
XX
DT   11-MAY-1999  (first entry)
XX
DE   RT-PCR primer of the invention SEQ ID 12.
XX
KW   RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS   Synthetic.
XX
PN   JP11032765-A.
XX
PD   09-FEB-1999.
XX
PF   18-JUL-1997;   97JP-00208312.
XX
PR   18-JUL-1997;   97JP-00208312.
XX
PA   (TAKI ) TAKARA SHUZO CO LTD.
XX
DR   WPI; 1999-183822/16.
XX
PT   Peptides having at least two new nucleotides - useful as primers in RT-
PT   PCR.
XX
PS   Disclosure; Page 11; 19pp; Japanese.
XX
CC   This sequence represents a primer of the invention. The invention relates
CC   to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC   -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC   a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC   natural number indicating the repetition of alpha; beta, delta = V or N;
CC   V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC   thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC   repetition of gamma, in which thymine expressed by gamma is composed of
CC   1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC   useful as primers for RT-PCR and determination of base sequences. The new
CC   sequences allow for reproductive and highly efficient analysis of gene
CC   sequences
XX
SQ   Sequence 17 BP; 1 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTA 2187
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTA 16


RESULT 2553
AAA30179
ID   AAA30179 standard; DNA; 17 BP.
XX
AC   AAA30179;
XX
DT   16-AUG-2000  (first entry)
XX
DE   PCR primer GT15A used in pollenosis associated gene identification.
XX
KW   Pollenosis-associated protein; high pollen-specific immunoglobulin E;
KW   IgE; diagnose; cedar pollenosis; treatment; human; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO200020575-A1.
XX
PD   13-APR-2000.
XX
PF   06-OCT-1999;   99WO-JP005506.
XX
PR   06-OCT-1998;   98JP-00284610.
XX
PA   (GENO-) GENOX RES INC.
XX
PI   Nagasu T,  Sugita Y,  Kashiwabara T,  Oshida T,  Obayashi M,  Gunji S;
PI   Obayashi I,  Imai Y,  Lu N,  Ogawa K;
XX
DR   WPI; 2000-317712/27.
XX
PT   Gene highly expressed in patients with high cedar pollen-specific IgE
PT   levels, useful for diagnosing pollenosis, and screening candidate
PT   compounds for pollenosis treatment.
XX
PS   Example 6; Page 38; 44pp; Japanese.
XX
CC   This sequence represents a PCR primer used in the identification of a
CC   human pollenosis associated gene. The gene is highly expressed in
CC   individuals with high pollen-specific immunoglobulin E (IgE) levels. The
CC   invention relates to the nucleotide sequence encoding the pollenosis
CC   associated protein, diagnosing pollenosis and screening candidate
CC   compounds for treating pollenosis. The gene can be used in diagnosing
CC   pollenosis, particularly cedar pollenosis, and screening candidate
CC   compounds for pollenosis treatment
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTA 2187
              ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTA 17


RESULT 2554
AAA30180/c
ID   AAA30180 standard; DNA; 17 BP.
XX
AC   AAA30180;
XX
DT   16-AUG-2000  (first entry)
XX
```

```
DE   PCR primer GT15C used in pollenosis associated gene identification.
XX
KW   Pollenosis-associated protein; high pollen-specific immunoglobulin E;
KW   IgE; diagnose; cedar pollenosis; treatment; human; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO200020575-A1.
XX
PD   13-APR-2000.
XX
PF   06-OCT-1999;   99WO-JP005506.
XX
PR   06-OCT-1998;   98JP-00284610.
XX
PA   (GENO-) GENOX RES INC.
XX
PI   Nagasu T,  Sugita Y,  Kashiwabara T,  Oshida T,  Obayashi M,  Gunji S;
PI   Obayashi I,  Imai Y,  Lu N,  Ogawa K;
XX
DR   WPI; 2000-317712/27.
XX
PT   Gene highly expressed in patients with high cedar pollen-specific IgE
PT   levels, useful for diagnosing pollenosis, and screening candidate
PT   compounds for pollenosis treatment.
XX
PS   Example 6; Page 38; 44pp; Japanese.
XX
CC   This sequence represents a PCR primer used in the identification of a
CC   human pollenosis associated gene. The gene is highly expressed in
CC   individuals with high pollen-specific immunoglobulin E (IgE) levels. The
CC   invention relates to the nucleotide sequence encoding the pollenosis
CC   associated protein, diagnosing pollenosis and screening candidate
CC   compounds for treating pollenosis. The gene can be used in diagnosing
CC   pollenosis, particularly cedar pollenosis, and screening candidate
CC   compounds for pollenosis treatment
XX
SQ   Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 2555
AAX82722/c
ID   AAX82722 standard; DNA; 17 BP.
XX
AC   AAX82722;
XX
DT   10-NOV-2000  (first entry)
XX
DE   Human IgA nephropathy-associated cDNA primer #63.
XX
KW   IgA nephropathy-associated protein; diagnosis; treatment; antisense;
KW   human; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9963085-A1.
XX
PD   09-DEC-1999.
XX
PF   28-MAY-1999;   99WO-JP002855.
XX
PR   02-JUN-1998;   98JP-00152603.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Ishiwata T,  Sakurada M,  Kawabata A,  Nakagawa S,  Nishi T,  Kuga T;
PI   Sawada S,  Takei M,  Shibata K,  Furuya A;
XX
DR   WPI; 2000-097328/08.
XX
PT   DNA sequences preferentially expressed in IgA nephropathy patients,
PT   proteins encoded by them, and antibodies to those proteins.
XX
PS   Claim 3; Page 170; 180pp; Japanese.
XX
CC   This invention describes novel DNA sequences preferentially expressed in
CC   IgA nephropathy patients, and DNA sequences stringently hybridizing to
CC   them. Independent claims cover diagnostic reagents for IgA nephropathy
CC   incorporating the antisense sequences; the treatment of IgA nephropathy
CC   using the antisense sequences for mRNA inhibition; proteins associated
CC   with IgA nephropathy, containing sequences encoded by the DNA sequences;
CC   antibodies recognizing these proteins; the production of the proteins by
CC   culture of host cells transformed with DNA encoding them; diagnostic
CC   reagents for IgA nephropathy containing the antibodies; and compositions
CC   for the treatment of IgA nephropathy which contain the antibodies. The
CC   products of the invention can be used for the diagnosis and treatment of
CC   IgA nephropathy. This sequence represents a primer used in the isolation
CC   and identification of the human IgA nephropathy-associated proteins
CC   described in the method of the invention
XX
SQ   Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 2556
AAX82720
ID   AAX82720 standard; DNA; 17 BP.
XX
AC   AAX82720;
XX
DT   10-NOV-2000  (first entry)
XX
DE   Human IgA nephropathy-associated cDNA primer #61.
XX
KW   IgA nephropathy-associated protein; diagnosis; treatment; antisense;
KW   human; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9963085-A1.
XX
PD   09-DEC-1999.
XX
PF   28-MAY-1999;   99WO-JP002855.
XX
PR   02-JUN-1998;   98JP-00152603.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Ishiwata T,  Sakurada M,  Kawabata A,  Nakagawa S,  Nishi T,  Kuga T;
PI   Sawada S,  Takei M,  Shibata K,  Furuya A;
XX
DR   WPI; 2000-097328/08.
XX
PT   DNA sequences preferentially expressed in IgA nephropathy patients,
PT   proteins encoded by them, and antibodies to those proteins.
XX
PS   Claim 3; Page 169; 180pp; Japanese.
XX
CC   This invention describes novel DNA sequences preferentially expressed in
CC   IgA nephropathy patients, and DNA sequences stringently hybridizing to
```

CC them. Independent claims cover diagnostic reagents for IgA nephropathy
CC incorporating the antisense sequences; the treatment of IgA nephropathy
CC using the antisense sequences for mRNA inhibition; proteins associated
CC with IgA nephropathy, containing sequences encoded by the DNA sequences;
CC antibodies recognizing these proteins; the production of the proteins by
CC culture of host cells transformed with DNA encoding them; diagnostic
CC reagents for IgA nephropathy containing the antibodies; and compositions
CC for the treatment of IgA nephropathy which contain the antibodies. The
CC products of the invention can be used for the diagnosis and treatment of
CC IgA nephropathy. This sequence represents a primer used in the isolation
CC and identification of the human IgA nephropathy-associated proteins
CC described in the method of the invention
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2172 TTTTTTTTTTTTTTTA 2187
||||||||||||||||
Db 2 TTTTTTTTTTTTTTTA 17

RESULT 2557
AAZ36739
ID AAZ36739 standard; DNA; 17 BP.
XX
AC AAZ36739;
XX
DT 13-MAR-2000 (first entry)
XX
DE Anchored oligo(dT) primer AT15A used for modified differential display.
XX
KW Stimulus-regulated nucleic acid; sequence profile; nucleic acid level;
KW differentially expressed nucleic acid; disease state; cancer;
KW autoimmune disease; infectious disease; aging; developmental disorder;
KW proliferative disorder; neurological disorder; toxicity; primer;
KW treatment resistance; differential expression; drug discovery;
KW growth factor; epidermal growth factor; radiation; stress; pathogen; ss.
XX
OS Synthetic.
XX
PN WO9955913-A2.
XX
PD 04-NOV-1999.
XX
PF 27-APR-1999; 99WO-US009119.
XX
PR 27-APR-1998; 98US-0083331P.
PR 27-AUG-1998; 98US-0098070P.
PR 04-FEB-1999; 99US-0118624P.
XX
PA (KIMM-) KIMMEL CANCER CENT SIDNEY.
XX
PI Mcclelland M, Welsh J, Trenkle T;
XX
DR WPI; 2000-086388/07.
XX
PT Measuring expression of low abundance reduced complexity target nucleic
PT acid molecules.
XX
PS Example 3; Page 91; 187pp; English.
XX
CC AAZ36739-41 represent oligo(dT) primers used for modified differential
CC display, in the method of the invention. The specification describes a
CC method for measuring the level of two or more nucleic acid molecules in a
CC target. The method comprises contacting a probe with an arbitrarily or
CC statistically sampled target and detecting the amount of specific binding
CC of the target to the probe. The methods can be used to identify
CC differentially expressed nucleic acid molecules associated with disease
CC states, such as cancer, autoimmune disease, infectious disease, aging,
CC developmental disorder, proliferative disorder or neurological disorder.
CC Alternatively the methods can be used to assess the efficacy or toxicity
CC of or a resistance to a treatment. Also the methods can be used to
CC determine differential expression of nucleic acid molecules in response
CC to a stimulus, e.g. a chemical, drug or growth factor (especially
CC epidermal growth factor), radiation, stress or a pathogen. The methods
CC can also be used to determine co-regulated genes that can be potential
CC targets for drug discovery
XX
SQ Sequence 17 BP; 2 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2172 TTTTTTTTTTTTTTTA 2187
||||||||||||||||
Db 2 TTTTTTTTTTTTTTTA 17

RESULT 2558
AAA25449
ID AAA25449 standard; DNA; 17 BP.
XX
AC AAA25449;
XX
DT 19-JUL-2000 (first entry)
XX
DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1947.
XX
KW Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW gene expression modification; cancer; phosphorothioate; endonuclease;
KW anticancer; breast cancer; endometrium cancer; ss.
XX
OS Homo sapiens.
XX
PN WO9954459-A2.
XX
PD 28-OCT-1999.
XX
PF 19-APR-1999; 99WO-US008547.
XX
PR 20-APR-1998; 98US-0082404P.
PR 23-JUN-1998; 98US-00103636.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haeberli P;
PI Matulic-Adamic J;
XX
DR WPI; 2000-013248/01.
XX
PT New nucleic acids that interact, and optionally cleave, target sequences,
PT used to treat cancer.
XX
PS Claim 77; Page 79; 148pp; English.
XX
CC The present invention describes nucleic acids (A) that interact stably
CC with a target sequence and contain at least one phosphoro(di)thioate
CC link, having endonuclease activity. (A), and more generally any catalytic
CC nucleic acid (A') that modulates expression of the oestrogen receptor
CC gene, are used to treat cancer (particularly of breast or endometrium),
CC in vivo or by transforming cells ex vivo and implanting treated cells, or
CC for other conditions associated with levels of oestrogen receptor.
CC Because of the high selectivity for targeted RNA, (A) can also be used to
CC correlate inhibition of gene expression with alterations in phenotype,
CC particularly for identification of therapeutic targets, and as research
CC reagents (for RNA, in the same way that restriction endonucleases are
CC used with DNA). The combination of modifications in (A) improves
CC resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
CC AAA24748 to AAA25992 represent their corresponding target sequences.

```
CC   AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC   sequences, and AAA26107 to AAA26218 represent their corresponding target
CC   sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC   antisense oligonucleotides used in the exemplification of the present
CC   invention
XX
SQ   Sequence 17 BP; 0 A; 0 C; 1 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTT 17


RESULT 2559
AAA25449/c
ID   AAA25449 standard; DNA; 17 BP.
XX
AC   AAA25449;
XX
DT   19-JUL-2000  (first entry)
XX
DE   Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1947.
XX
KW   Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW   hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW   gene expression modification; cancer; phosphorothioate; endonuclease;
KW   anticancer; breast cancer; endometrium cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9954459-A2.
XX
PD   28-OCT-1999.
XX
PF   19-APR-1999;   99WO-US008547.
XX
PR   20-APR-1998;   98US-0082404P.
PR   23-JUN-1998;   98US-00103636.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Thompson JD,  Beigelman L,  Mcswiggen JA,  Karpeisky A,  Bellon L;
PI   Reynolds M,  Zwick M,  Jarvis T,  Woolf T,  Haeberli P;
PI   Matulic-Adamic J;
XX
DR   WPI; 2000-013248/01.
XX
PT   New nucleic acids that interact, and optionally cleave, target sequences,
PT   used to treat cancer.
XX
PS   Claim 77; Page 79; 148pp; English.
XX
CC   The present invention describes nucleic acids (A) that interact stably
CC   with a target sequence and contain at least one phosphoro(di)thioate
CC   link, having endonuclease activity. (A), and more generally any catalytic
CC   nucleic acid (A') that modulates expression of the oestrogen receptor
CC   gene, are used to treat cancer (particularly of breast or endometrium),
CC   in vivo or by transforming cells ex vivo and implanting treated cells, or
CC   for other conditions associated with levels of oestrogen receptor.
CC   Because of the high selectivity for targeted RNA, (A) can also be used to
CC   correlate inhibition of gene expression with alterations in phenotype,
CC   particularly for identification of therapeutic targets, and as research
CC   reagents (for RNA, in the same way that restriction endonucleases are
CC   used with DNA). The combination of modifications in (A) improves
CC   resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC   AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
CC   AAA24748 to AAA25992 represent their corresponding target sequences.
CC   AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC   sequences, and AAA26107 to AAA26218 represent their corresponding target
CC   sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC   antisense oligonucleotides used in the exemplification of the present
CC   invention
XX
SQ   Sequence 17 BP; 0 A; 0 C; 1 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         17 AAAAAAAAAAAAAAAA 2


RESULT 2560
AAA25451
ID   AAA25451 standard; DNA; 17 BP.
XX
AC   AAA25451;
XX
DT   19-JUL-2000  (first entry)
XX
DE   Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1949.
XX
KW   Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW   hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW   gene expression modification; cancer; phosphorothioate; endonuclease;
KW   anticancer; breast cancer; endometrium cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9954459-A2.
XX
PD   28-OCT-1999.
XX
PF   19-APR-1999;   99WO-US008547.
XX
PR   20-APR-1998;   98US-0082404P.
PR   23-JUN-1998;   98US-00103636.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Thompson JD,  Beigelman L,  Mcswiggen JA,  Karpeisky A,  Bellon L;
PI   Reynolds M,  Zwick M,  Jarvis T,  Woolf T,  Haeberli P;
PI   Matulic-Adamic J;
XX
DR   WPI; 2000-013248/01.
XX
PT   New nucleic acids that interact, and optionally cleave, target sequences,
PT   used to treat cancer.
XX
PS   Claim 77; Page 79; 148pp; English.
XX
CC   The present invention describes nucleic acids (A) that interact stably
CC   with a target sequence and contain at least one phosphoro(di)thioate
CC   link, having endonuclease activity. (A), and more generally any catalytic
CC   nucleic acid (A') that modulates expression of the oestrogen receptor
CC   gene, are used to treat cancer (particularly of breast or endometrium),
CC   in vivo or by transforming cells ex vivo and implanting treated cells, or
CC   for other conditions associated with levels of oestrogen receptor.
CC   Because of the high selectivity for targeted RNA, (A) can also be used to
CC   correlate inhibition of gene expression with alterations in phenotype,
CC   particularly for identification of therapeutic targets, and as research
CC   reagents (for RNA, in the same way that restriction endonucleases are
CC   used with DNA). The combination of modifications in (A) improves
CC   resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC   AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
CC   AAA24748 to AAA25992 represent their corresponding target sequences.
CC   AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC   sequences, and AAA26107 to AAA26218 represent their corresponding target
CC   sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC   antisense oligonucleotides used in the exemplification of the present
```

```
CC   invention
XX
SQ   Sequence 17 BP; 0 A; 0 C; 1 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 16


RESULT 2561
AAA25451/c
ID   AAA25451 standard; DNA; 17 BP.
XX
AC   AAA25451;
XX
DT   19-JUL-2000  (first entry)
XX
DE   Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1949.
XX
KW   Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW   hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW   gene expression modification; cancer; phosphorothioate; endonuclease;
KW   anticancer; breast cancer; endometrium cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9954459-A2.
XX
PD   28-OCT-1999.
XX
PF   19-APR-1999;   99WO-US008547.
XX
PR   20-APR-1998;   98US-0082404P.
PR   23-JUN-1998;   98US-00103636.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Thompson JD,  Beigelman L,  Mcswiggen JA,  Karpeisky A,  Bellon L;
PI   Reynolds M,  Zwick M,  Jarvis T,  Woolf T,  Haeberli P;
PI   Matulic-Adamic J;
XX
DR   WPI; 2000-013248/01.
XX
PT   New nucleic acids that interact, and optionally cleave, target sequences,
PT   used to treat cancer.
XX
PS   Claim 77; Page 79; 148pp; English.
XX
CC   The present invention describes nucleic acids (A) that interact stably
CC   with a target sequence and contain at least one phosphoro(di)thioate
CC   link, having endonuclease activity. (A), and more generally any catalytic
CC   nucleic acid (A') that modulates expression of the oestrogen receptor
CC   gene, are used to treat cancer (particularly of breast or endometrium),
CC   in vivo or by transforming cells ex vivo and implanting treated cells, or
CC   for other conditions associated with levels of oestrogen receptor.
CC   Because of the high selectivity for targeted RNA, (A) can also be used to
CC   correlate inhibition of gene expression with alterations in phenotype,
CC   particularly for identification of therapeutic targets, and as research
CC   reagents (for RNA, in the same way that restriction endonucleases are
CC   used with DNA). The combination of modifications in (A) improves
CC   resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC   AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
CC   AAA24748 to AAA25992 represent their corresponding target sequences.
CC   AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC   sequences, and AAA26107 to AAA26218 represent their corresponding target
CC   sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC   antisense oligonucleotides used in the exemplification of the present
CC   invention
XX
SQ   Sequence 17 BP; 0 A; 0 C; 1 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         16 AAAAAAAAAAAAAAAA 1


RESULT 2562
AAC64202
ID   AAC64202 standard; DNA; 17 BP.
XX
AC   AAC64202;
XX
DT   21-FEB-2001  (first entry)
XX
DE   PCR anchor primer, SEQ ID NO:3, used in human gene 373 isolation.
XX
KW   Human; pollinosis-associated gene 373; IgE; immunoglobulin E;
KW   cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW   drug screening; allergic disease; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO200065046-A1.
XX
PD   02-NOV-2000.
XX
PF   26-APR-2000; 2000WO-JP002730.
XX
PR   27-APR-1999;   99JP-00120489.
XX
PA   (GENO-) GENOX RES INC.
XX
PI   Nagasu T,  Sugita Y,  Kashiwabara T,  Oshida T,  Obayashi M,  Gunji S;
PI   Obayashi I,  Imai Y,  Yoshida N,  Ogawa K,  Matsui K;
XX
DR   WPI; 2000-687339/67.
XX
PT   Pollinosis-associated gene 373 undergoing significantly low expression in
PT   subjects with high cedar pollen-specific immunoglobulin-E levels, useful
PT   in diagnosis of allergic diseases and screening drug candidates.
XX
PS   Example 6; Page 69; 80pp; Japanese.
XX
CC   The invention relates to the human pollinosis-associated gene 373 which
CC   exhibits significantly reduced expression in the T-cells of individuals
CC   with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC   was isolated from T-cells from individuals allergic to cedar pollen using
CC   the differential display method. The invention also relates also relates
CC   to the protein encoded by pollinosis gene 373; expression constructs and
CC   host cells comprising pollinosis-associated gene 373 nucleic acids;
CC   pollinosis-associated gene 373 primers and probes; antibodies against the
CC   protein encoded by the gene; methods of detection of pollinosis-
CC   associated gene 373 nucleic acids; and a method of diagnosis of allergic
CC   diseases via the detection of pollinosis-associated gene 373 nucleic
CC   acids. The invention additionally encompasses methods of screening drug
CC   candidates for the treatment of allergic disease by measuring the
CC   expression of pollinosis-associated gene 373 in pollen antigen-stimulated
CC   T-cells in the presence of a test compound relative to a control.
CC   Pollinosis-associated gene 373 is useful in the diagnosis of allergic
CC   diseases and in the screening of drug candidates for the treatment of
CC   such diseases. The present sequence represents a PCR primer used in the
CC   isolation of human pollinosis-associated gene 373 cDNA
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy       2172 TTTTTTTTTTTTTTA 2187
              ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTA 17
```

RESULT 2563
AAC64203/c
ID AAC64203 standard; DNA; 17 BP.
XX
AC AAC64203;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:4, used in human gene 373 isolation.
XX
KW Human; pollinosis-associated gene 373; IgE; immunoglobulin E;
KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW drug screening; allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065046-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP002730.
XX
PR 27-APR-1999; 99JP-00120489.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
DR WPI; 2000-687339/67.
XX
PT Pollinosis-associated gene 373 undergoing significantly low expression in
PT subjects with high cedar pollen-specific immunoglobulin-E levels, useful
PT in diagnosis of allergic diseases and screening drug candidates.
XX
PS Example 6; Page 70; 80pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 373 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. The invention also relates also relates
CC to the protein encoded by pollinosis gene 373; expression constructs and
CC host cells comprising pollinosis-associated gene 373 nucleic acids;
CC pollinosis-associated gene 373 primers and probes; antibodies against the
CC protein encoded by the gene; methods of detection of pollinosis-
CC associated gene 373 nucleic acids; and a method of diagnosis of allergic
CC diseases via the detection of pollinosis-associated gene 373 nucleic
CC acids. The invention additionally encompasses methods of screening drug
CC candidates for the treatment of allergic disease by measuring the
CC expression of pollinosis-associated gene 373 in pollen antigen-stimulated
CC T-cells in the presence of a test compound relative to a control.
CC Pollinosis-associated gene 373 is useful in the diagnosis of allergic
CC diseases and in the screening of drug candidates for the treatment of
CC such diseases. The present sequence represents a PCR primer used in the
CC isolation of human pollinosis-associated gene 373 cDNA
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

```
  Query Match              0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         17 GAAAAAAAAAAAAAAA 2
```

RESULT 2564
AAC64181
ID AAC64181 standard; DNA; 17 BP.
XX
AC AAC64181;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:2, used in human gene 419 isolation.
XX
KW Human; pollinosis-associated gene 419; FAF-1 homologue;
KW Fas-associated factor-1; IgE; immunoglobulin E; cedar pollen allergy;
KW T-cell; reduced expression; detection; diagnosis; drug screening;
KW allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065045-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP002729.
XX
PR 27-APR-1999; 99JP-00120490.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
DR WPI; 2000-687338/67.
XX
PT Pollinosis-associated gene 419 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
PS Example 6; Page 49; 77pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 419 which
CC exhibits reduced expression in the T-cells of individuals with high cedar
CC pollen-specific IgE (immunoglobulin E) levels. The gene was isolated from
CC T-cells from individuals allergic to cedar pollen using the differential
CC display method. Pollinosis-associated gene 419 has homology with the gene
CC encoding human Fas-associated factor-1 (FAF-1). The invention also
CC relates to the protein encoded by pollinosis gene 419; expression
CC constructs and host cells comprising pollinosis- associated gene 419
CC nucleic acids; pollinosis-associated gene 419 primers and probes;
CC antibodies against the protein encoded by the gene; methods of detection
CC of pollinosis-associated gene 419 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-
CC associated gene 419 nucleic acids. The invention additionally encompasses
CC methods of screening drug candidates for the treatment of allergic
CC disease by measuring the expression of pollinosis-associated gene 419 in
CC pollen antigen-stimulated T-cells in the presence of a test compound
CC relative to a control.Pollinosis-associated gene 419 is useful in the
CC diagnosis of allergic diseases and in the screening of drug candidates
CC for the treatment of such diseases. The present sequence represents a PCR
CC primer used in the isolation of human pollinosis-associated gene 419 cDNA
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

```
  Query Match              0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTA 2187
              ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTA 17
```

RESULT 2565
AAC64182/c

ID AAC64182 standard; DNA; 17 BP.
XX
AC AAC64182;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:3, used in human gene 419 isolation.
XX
KW Human; pollinosis-associated gene 419; FAF-1 homologue;
KW Fas-associated factor-1; IgE; immunoglobulin E; cedar pollen allergy;
KW T-cell; reduced expression; detection; diagnosis; drug screening;
KW allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065045-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP002729.
XX
PR 27-APR-1999; 99JP-00120490.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
DR WPI; 2000-687338/67.
XX
PT Pollinosis-associated gene 419 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
PS Example 6; Page 49; 77pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 419 which
CC exhibits reduced expression in the T-cells of individuals with high cedar
CC pollen-specific IgE (immunoglobulin E) levels. The gene was isolated from
CC T-cells from individuals allergic to cedar pollen using the differential
CC display method. Pollinosis-associated gene 419 has homology with the gene
CC encoding human Fas-associated factor-1 (FAF-1). The invention also
CC relates to the protein encoded by pollinosis gene 419; expression
CC constructs and host cells comprising pollinosis- associated gene 419
CC nucleic acids; pollinosis-associated gene 419 primers and probes;
CC antibodies against the protein encoded by the gene; methods of detection
CC of pollinosis-associated gene 419 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-
CC associated gene 419 nucleic acids. The invention additionally encompasses
CC methods of screening drug candidates for the treatment of allergic
CC disease by measuring the expression of pollinosis-associated gene 419 in
CC pollen antigen-stimulated T-cells in the presence of a test compound
CC relative to a control.Pollinosis-associated gene 419 is useful in the
CC diagnosis of allergic diseases and in the screening of drug candidates
CC for the treatment of such diseases. The present sequence represents a PCR
CC primer used in the isolation of human pollinosis-associated gene 419 cDNA
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAAAAAA 2800
||||||||||||||||
Db 17 GAAAAAAAAAAAAAAA 2

RESULT 2566
AAC64171
ID AAC64171 standard; DNA; 17 BP.
XX
AC AAC64171;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:2, used in human gene 513 isolation.
XX
KW Human; pollinosis-associated gene 513; IgE; immunoglobulin E;
KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW drug screening; allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065049-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP002733.
XX
PR 27-APR-1999; 99JP-00120491.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
DR WPI; 2000-687342/67.
XX
PT Pollinosis-associated gene 513 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
PS Example 6; Page 38; 46pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 513 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. The invention also relates to methods of
CC detection of pollinosis-associated gene 513 nucleic acids; a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 513 nucleic acids; and methods of screening drug candidates for the
CC treatment of allergic disease by measuring the expression of pollinosis-
CC associated gene 513 in pollen antigen-stimulated T-cells in the presence
CC of a test compound relative to a control. Pollinosis-associated gene 513
CC is useful in the diagnosis of allergic diseases and in the screening of
CC drug candidates for the treatment of such diseases. The present sequence
CC represents a PCR primer used in the isolation of human pollinosis-
CC associated gene 513 cDNA
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2172 TTTTTTTTTTTTTTTA 2187
||||||||||||||||
Db 2 TTTTTTTTTTTTTTTA 17

RESULT 2567
AAC64172/c
ID AAC64172 standard; DNA; 17 BP.
XX
AC AAC64172;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:3, used in human gene 513 isolation.
XX
KW Human; pollinosis-associated gene 513; IgE; immunoglobulin E;
KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW drug screening; allergic disease; PCR primer; ss.
XX

```
OS   Synthetic.
XX
PN   WO200065049-A1.
XX
PD   02-NOV-2000.
XX
PF   26-APR-2000; 2000WO-JP002733.
XX
PR   27-APR-1999;   99JP-00120491.
XX
PA   (GENO-) GENOX RES INC.
XX
PI   Nagasu T,  Sugita Y,  Kashiwabara T,  Oshida T,  Obayashi M,  Gunji S;
PI   Obayashi I,  Imai Y,  Yoshida N,  Ogawa K,  Matsui K;
XX
DR   WPI; 2000-687342/67.
XX
PT   Pollinosis-associated gene 513 undergoing significantly low expression in
PT   subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT   of allergic diseases and screening drug candidates.
XX
PS   Example 6; Page 38; 46pp; Japanese.
XX
CC   The invention relates to the human pollinosis-associated gene 513 which
CC   exhibits significantly reduced expression in the T-cells of individuals
CC   with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC   was isolated from T-cells from individuals allergic to cedar pollen using
CC   the differential display method. The invention also relates to methods of
CC   detection of pollinosis-associated gene 513 nucleic acids; a method of
CC   diagnosis of allergic diseases via the detection of pollinosis-associated
CC   gene 513 nucleic acids; and methods of screening drug candidates for the
CC   treatment of allergic disease by measuring the expression of pollinosis-
CC   associated gene 513 in pollen antigen-stimulated T-cells in the presence
CC   of a test compound relative to a control. Pollinosis-associated gene 513
CC   is useful in the diagnosis of allergic diseases and in the screening of
CC   drug candidates for the treatment of such diseases. The present sequence
CC   represents a PCR primer used in the isolation of human pollinosis-
CC   associated gene 513 cDNA
XX
SQ   Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         17 GAAAAAAAAAAAAAAA 2

RESULT 2568
AAC64161
ID   AAC64161 standard; DNA; 17 BP.
XX
AC   AAC64161;
XX
DT   21-FEB-2001  (first entry)
XX
DE   PCR anchor primer, SEQ ID NO:2, used in human gene 581 isolation.
XX
KW   Human; pollinosis-associated gene 581; IgE; immunoglobulin E;
KW   cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW   drug screening; allergic disease; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO200065048-A1.
XX
PD   02-NOV-2000.
XX
PF   26-APR-2000; 2000WO-JP002732.
XX
PR   27-APR-1999;   99JP-00120492.
XX
PA   (GENO-) GENOX RES INC.
XX
PI   Nagasu T,  Sugita Y,  Kashiwabara T,  Oshida T,  Obayashi M,  Gunji S;
PI   Obayashi I,  Imai Y,  Yoshida N,  Ogawa K,  Matsui K;
XX
DR   WPI; 2000-687341/67.
XX
PT   Pollenosis-associated gene 581 undergoing significantly low expression in
PT   subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT   of allergic diseases and screening drug candidates.
XX
PS   Example 6; Page 39; 69pp; Japanese.
XX
CC   The invention relates to the human pollinosis-associated gene 581 which
CC   exhibits significantly reduced expression in the T-cells of individuals
CC   with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC   was isolated from T-cells from individuals allergic to cedar pollen using
CC   the differential display method. The invention also relates also relates
CC   to the protein encoded by pollinosis-associated gene 581; to expression
CC   constructs and host cells comprising pollinosis-associated gene 581
CC   nucleic acids; pollinosis-associated gene 581 primers and probes;
CC   antibodies against the protein encoded by the gene; methods of detection
CC   of pollinosis-associated gene 581 nucleic acids; and a method of
CC   diagnosis of allergic diseases via the detection of pollinosis-associated
CC   gene 581 nucleic acids. The invention additionally encompasses methods of
CC   screening drug candidates for the treatment of allergic disease by
CC   measuring the expression of pollinosis-associated gene 581 in pollen
CC   antigen-stimulated T-cells in the presence of a test compound relative to
CC   a control.Pollinosis-associated gene 581 is useful in the diagnosis of
CC   allergic diseases and in the screening of drug candidates for the
CC   treatment of such diseases. The present sequence represents a PCR primer
CC   used in the isolation of human pollinosis-associated gene 581 cDNA
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTA 2187
              ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTA 17

RESULT 2569
AAC64162/c
ID   AAC64162 standard; DNA; 17 BP.
XX
AC   AAC64162;
XX
DT   21-FEB-2001  (first entry)
XX
DE   PCR anchor primer, SEQ ID NO:3, used in human gene 581 isolation.
XX
KW   Human; pollinosis-associated gene 581; IgE; immunoglobulin E;
KW   cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW   drug screening; allergic disease; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO200065048-A1.
XX
PD   02-NOV-2000.
XX
PF   26-APR-2000; 2000WO-JP002732.
XX
PR   27-APR-1999;   99JP-00120492.
XX
PA   (GENO-) GENOX RES INC.
XX
PI   Nagasu T,  Sugita Y,  Kashiwabara T,  Oshida T,  Obayashi M,  Gunji S;
PI   Obayashi I,  Imai Y,  Yoshida N,  Ogawa K,  Matsui K;
```

```
XX
DR   WPI; 2000-687341/67.
XX
PT   Pollenosis-associated gene 581 undergoing significantly low expression in
PT   subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT   of allergic diseases and screening drug candidates.
XX
PS   Example 6; Page 40; 69pp; Japanese.
XX
CC   The invention relates to the human pollinosis-associated gene 581 which
CC   exhibits significantly reduced expression in the T-cells of individuals
CC   with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC   was isolated from T-cells from individuals allergic to cedar pollen using
CC   the differential display method. The invention also relates also relates
CC   to the protein encoded by pollinosis-associated gene 581; to expression
CC   constructs and host cells comprising pollinosis-associated gene 581
CC   nucleic acids; pollinosis-associated gene 581 primers and probes;
CC   antibodies against the protein encoded by the gene; methods of detection
CC   of pollinosis-associated gene 581 nucleic acids; and a method of
CC   diagnosis of allergic diseases via the detection of pollinosis-associated
CC   gene 581 nucleic acids. The invention additionally encompasses methods of
CC   screening drug candidates for the treatment of allergic disease by
CC   measuring the expression of pollinosis-associated gene 581 in pollen
CC   antigen-stimulated T-cells in the presence of a test compound relative to
CC   a control.Pollinosis-associated gene 581 is useful in the diagnosis of
CC   allergic diseases and in the screening of drug candidates for the
CC   treatment of such diseases. The present sequence represents a PCR primer
CC   used in the isolation of human pollinosis-associated gene 581 cDNA
XX
SQ   Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 2570
AAC64213
ID   AAC64213 standard; DNA; 17 BP.
XX
AC   AAC64213;
XX
DT   21-FEB-2001  (first entry)
XX
DE   PCR anchor primer, SEQ ID NO:2, used in human gene 627 isolation.
XX
KW   Human; pollinosis-associated gene 627; IgE; immunoglobulin E;
KW   cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW   drug screening; allergic disease; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO200065051-A1.
XX
PD   02-NOV-2000.
XX
PF   26-APR-2000; 2000WO-JP002735.
XX
PR   27-APR-1999;   99JP-00120493.
XX
PA   (GENO-) GENOX RES INC.
XX
PI   Nagasu T,  Sugita Y,  Kashiwabara T,  Oshida T,  Obayashi M,  Gunji S;
PI   Obayashi I,  Imai Y,  Yoshida N,  Ogawa K,  Matsui K;
XX
DR   WPI; 2000-687344/67.
XX
PT   Pollinosis-associated gene 627 undergoing significantly low expression in
PT   subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT   of allergic diseases and screening drug candidates.
XX
PS   Example 6; Page 41; 51pp; Japanese.
XX
CC   The invention relates to the human pollinosis-associated gene 627 which
CC   exhibits significantly reduced expression in the T-cells of individuals
CC   with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC   was isolated from T-cells from individuals allergic to cedar pollen using
CC   the differential display method. The invention also relates to methods of
CC   detection of pollinosis-associated gene 627 nucleic acids; a method of
CC   diagnosis of allergic diseases via the detection of pollinosis-associated
CC   gene 627 nucleic acids; and a method of screening drug candidates for the
CC   treatment of allergic disease by measuring the expression of pollinosis-
CC   associated gene 627 in pollen antigen-stimulated T-cells in the presence
CC   of a test compound relative to a control. Pollinosis-associated gene 627
CC   is useful in the diagnosis of allergic diseases and in the screening of
CC   drug candidates for the treatment of such diseases. The present sequence
CC   represents a PCR primer used in the isolation of human pollinosis-
CC   associated gene 627 cDNA
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTA 2187
              ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTA 17


RESULT 2571
AAC64214/c
ID   AAC64214 standard; DNA; 17 BP.
XX
AC   AAC64214;
XX
DT   21-FEB-2001  (first entry)
XX
DE   PCR anchor primer, SEQ ID NO:3, used in human gene 627 isolation.
XX
KW   Human; pollinosis-associated gene 627; IgE; immunoglobulin E;
KW   cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW   drug screening; allergic disease; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO200065051-A1.
XX
PD   02-NOV-2000.
XX
PF   26-APR-2000; 2000WO-JP002735.
XX
PR   27-APR-1999;   99JP-00120493.
XX
PA   (GENO-) GENOX RES INC.
XX
PI   Nagasu T,  Sugita Y,  Kashiwabara T,  Oshida T,  Obayashi M,  Gunji S;
PI   Obayashi I,  Imai Y,  Yoshida N,  Ogawa K,  Matsui K;
XX
DR   WPI; 2000-687344/67.
XX
PT   Pollinosis-associated gene 627 undergoing significantly low expression in
PT   subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT   of allergic diseases and screening drug candidates.
XX
PS   Example 6; Page 42; 51pp; Japanese.
XX
CC   The invention relates to the human pollinosis-associated gene 627 which
CC   exhibits significantly reduced expression in the T-cells of individuals
CC   with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC   was isolated from T-cells from individuals allergic to cedar pollen using
CC   the differential display method. The invention also relates to methods of
```

CC detection of pollinosis-associated gene 627 nucleic acids; a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 627 nucleic acids; and a method of screening drug candidates for the
CC treatment of allergic disease by measuring the expression of pollinosis-
CC associated gene 627 in pollen antigen-stimulated T-cells in the presence
CC of a test compound relative to a control. Pollinosis-associated gene 627
CC is useful in the diagnosis of allergic diseases and in the screening of
CC drug candidates for the treatment of such diseases. The present sequence
CC represents a PCR primer used in the isolation of human pollinosis-
CC associated gene 627 cDNA
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAAAAAA 2800
||||||||||||||||
Db 17 GAAAAAAAAAAAAAAA 2

RESULT 2572
AAC64231/c
ID AAC64231 standard; DNA; 17 BP.
XX
AC AAC64231;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:3, used in human gene 795 isolation.
XX
KW Human; pollinosis-associated gene 795; vimentin homologue; IgE;
KW immunoglobulin E; cedar pollen allergy; T-cell; reduced expression;
KW detection; diagnosis; drug screening; allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065050-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP002734.
XX
PR 27-APR-1999; 99JP-00120494.
XX
PA (GENO-) GENOX RES INC.
PA (EISA) EISAI CO LTD.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
PI Yokoi A;
XX
DR WPI; 2000-687343/67.
XX
PT Pollinosis-associated gene 795 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
PS Page 45; Example 6; 73pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 795 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. Pollinosis-associated gene 795 has
CC homology with the human vimentin gene. The invention also relates also
CC relates to the protein encoded by pollinosis gene 795; to expression
CC constructs and host cells comprising pollinosis-associated gene 795
CC nucleic acids; pollinosis-associated gene 795 primers and probes;
CC antibodies against the protein encoded by the gene; methods of detection
CC of pollinosis-associated gene 795 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 795 nucleic acids. The invention additionally encompasses methods of
CC screening drug candidates for the treatment of allergic disease by
CC measuring the expression of pollinosis-associated gene 795 in pollen
CC antigen-stimulated T-cells in the presence of a test compound relative to
CC a control. Pollinosis-associated gene 795 is useful in the diagnosis of
CC allergic diseases and in the screening of drug candidates for the
CC treatment of such diseases. The present sequence represents a PCR primer
CC used in the isolation of human pollinosis-associated gene 795 cDNA
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAAAAAA 2800
||||||||||||||||
Db 17 GAAAAAAAAAAAAAAA 2

RESULT 2573
AAC64230
ID AAC64230 standard; DNA; 17 BP.
XX
AC AAC64230;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:2, used in human gene 795 isolation.
XX
KW Human; pollinosis-associated gene 795; vimentin homologue; IgE;
KW immunoglobulin E; cedar pollen allergy; T-cell; reduced expression;
KW detection; diagnosis; drug screening; allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065050-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP002734.
XX
PR 27-APR-1999; 99JP-00120494.
XX
PA (GENO-) GENOX RES INC.
PA (EISA) EISAI CO LTD.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
PI Yokoi A;
XX
DR WPI; 2000-687343/67.
XX
PT Pollinosis-associated gene 795 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
PS Page 45; Example 6; 73pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 795 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. Pollinosis-associated gene 795 has
CC homology with the human vimentin gene. The invention also relates also
CC relates to the protein encoded by pollinosis gene 795; to expression
CC constructs and host cells comprising pollinosis-associated gene 795
CC nucleic acids; pollinosis-associated gene 795 primers and probes;
CC antibodies against the protein encoded by the gene; methods of detection
CC of pollinosis-associated gene 795 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 795 nucleic acids. The invention additionally encompasses methods of
CC screening drug candidates for the treatment of allergic disease by

```
CC   measuring the expression of pollinosis-associated gene 795 in pollen
CC   antigen-stimulated T-cells in the presence of a test compound relative to
CC   a control. Pollinosis-associated gene 795 is useful in the diagnosis of
CC   allergic diseases and in the screening of drug candidates for the
CC   treatment of such diseases. The present sequence represents a PCR primer
CC   used in the isolation of human pollinosis-associated gene 795 cDNA
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTA 2187
              ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTA 17


RESULT 2574
AAC92292
ID   AAC92292 standard; DNA; 17 BP.
XX
AC   AAC92292;
XX
DT   22-MAR-2001  (first entry)
XX
DE   Human pollinosis-associated gene 465 related PCR primer SEQ ID NO:2.
XX
KW   Human; pollinosis-associated gene 465; pollen scattering; allergy;
KW   allergic disease; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200073439-A1.
XX
PD   07-DEC-2000.
XX
PF   18-MAY-2000; 2000WO-JP003191.
XX
PR   27-MAY-1999;   99JP-00148784.
XX
PA   (GENO-) GENOX RES INC.
PA   (EISA ) EISAI CO LTD.
XX
PI   Nagasu T,  Sugita Y,  Kashiwabara T,  Oshida T,  Obayashi M,  Gunji S;
PI   Obayashi I,  Imai Y,  Yoshida N,  Ogawa K,  Matsui K,  Takahashi E;
PI   Yokoi A;
XX
DR   WPI; 2001-061528/07.
XX
PT   Pollinosis-associated gene 465 undergoing significantly low expression in
PT   subjects after pollen scattering, useful in diagnosis of allergic
PT   diseases and screening candidate compounds to regulate response of T
PT   cells to antigen stimulus.
XX
PS   Example 6; Page 43; 61pp; Japanese.
XX
CC   The present invention describes the human pollinosis-associated gene 465
CC   which has a nucleic acid sequence of 3442 base pairs (bp), given in
CC   (AAC92291), that undergoes significantly low expression in subjects after
CC   pollen scattering, and is useful in the diagnosis of allergic diseases
CC   and screening candidate compounds for remedies capable of regulating the
CC   response of T cells to the stimulus by an antigen. The gene is useful in
CC   the diagnosis of allergic diseases and screening candidate compounds for
CC   remedies capable of regulating the response of T cells to the stimulus by
CC   an antigen. The present sequence represents a PCR primer which is used in
CC   an example from the present invention
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTA 2187
              ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTA 17


RESULT 2575
AAC92293/c
ID   AAC92293 standard; DNA; 17 BP.
XX
AC   AAC92293;
XX
DT   22-MAR-2001  (first entry)
XX
DE   Human pollinosis-associated gene 465 related PCR primer SEQ ID NO:3.
XX
KW   Human; pollinosis-associated gene 465; pollen scattering; allergy;
KW   allergic disease; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200073439-A1.
XX
PD   07-DEC-2000.
XX
PF   18-MAY-2000; 2000WO-JP003191.
XX
PR   27-MAY-1999;   99JP-00148784.
XX
PA   (GENO-) GENOX RES INC.
PA   (EISA ) EISAI CO LTD.
XX
PI   Nagasu T,  Sugita Y,  Kashiwabara T,  Oshida T,  Obayashi M,  Gunji S;
PI   Obayashi I,  Imai Y,  Yoshida N,  Ogawa K,  Matsui K,  Takahashi E;
PI   Yokoi A;
XX
DR   WPI; 2001-061528/07.
XX
PT   Pollinosis-associated gene 465 undergoing significantly low expression in
PT   subjects after pollen scattering, useful in diagnosis of allergic
PT   diseases and screening candidate compounds to regulate response of T
PT   cells to antigen stimulus.
XX
PS   Example 6; Page 44; 61pp; Japanese.
XX
CC   The present invention describes the human pollinosis-associated gene 465
CC   which has a nucleic acid sequence of 3442 base pairs (bp), given in
CC   (AAC92291), that undergoes significantly low expression in subjects after
CC   pollen scattering, and is useful in the diagnosis of allergic diseases
CC   and screening candidate compounds for remedies capable of regulating the
CC   response of T cells to the stimulus by an antigen. The gene is useful in
CC   the diagnosis of allergic diseases and screening candidate compounds for
CC   remedies capable of regulating the response of T cells to the stimulus by
CC   an antigen. The present sequence represents a PCR primer which is used in
CC   an example from the present invention
XX
SQ   Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 2576
AAS06655
ID   AAS06655 standard; DNA; 17 BP.
XX
AC   AAS06655;
XX
```

DT 12-SEP-2001 (first entry)
XX
DE Human cDNA synthesis and differential display primer, HT11GG.
XX
KW Human; Estrogen response element; ERE; DDRT-PCR; ss; PCR primer;
KW differential display of reverse transcribed mRNAs by PCR;
KW testicular cancer; breast cancer; prostate cancer; endometrial cancer;
KW asthma; hypospadia; cryptorchism; allergy; hormone replacement therapy;
KW HRT; endocrine system; HT11GG.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200134834-A2.
XX
PD 17-MAY-2001.
XX
PF 10-NOV-2000; 2000WO-DK000628.
XX
PR 11-NOV-1999; 99DK-00001626.
XX
PA (RIGS-) RIGSHOSPITALET.
XX
PI Leffers H, Jorgensen M, Skakkebaek NE;
XX
DR WPI; 2001-335941/35.
XX
PT Evaluating a cellular response to an environmental compound, for use in
PT toxicological analysis, involves determining or comparing the expression
PT levels of at least one endogenous gene.
XX
PS Example 3; Page 27; 77pp; English.
XX
CC The sequence represents a downstream PCR primer used in a DDRT-PCR
CC experiment (and in cDNA synthesis), demonstrating the method of the
CC invention. The method relates to evaluating a cellular response to an
CC environmental compound, comprising determining or comparing the
CC expression levels of at least one endogenous gene e.g by differential
CC display of reverse transcribed mRNAs by PCR (DDRT-PCR). The method can be
CC adapted to identify compounds that act on the level of endogenous gene
CC expression through activating nuclear receptors. The method is useful in
CC toxicological analysis, diagnostics, for diagnosing cancer (e.g.
CC testicular, breast, prostate and endometrium), asthma, hypospadia,
CC cryptorchism and/or allergy, and for evaluating the efficiency of a
CC treatment for hormonal deficiency or hormonal replacement therapy, in a
CC human such as a post-menopausal female. The method is also useful for
CC identifying environmental chemicals or pharmaceutical compositions that
CC interact with endocrine systems, and for detecting chemicals that pose a
CC health threat. Expression levels of endogenous genes are determined
CC rapidly using a sensitive technique, and the expression of any gene can
CC be monitored. The assays are far more informative than the currently used
CC assays, and significantly reduces the number of animals required for the
CC testing, as it is expected that essentially all the animals in a test
CC group will respond to the compound
XX
SQ Sequence 17 BP; 2 A; 1 C; 3 G; 11 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1767 AAGCTTTTTTTTTTG 1782
||||||||||||||||
Db 1 AAGCTTTTTTTTTTG 16

RESULT 2577
AAC91720/c
ID AAC91720 standard; DNA; 17 BP.
XX
AC AAC91720;
XX
DT 27-MAR-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:3, used in human gene 787 isolation.
XX
KW Human; pollinosis-associated gene 787; pollen allergy; T-cell;
KW reduced expression; detection; diagnosis; drug screening;
KW allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200073440-A1.
XX
PD 07-DEC-2000.
XX
PF 18-MAY-2000; 2000WO-JP003192.
XX
PR 27-MAY-1999; 99JP-00148785.
XX
PA (GENO-) GENOX RES INC.
PA (EISA) EISAI CO LTD.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
PI Yokoi A;
XX
DR WPI; 2001-032159/04.
XX
PT Pollinosis-associated gene 787 undergoing significantly low expression in
PT subjects after pollen scattering, useful in diagnosis of allergic
PT diseases and screening candidate compounds to regulate response of T
PT cells to antigen stimulus.
XX
PS Example 6; Page 40; 54pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 787 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC after the pollen-scattering season, relative to expression levels in T-
CC cells before the pollen-scattering season. The gene was isolated from T-
CC cells from individuals allergic to pollen using the differential display
CC method. The invention also relates to pollinosis-associated gene 787
CC primers and probes; methods of detection of pollinosis-associated gene
CC 787 nucleic acids; and a method of diagnosis of allergic diseases via the
CC detection of pollinosis-associated gene 787 nucleic acids. The invention
CC additionally encompasses a method of screening drug candidates for the
CC treatment of allergic disease by measuring the expression of pollinosis-
CC associated gene 787 in pollen antigen-stimulated T-cells in the presence
CC of a test compound relative to a control. Pollinosis- associated gene 787
CC is useful in the diagnosis of allergic diseases and in the screening of
CC drug candidates for the treatment of such diseases. The present sequence
CC represents a PCR primer used in the isolation of human pollinosis-
CC associated gene 787 cDNA
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAAAAAA 2800
||||||||||||||||
Db 17 GAAAAAAAAAAAAAAA 2

RESULT 2578
AAC91719
ID AAC91719 standard; DNA; 17 BP.
XX
AC AAC91719;
XX
DT 27-MAR-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:2, used in human gene 787 isolation.
XX
KW Human; pollinosis-associated gene 787; pollen allergy; T-cell;

KW reduced expression; detection; diagnosis; drug screening;
KW allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200073440-A1.
XX
PD 07-DEC-2000.
XX
PF 18-MAY-2000; 2000WO-JP003192.
XX
PR 27-MAY-1999; 99JP-00148785.
XX
PA (GENO-) GENOX RES INC.
PA (EISA) EISAI CO LTD.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
PI Yokoi A;
XX
DR WPI; 2001-032159/04.
XX
PT Pollinosis-associated gene 787 undergoing significantly low expression in
PT subjects after pollen scattering, useful in diagnosis of allergic
PT diseases and screening candidate compounds to regulate response of T
PT cells to antigen stimulus.
XX
PS Example 6; Page 40; 54pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 787 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC after the pollen-scattering season, relative to expression levels in T-
CC cells before the pollen-scattering season. The gene was isolated from T-
CC cells from individuals allergic to pollen using the differential display
CC method. The invention also relates to pollinosis-associated gene 787
CC primers and probes; methods of detection of pollinosis-associated gene
CC 787 nucleic acids; and a method of diagnosis of allergic diseases via the
CC detection of pollinosis-associated gene 787 nucleic acids. The invention
CC additionally encompasses a method of screening drug candidates for the
CC treatment of allergic disease by measuring the expression of pollinosis-
CC associated gene 787 in pollen antigen-stimulated T-cells in the presence
CC of a test compound relative to a control. Pollinosis- associated gene 787
CC is useful in the diagnosis of allergic diseases and in the screening of
CC drug candidates for the treatment of such diseases. The present sequence
CC represents a PCR primer used in the isolation of human pollinosis-
CC associated gene 787 cDNA
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2172 TTTTTTTTTTTTTTTA 2187
||||||||||||||||
Db 2 TTTTTTTTTTTTTTTA 17

RESULT 2579
AAC82875/c
ID AAC82875 standard; DNA; 17 BP.
XX
AC AAC82875;
XX
DT 20-MAR-2001 (first entry)
XX
DE Human pollinosis-associated gene 441 primer #2.
XX
KW Pollinosis; pollinosis-associated gene 441; allergy; T cell;
KW pollen scattering; antigen; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200073435-A1.
XX
PD 07-DEC-2000.
XX
PF 18-MAY-2000; 2000WO-JP003190.
XX
PR 27-MAY-1999; 99JP-00148783.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
DR WPI; 2001-061526/07.
XX
PT Pollinosis-associated gene 441 which undergoes lower expression in
PT subjects after pollen scattering, useful in diagnosis of allergic
PT diseases and screening candidate compounds to regulate response of T
PT cells to antigen stimulus.
XX
PS Example 6; Page 35; 42pp; Japanese.
XX
CC This invention describes a novel nucleic acid molecule comprising a
CC sequence (I) which undergoes significantly low expression in subjects
CC after pollen scattering, and is useful in diagnosis of allergic diseases
CC and screening candidate compounds for remedies capable of regulating the
CC response of T cells to the stimulus by an antigen
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAAAAAA 2800
||||||||||||||||
Db 17 GAAAAAAAAAAAAAAA 2

RESULT 2580
AAC82874
ID AAC82874 standard; DNA; 17 BP.
XX
AC AAC82874;
XX
DT 20-MAR-2001 (first entry)
XX
DE Human pollinosis-associated gene 441 primer #1.
XX
KW Pollinosis; pollinosis-associated gene 441; allergy; T cell;
KW pollen scattering; antigen; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200073435-A1.
XX
PD 07-DEC-2000.
XX
PF 18-MAY-2000; 2000WO-JP003190.
XX
PR 27-MAY-1999; 99JP-00148783.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
DR WPI; 2001-061526/07.
XX
PT Pollinosis-associated gene 441 which undergoes lower expression in
PT subjects after pollen scattering, useful in diagnosis of allergic
PT diseases and screening candidate compounds to regulate response of T
PT cells to antigen stimulus.

```
XX
PS   Example 6; Page 35; 42pp; Japanese.
XX
CC   This invention describes a novel nucleic acid molecule comprising a
CC   sequence (I) which undergoes significantly low expression in subjects
CC   after pollen scattering, and is useful in diagnosis of allergic diseases
CC   and screening candidate compounds for remedies capable of regulating the
CC   response of T cells to the stimulus by an antigen
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTA 2187
              ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTA 17


RESULT 2581
AAH47127/c
ID   AAH47127 standard; DNA; 17 BP.
XX
AC   AAH47127;
XX
DT   30-NOV-2001  (first entry)
XX
DE   Nucleotide sequence of primer GT15C.
XX
KW   B1001; B1466; B1072; B1151; T-cell; allergy; atopic dermatitis; human;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200165259-A1.
XX
PD   07-SEP-2001.
XX
PF   23-FEB-2001; 2001WO-JP001372.
XX
PR   02-MAR-2000; 2000JP-00061832.
XX
PA   (GENO-) GENOX RES INC.
PA   (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
PI   Nagasu T,  Oshida T,  Obayashi I,  Matsui K,  Saito H;
XX
DR   WPI; 2001-557789/62.
XX
PT   Diagnosis of allergies including atopic dermatitis.
XX
PS   Example 6; Page 66; 83pp; Japanese.
XX
CC   The invention provides a method of diagnosis of allergies that involves:
CC   assaying the levels of expression of genes B1001, B1466, B1072 or B1151
CC   in T-cells; and comparing them with the level of expression in healthy T-
CC   cells. The method is useful for diagnosing allergies, particularly atopic
CC   dermatitis. The present sequence represents a PCR primer used for
CC   analysis of the expression of the above genes
XX
SQ   Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 2582
```

```
AAH47126
ID   AAH47126 standard; DNA; 17 BP.
XX
AC   AAH47126;
XX
DT   30-NOV-2001  (first entry)
XX
DE   Nucleotide sequence of primer GT15A.
XX
KW   B1001; B1466; B1072; B1151; T-cell; allergy; atopic dermatitis; human;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200165259-A1.
XX
PD   07-SEP-2001.
XX
PF   23-FEB-2001; 2001WO-JP001372.
XX
PR   02-MAR-2000; 2000JP-00061832.
XX
PA   (GENO-) GENOX RES INC.
PA   (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
PI   Nagasu T,  Oshida T,  Obayashi I,  Matsui K,  Saito H;
XX
DR   WPI; 2001-557789/62.
XX
PT   Diagnosis of allergies including atopic dermatitis.
XX
PS   Example 6; Page 65; 83pp; Japanese.
XX
CC   The invention provides a method of diagnosis of allergies that involves:
CC   assaying the levels of expression of genes B1001, B1466, B1072 or B1151
CC   in T-cells; and comparing them with the level of expression in healthy T-
CC   cells. The method is useful for diagnosing allergies, particularly atopic
CC   dermatitis. The present sequence represents a PCR primer used for
CC   analysis of the expression of the above genes
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTA 2187
              ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTA 17


RESULT 2583
ABK49634
ID   ABK49634 standard; DNA; 17 BP.
XX
AC   ABK49634;
XX
DT   15-JUL-2002  (first entry)
XX
DE   Human Acetyltransferase-like protein 20-90-05 PCR primer GT15A.
XX
KW   Human; ss; PCR; acetyltransferase; 20-90-05; allergic disease; primer;
KW   differential display; eosinophil; antiallergic; atopic dermatitis; GT15A.
XX
OS   Homo sapiens.
XX
PN   WO200224903-A1.
XX
PD   28-MAR-2002.
XX
PF   21-SEP-2001; 2001WO-JP008246.
XX
PR   25-SEP-2000; 2000JP-00291318.
```

XX
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
PA (EISA) EISAI CO LTD.
XX
PI Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Tsujimoto G;
PI Takahashi E;
XX
DR WPI; 2002-315738/35.
XX
PT Examining allergic diseases by differential display of gene showing
PT different expression particularly increased expression in remission stage
PT in eosinophils of patients, also applicable in screening candidate
PT compounds for remedies.
XX
PS Example 1; Page 56; 72pp; Japanese.
XX
CC The invention relates to a method for examining allergic diseases
CC comprises determining the expression level of a gene containing, the
CC human cDNA appearing as ABK49633 which has homology with
CC acetyltransferases in the eosinophils of a patient and comparing the
CC expression level with that in the eosinophils of a healthy individual
CC (i.e. differential display). Also included are methods of screening for
CC candidate compounds which affect the expression level of the gene or the
CC activity of the protein encoded by the gene (including related proteins
CC and mutants), the use of probes based on the gene sequence in the
CC examination of allergic diseases, the use of reporter constructs in the
CC screening of candidate compounds, a vector containing a the transcription
CC -controlling region of the gene, cells transformed with the vector, an
CC antibody against the protein and a model animal for allergic diseases
CC which is a transgenic non-human vertebrate with lowering of expression
CC intensity of the gene in eosinophils. The method is examining allergic
CC diseases particularly atopic dermatitis which is also applicable in
CC screening candidate compounds for remedies. Such method can be performed
CC in high throughput, at low cost. The present sequence is a differential
CC display PCR primer for the cDNA encoding the human acetyltransferase-like
CC protein 20-90-05
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2172 TTTTTTTTTTTTTTTA 2187
||||||||||||||||
Db 2 TTTTTTTTTTTTTTTA 17

RESULT 2584
ABK49635/c
ID ABK49635 standard; DNA; 17 BP.
XX
AC ABK49635;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human Acetyltransferase-like protein 20-90-05 PCR primer GT15C.
XX
KW Human; ss; PCR; acetyltransferase; 20-90-05; allergic disease; primer;
KW differential display; eosinophil; antiallergic; atopic dermatitis; GT15C.
XX
OS Homo sapiens.
XX
PN WO200224903-A1.
XX
PD 28-MAR-2002.
XX
PF 21-SEP-2001; 2001WO-JP008246.
XX
PR 25-SEP-2000; 2000JP-00291318.
XX
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
PA (EISA) EISAI CO LTD.
XX
PI Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Tsujimoto G;
PI Takahashi E;
XX
DR WPI; 2002-315738/35.
XX
PT Examining allergic diseases by differential display of gene showing
PT different expression particularly increased expression in remission stage
PT in eosinophils of patients, also applicable in screening candidate
PT compounds for remedies.
XX
PS Example 1; Page 56; 72pp; Japanese.
XX
CC The invention relates to a method for examining allergic diseases
CC comprises determining the expression level of a gene containing, the
CC human cDNA appearing as ABK49633 which has homology with
CC acetyltransferases in the eosinophils of a patient and comparing the
CC expression level with that in the eosinophils of a healthy individual
CC (i.e. differential display). Also included are methods of screening for
CC candidate compounds which affect the expression level of the gene or the
CC activity of the protein encoded by the gene (including related proteins
CC and mutants), the use of probes based on the gene sequence in the
CC examination of allergic diseases, the use of reporter constructs in the
CC screening of candidate compounds, a vector containing a the transcription
CC -controlling region of the gene, cells transformed with the vector, an
CC antibody against the protein and a model animal for allergic diseases
CC which is a transgenic non-human vertebrate with lowering of expression
CC intensity of the gene in eosinophils. The method is examining allergic
CC diseases particularly atopic dermatitis which is also applicable in
CC screening candidate compounds for remedies. Such method can be performed
CC in high throughput, at low cost. The present sequence is a differential
CC display PCR primer for the cDNA encoding the human acetyltransferase-like
CC protein 20-90-05
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAAAAAA 2800
||||||||||||||||
Db 17 GAAAAAAAAAAAAAAA 2

RESULT 2585
ABL59038
ID ABL59038 standard; DNA; 17 BP.
XX
AC ABL59038;
XX
DT 20-AUG-2002 (first entry)
XX
DE Nucleotide sequence of PCR primer GT15A.
XX
KW Human; allergosis; eosinophil; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN JP2002095500-A.
XX
PD 02-APR-2002.
XX
PF 25-SEP-2000; 2000JP-00291316.
XX
PR 25-SEP-2000; 2000JP-00291316.
XX
PA (GENO-) GENOX SOYAKU KENKYUSHO KK.
PA (KOKU-) KOKURITSU SHONI BYOIN INCHO.
XX
DR WPI; 2002-439993/47.

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XX
PT   Examining allergosis, involves measuring the expression levels of a
PT   specific gene, and comparing it to the levels in the eosinophils of a
PT   healthy control.
XX
PS   Example 1; Page 17; 20pp; Japanese.
XX
CC   The specification describes a method for examining allergosis. The method
CC   comprises measuring the expression level of the gene given in ABL59037,
CC   and comparing it with the expression level of the gene in the eosinophils
CC   of a healthy person. The method is used for the examination of
CC   allergosis. The present sequence represents a PCR primer, which is used
CC   in the course of the invention
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTA 2187
              ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTA 17


RESULT 2586
ABL59039/c
ID   ABL59039 standard; DNA; 17 BP.
XX
AC   ABL59039;
XX
DT   20-AUG-2002  (first entry)
XX
DE   Nucleotide sequence of PCR primer GT15C.
XX
KW   Human; allergosis; eosinophil; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2002095500-A.
XX
PD   02-APR-2002.
XX
PF   25-SEP-2000; 2000JP-00291316.
XX
PR   25-SEP-2000; 2000JP-00291316.
XX
PA   (GENO-) GENOX SOYAKU KENKYUSHO KK.
PA   (KOKU-) KOKURITSU SHONI BYOIN INCHO.
XX
DR   WPI; 2002-439993/47.
XX
PT   Examining allergosis, involves measuring the expression levels of a
PT   specific gene, and comparing it to the levels in the eosinophils of a
PT   healthy control.
XX
PS   Example 1; Page 17; 20pp; Japanese.
XX
CC   The specification describes a method for examining allergosis. The method
CC   comprises measuring the expression level of the gene given in ABL59037,
CC   and comparing it with the expression level of the gene in the eosinophils
CC   of a healthy person. The method is used for the examination of
CC   allergosis. The present sequence represents a PCR primer, which is used
CC   in the course of the invention
XX
SQ   Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db          17 GAAAAAAAAAAAAAAA 2


RESULT 2587
ABN99829
ID   ABN99829 standard; DNA; 17 BP.
XX
AC   ABN99829;
XX
DT   15-AUG-2002  (first entry)
XX
DE   Human allergic disease related PCR primer SEQ ID NO: 18.
XX
KW   Human; allergy; atopic dermatitis; eosinophil; anti-allergic; PCR;
KW   primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200233069-A1.
XX
PD   25-APR-2002.
XX
PF   28-SEP-2001; 2001WO-JP008574.
XX
PR   13-OCT-2000; 2000JP-00314093.
XX
PA   (GENO-) GENOX RES INC.
PA   (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
PI   Sugita Y,  Hashida R,  Ogawa K,  Obayashi M,  Nagasu T,  Saito H;
XX
DR   WPI; 2002-372311/40.
XX
PT   Method for examining allergic diseases by differential display of
PT   seventeen genes showing different expression particularly significant
PT   increase in eosinophils in patients with mild atopic dermatitis, also
PT   applicable in screening compounds.
XX
PS   Example 1; Page 109; 165pp; Japanese.
XX
CC   The present invention relates to a method for examining allergic diseases
CC   which involves determining the expression level of a gene, having one of
CC   the 17 nucleotide sequences shown in ABN99812-ABN99828, in the
CC   eosinophils in a patient and comparing the expression level with that in
CC   the eosinophils of a healthy individual. The method can be used to
CC   examine allergic diseases, particularly atopic dermatitis, and its early
CC   diagnosis, which is also applicable in screening candidate compounds for
CC   remedies. The present sequence is a PCR primer described in the
CC   exemplification of the invention
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTA 2187
              ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTA 17


RESULT 2588
ABN99830/c
ID   ABN99830 standard; DNA; 17 BP.
XX
AC   ABN99830;
XX
DT   15-AUG-2002  (first entry)
XX
DE   Human allergic disease related PCR primer SEQ ID NO: 19.
XX
KW   Human; allergy; atopic dermatitis; eosinophil; anti-allergic; PCR;
KW   primer; ss.
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